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(54) Title: NOVEL COMPOUNDS (57) Abstract <p>This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.</p>		

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NOVEL COMPOUNDS

Field of the Invention:

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the
5 production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy. Preferred embodiments of the invention include Streptococcal polypeptides and polynucleotides, particularly those of *Streptococcus pneumoniae*.

Background of the Invention:

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including otitis media, pneumonia and meningitis. Since its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that
15 DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain.

While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement
20 factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established, provides
25 critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognized targets.

Brief Description of the Invention:

This invention provides novel proteins, particularly those from *Streptococcus pneumoniae*, strain 0100993, characterised in that it comprises the amino acid sequences
30 given herein or fragments, analogues or derivatives thereof.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

In particular the invention provides polynucleotides having the DNA sequences given herein.

The invention also relates to novel oligonucleotides derived from the sequences given herein which can act as PCR primers in the process herein described to determine whether or not the *Streptococcus pneumoniae* gene identified herein in whole or in part is expressed in infected tissue. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. The proteins so identified are also useful as targets in screens designed to identify antimicrobial compounds.

It is an object of the invention to provide polypeptides that have been identified as novel polypeptides by homology between the amino acid sequence set out in the Sequence Listing and a known amino acid sequence or sequences of other proteins such as the proteins identified under the heading Identity in Table 1.

It is a further object of the invention to provide polynucleotides that encode polypeptides set forth in the Sequence Listing, particularly polynucleotides that encode the polypeptide set forth in the Sequence Listing.

In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding polypeptides comprising the sequence set out in the Sequence Listing, or a variant thereof.

In another particularly preferred embodiment of the invention there is a novel protein from comprising an amino acid sequence of the Sequence Listing, or a variant thereof.

In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants the polynucleotides set forth in the Sequence Listing and polypeptides encoded thereby.

In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing expression of the sequences the Sequence Listing, treating disease, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and

administering a polypeptide or polynucleotide of the invention to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to polynucleotide sequences of the invention, particularly under stringent conditions.

In certain preferred embodiments of the invention there are provided antibodies against polypeptides of the invention.

In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided agonists and antagonists of the polynucleotide and/or polypeptides of the invention, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a polynucleotide or a polypeptide of the invention for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

Detailed Description of the Invention:

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) with appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding preferably the amino terminal regions of the encoded protein or the Shine-Delgarno region can be used to construct antisense sequences

to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by
5 restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this
10 invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine
15 candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or
20 essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

1) Signature Tagged Mutagenesis (STM)

25 This technique is described by Hensel *et al.*, Science 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

The basis of the technique is the random mutagenesis of target organism by various
30 means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridisation analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

In Streptococcus pneumoniae, because the transposon system is less well developed, a more efficient way of creating the tagged mutants is to use the insertion-duplication mutagenesis technique as described by Morrison et al., J. Bacteriol. 159:870 (1984) the contents of which is incorporated by reference for background purposes.

5 **2) In Vivo Expression Technology (IVET)**

This technique is described by Camilli et al., Proc. Nat'l. Acad. Sci. USA. 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes. IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are
10 implied to have a significant role in infection establishment/maintenance.

In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is introduced into the target organism which carries an antibiotic resistance gene flanked by resolvase sites. Growth in the presence of the antibiotic removes from the population those
15 fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool is introduced into a host and at various times after infection bacteria may be recovered and assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally
20 upregulated during infection. Sequencing upstream of the recombinase gene allows identification of the up regulated gene.

3) Differential display

This technique is described by Chuang et al., J. Bacteriol. 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method
25 identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

4) **Generation of conditional lethal mutants by transposon mutagenesis.**

This technique, described by de Lorenzo, V. *et al.*, Gene 123:17-24 (1993); Neuwald, A. F. *et al.*, Gene 125: 69-73(1993); and Takiff, H. E. *et al.*, J. Bacteriol. 174:1544-1553(1992), the contents of which is incorporated by reference for

5 background purposes, identifies genes whose expression are essential for cell viability.

In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which
10 separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the
15 absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid, peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.

20 5) **Generation of conditional lethal mutants by chemical mutagenesis.**

This technique is described by Beckwith, L. Methods in Enzymology 204: 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at temperature other than physiological temperature (permissive temperature) and subsequent
25 replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene
30 allows matching with unknown ORF.

6) RT-PCR

Streptococcus pneumoniae messenger RNA is isolated from bacterial infected tissue e.g. 48 hour murine lung infections, and the amount of each mRNA species assessed by reverse transcription of the RNA sample primed with random hexanucleotides followed by PCR

with gene specific primer pairs. The determination of the presence and amount of a particular mRNA species by quantification of the resultant PCR product provides information on the bacterial genes which are transcribed in the infected tissue. Analysis of gene transcription can be carried out at different times of infection to gain a detailed knowledge of gene regulation in bacterial pathogenesis allowing for a clearer understanding of which gene products represent targets for screens for novel antibacterials. Because of the gene specific nature of the PCR primers employed it should be understood that the bacterial mRNA preparation need not be free of mammalian RNA. This allows the investigator to carry out a simple and quick RNA preparation from infected tissue to obtain bacterial mRNA species which are very short lived in the bacterium (in the order of 2 minute half-lives). Optimally the bacterial mRNA is prepared from infected murine lung tissue by mechanical disruption in the presence of TRIzol (GIBCO-BRL) for very short periods of time, subsequent processing according to the manufacturers of TRIzol reagent and DNAase treatment to remove contaminating DNA. Preferably the process is optimised by finding those conditions which give a maximum amount of *S.pneumoniae* 16S ribosomal RNA as detected by probing Northern blots with a suitably labelled sequence specific oligonucleotide probe. Typically a 5' dye labelled primer is used in each PCR primer pair in a PCR reaction which is terminated optimally between 8 and 25 cycles. The PCR products are separated on 6% polyacrylamide gels with detection and quantification using GeneScanner (manufactured by ABI).

Each of these techniques may have advantages or disadvantages depending on the particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind. For example, some genes might be recognised as essential for infection but in reality are only necessary for the initiation of infection and so their products would represent relatively unattractive targets for antibacterials developed to cure established and chronic infections.

Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

Streptococcus pneumoniae, strain 0100993 has been deposited at the National Collection of Industrial and Marine Bacteria Ltd. (NCIMB), Aberdeen, Scotland under NCIMB number 40794 on 11 April 1996, and a *Streptococcus pneumoniae*, strain 0100993 DNA library in *E. coli* was similarly deposited on 17 April 1996 under NCIMB number 40800.

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *Streptococcus pneumoniae*, strain 0100993 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given herein typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae*, strain 0100993 in *E. coli* or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a 17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using high stringency washes. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook, J. in MOLECULAR CLONING, A Laboratory Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70).

A polynucleotide of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide may be identical to the coding sequence shown or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encoding the same polypeptide.

The present invention includes variants of the hereinabove described polynucleotides which encode fragments, analogues and derivatives of the polypeptide characterized by the deduced amino acid sequence given herein. The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide. In addition to the standard A, G, C, T/U representations for nucleic acid bases, the term "N" is also used. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA

sequence, except that N cannot be a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

Thus, the present invention includes polynucleotides encoding the same
5 polypeptide characterized by the deduced amino acid sequence given herein as well as variants of such polynucleotides which variants encode for a fragment, derivative or analogue of the polypeptide. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

The polynucleotide may have a coding sequence which is a naturally occurring
10 allelic variant of the coding sequence characterized by the DNA sequence disclosed herein. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The polynucleotide which encodes for the mature polypeptide, may include only
15 the coding sequence for the mature polypeptide or the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a
polynucleotide which includes only coding sequence for the polypeptide as well as a
20 polynucleotide which includes additional coding and/or non-coding sequence.

The present invention therefore includes polynucleotides, wherein the coding
sequence for the mature polypeptide may be fused in the same reading frame to a
polynucleotide sequence which aids in expression and secretion of a polypeptide from a
host cell, for example, a leader sequence which functions as a secretory sequence for
25 controlling transport of a polypeptide from the cell. The polypeptide having a leader
sequence is a preprotein and may have the leader sequence cleaved by the host cell to form
the mature form of the polypeptide. The polynucleotides may also encode for a proprotein
which is the mature protein plus additional 5' amino acid residues. A mature protein having
a prosequence is a proprotein and may be an inactive form of the protein. Once the
30 prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may code for a
mature protein, or for a protein having a prosequence or for a protein having both a
prosequence and a presequence (leader sequence). Further, the amino acid sequences
provided herein show a methionine residue at the NH₂-terminus. It is appreciated, however,

that during post-translational modification of the peptide, this residue may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of each protein disclosed herein.

The polynucleotides of the present invention may also have the coding sequence
5 fused in frame to a marker sequence at either the 5' or 3' terminus of the gene which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by the pQE series of vectors (supplied commercially by Quiagen Inc.) to provide for purification of the polypeptide fused to the marker in the case of a bacterial host.

10 The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably at least 70% identity between the sequences. The present invention particularly relates to polynucleotides, particularly Streptococcal polynucleotides, which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions"
15 means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterised by the deduced amino acid sequence given herein. An example of stringent hybridization
20 conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*,
25 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence selected from the group consisting of the
30 polynucleotides of the Sequence Listing under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in said polynucleotide of the Sequence Listing or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

"Identity," as known in the art and used herein, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match

5 between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds.,

10 Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity

15 are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990)). The BLAST X program is publicly available from NCBI and other sources (*BLAST*

20 *Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990)).

As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence selected from the group consisting of the polynucleotide of the Sequence Listing is intended that the nucleotide

25 sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another

30 nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among

nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of selected from the group consisting of the amino acids of the Sequence Listing is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

The deposit referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The terms "fragment," "derivative" and "analogue" when referring to the polypeptide characterized by the deduced amino acid sequence herein, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analogue includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analogue of the polypeptide characterized by the deduced amino acid sequence herein may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogues are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

In accordance with yet a further aspect of the present invention, there is therefore provided a process for producing the polypeptide of the invention by recombinant techniques by expressing a polynucleotide encoding said polypeptide in a host and recovering the expressed product. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a cosmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the

genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

Suitable expression vectors include chromosomal, nonchromosomal and synthetic
5 DNA sequences, e.g., bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction
10 endonuclease site(s) by procedures known in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli* *lac* or *trp*, the phage lambda P_L promoter and other promoters known to control expression
15 of genes in eukaryotic or prokaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as
20 dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control" elements), so that the DNA sequence encoding the desired protein is transcribed into RNA
25 in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. The polypeptides of the present invention can be expressed using, for example, the *E. coli* *tac* promoter or the protein A gene (*spa*) promoter and signal sequence. Leader sequences can be removed by the bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739;
30 4,425,437; 4,338,397. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are PKK232-8 and PCM7. Particular named bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, lambda P_R , P_L and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and

mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding sequence). Modification of the coding sequences may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this
5 embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pET-3 vectors (Stratagene), pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks,
10 pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pBlueBacIII (Invitrogen), pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

15 Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage λ (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5
20 (*Saccharomyces*), a baculovirus insect cell system, YCp19 (*Saccharomyces*). See, generally, "DNA Cloning": Vols. I & II, Glover *et al.* ed. IRL Press Oxford (1985) (1987) and; T. Maniatis *et al.* ("Molecular Cloning" Cold Spring Harbor Laboratory (1982).

In some cases, it may be desirable to add sequences which cause the secretion of the polypeptide from the host organism, with subsequent cleavage of the secretory signal.

25 Polypeptides can be expressed in host cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrock, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold
30 Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Depending on the expression system and host selected, the polypeptide of the present invention may be produced by growing host cells transformed by an expression vector described above under conditions whereby the polypeptide of interest is expressed. The polypeptide is then isolated from the host cells and purified. If the expression system secretes the polypeptide into growth media, the polypeptide can be purified directly from the media. If the polypeptide is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. Where the polypeptide is localized to the cell surface, whole cells or isolated membranes can be used as an assayable source of the desired gene product. Polypeptide expressed in bacterial hosts such as *E. coli* may require isolation from inclusion bodies and refolding. Where the mature protein has a very hydrophobic region which leads to an insoluble product of overexpression, it may be desirable to express a truncated protein in which the hydrophobic region has been deleted. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

The polypeptide can be recovered and purified from recombinant cell cultures by methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "double-stranded DNA molecule" refers to the polymeric form of deoxyribonucleotides (bases adenine, guanine, thymine, or cytosine) in a double-stranded helix, both relaxed and supercoiled. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having the sequence homologous to the mRNA).

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

A control sequence "directs the expression" of a coding sequence in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

10 A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature.

15 This invention is also related to the use of the polynucleotides of the invention for use as diagnostic reagents. Detection of a polynucleotide or polypeptide of the invention in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with an organism comprising a polynucleotide of the invention may be detected at the nucleic acid level by a variety of techniques.

20 Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled polynucleotide sequences of the invention. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, *e.g.*, Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be

revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

5 Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to used RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding a polypeptide of the invention can be used to identify and analyze mutations. These primers may be used for, among other things, amplifying DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

15 The invention further provides a process for diagnosing, disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having a sequence set forth in the Sequence Listing or a sequence of the invention. Increased or decreased expression of a polynucleotide of the invention can be measured using any one of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

20 In addition, a diagnostic assay in accordance with the invention for detecting over-expression of a polypeptide of the invention compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a polypeptide of the invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

25 In accordance with yet a further aspect of the present invention, there is provided the use of a polypeptide of the invention for therapeutic or prophylactic purposes, for example, as an antibacterial agent or a vaccine.

30 In accordance with another aspect of the present invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunisation.

In accordance with yet another aspect of the present invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents. In particular, there are provided antibodies against such polypeptides.

Polypeptides of the invention may also be used to assess the binding of small molecule
5 substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The invention also provides a method of screening compounds to identify those which
10 enhance (agonist) or block (antagonist) the action of polypeptides or polynucleotides of the invention, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising a polypeptide of the invention and a
15 labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be an agonist or antagonist of a polypeptide of the invention. The ability of the candidate molecule to agonize or antagonize a polypeptide of the invention is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of a polypeptide of
20 the invention are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in polynucleotide or
25 polypeptide activity, and binding assays known in the art.

Another example of an assay for antagonists of a polypeptide of the invention is a competitive assay that combines such polypeptide and a potential antagonist with polypeptide-binding molecules, recombinant polypeptide-binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay.
30 Polypeptides of the invention can be labeled, such as by radioactivity or a colorimetric compound, such that the number of such polypeptide molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, without inducing an activities of a polypeptide of the invention, thereby preventing the action of such polypeptide by excluding it from binding.

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of the polypeptides of the invention.

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage and; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural

empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

Another aspect of the invention is a pharmaceutical composition comprising the above polypeptide, polynucleotide or inhibitor of the invention and a pharmaceutically acceptable carrier.

In a particular aspect the invention provides the use of an inhibitor of the invention as an antibacterial agent.

The invention further relates to the manufacture of a medicament for such uses.

The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which have anti-bacterial action. This invention also contemplates the use of the DNA encoding the antigen as a component in a DNA vaccine as discussed more fully below.

The polypeptides or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The term antibodies also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

Polypeptide derivatives include antigenically or immunologically equivalent derivatives which form a particular aspect of this invention.

The term 'antigenically equivalent derivative' as used herein encompasses a polypeptide or its equivalent which will be specifically recognised by certain antibodies which, when raised to the protein or polypeptide according to the present invention, interfere with the interaction between pathogen and mammalian host.

The term 'immunologically equivalent derivative' as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a

vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

In particular derivatives which are slightly longer or slightly shorter than the native protein or polypeptide fragment of the present invention may be used. In addition,
5 polypeptides in which one or more of the amino acid residues are modified may be used. Such peptides may, for example, be prepared by substitution, addition, or rearrangement of amino acids or by chemical modification thereof. All such substitutions and modifications are generally well known to those skilled in the art of peptide chemistry.

The polypeptide, such as an antigenically or immunologically equivalent derivative
10 or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or
15 polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497(1975)), the trioma technique, the
20 human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72(1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide
25 products of this invention.

Using the procedure of Kohler and Milstein (*supra*, (1975)), antibody-containing cells from the immunised mammal are fused with myeloma cells to create hybridoma cells secreting monoclonal antibodies.

The hybridomas are screened to select a cell line with high binding affinity and
30 favorable cross reaction with other Streptococcal species using one or more of the original polypeptide and/or the fusion protein. The selected cell line is cultured to obtain the desired Mab.

Hybridoma cell lines secreting the monoclonal antibody are another aspect of this invention.

Alternatively phage display technology could be utilised to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Fbp or from naive libraries (McCafferty, J. *et al.*, Nature 348:552-554(1990), and Marks, J. *et al.*, Biotechnology 10:779-783(1992)). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. *et al.*, Nature 352:624-628(1991)).

The antibody should be screened again for high affinity to the polypeptide and/or fusion protein.

As mentioned above, a fragment of the final antibody may be prepared.

The antibody may be either intact antibody of M_r approx 150,000 or a derivative of it, for example a Fab fragment or a Fv fragment as described in Skerra, A and Pluckthun, A., Science 240:1038-1040 (1988). If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

The antibody of the invention may be prepared by conventional means for example by established monoclonal antibody technology (Kohler, G. and Milstein, C. (*supra*, (1975) or using recombinant means e.g. combinatorial libraries, for example as described in Huse, W.D. *et al.*, Science 246:1275-1281 (1989).

Preferably the antibody is prepared by expression of a DNA polymer encoding said antibody in an appropriate expression system such as described above for the expression of polypeptides of the invention. The choice of vector for the expression system will be determined in part by the host, which may be a prokaryotic cell, such as *E. coli* (preferably strain B) or *Streptomyces sp.* or a eukaryotic cell, such as a mouse C127, mouse myeloma, human HeLa, Chinese hamster ovary, filamentous or unicellular fungi or insect cell. The host may also be a transgenic animal or a transgenic plant (for example, as described in Hiatt, A. *et al.*, Nature 340:76-78(1989). Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses, derived from, for example, baculoviruses and vaccinia.

The Fab fragment may also be prepared from its parent monoclonal antibody by enzyme treatment, for example using papain to cleave the Fab portion from the Fc portion.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the patient. For example, if the patient is human the antibody may most preferably be 'humanised'; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. *et al.*, Nature 321:522-525 (1986), or Tempest *et al.*, Biotechnology 9:266-273 (1991).

The modification need not be restricted to one of 'humanisation' ; other primate sequences (for example Newman, R. *et al.*, Biotechnology 10:1455-1460 (1992)) may also be used.

5 The humanised monoclonal antibody, or its fragment having binding activity, form a particular aspect of this invention.

This invention provides a method of screening drugs to identify those which interfere with the proteins selected as targets herein, which method comprises measuring the interference of the activity of the protein by a test drug. For example if the protein selected has a catalytic activity, after suitable purification and formulation the activity of the enzyme
10 can be followed by its ability to convert its natural substrates. By incorporating different chemically synthesised test compounds or natural products into such an assay of enzymatic activity one is able to detect those additives which compete with the natural substrate or otherwise inhibit enzymatic activity.

The invention also relates to inhibitors identified thereby.

15 The use of a polynucleotide of the invention in genetic immunisation will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, Hum. Mol. Genet. 1:363 (1992); Manthorpe *et al.*, Hum. Gene Ther. 4:419 (1993)), delivery of DNA complexed with specific protein carriers (Wu *et al.*, J. Biol. Chem. 264:16985 (1989)), coprecipitation of DNA with calcium phosphate
20 (Benvenisty & Reshef, Proc. Nat'l Acad. Sci. USA, 83:9551 (1986)), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, Science 243:375 (1989)), particle bombardment (Tang *et al.*, Nature 356:152 (1992)); Eisenbraun *et al.*, DNA Cell Biol. 12:791 (1993)) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, Proc. Nat'l Acad. Sci. USA 81:5849 (1984)). Suitable promoters for muscle transfection include
25 CMV, RSV, SRa, actin, MCK, alpha globin, adenovirus and dihydrofolate reductase.

In therapy or as a prophylactic, the active agent i.e., the polypeptide, polynucleotide or inhibitor of the invention, may be administered to a patient as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application
30 for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol

or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

For administration to human patients, it is expected that the daily dosage level of the active agent will be from 0.01 to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual patient and will vary with the age, weight and response of the particular patient. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response.

A suitable unit dose for vaccination is 0.5-5 μ g/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

Within the indicated dosage range, no adverse toxicological effects are expected with the compounds of the invention which would preclude their administration to suitable patients.

The individual full length sequences given herein are summarized in the following Tables (Table 1 and Table 2). Under the column in Table 1 labeled "Identity" there is the deduced identity of each open reading frame of the invention determined using Blastp and/or MPSearch. The ORF# column indicates whether the polynucleotide encoding each ORF encodes more than one ORF. For example, SEQ ID NO: 263 has an ORF# 1 but no #2; thus the polynucleotide encodes this ORF#1, but no other ORF was detected. On the other hand, SEQ ID NO:286 and 287 have ORF#s 1 and 2 respectively, indicating that they were both encoded by the same polynucleotide. This can also be seen in Table 2 where the polynucleotide of SEQ ID NO: 24 encodes the ORFs of SEQ ID NOS: 286 and 287. Table 1 also shows in the position ("POSITION" columns) the start ("START" column) and stop ("STOP" column) codons for each ORF and their positions in the encoding polynucleotide sequence. The SEQ ID NOS of the polypeptides of this table are linked to both a deduced identity in this table and a polynucleotide sequence in Table 2 which encodes each polypeptide. The "Direction" column in Table 1 shows the direction of the ORF encoding each polypeptide in this table. "Forward" denotes the sense orientation and "Reverse" denotes the antisense orientation of the ORF. Table 1 also provides an "Assembly ID" which is a unique numerical descriptor for each polynucleotide sequence of the invention.

TABLE 1

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
263.	probable transposase (insertion sequence IS861) - Streptococcus agalactiae (strain COH-1)	3112224	1	ATG	TAA	258	746	Forward
264.	Unknown	3112506	1	~CAT	CTA~	414	554	Reverse
265.	SUCCINYLDIAMINOPIMELATE DESUCCINYLA SE (EC 3.5.1.18) (SDAP). - ESCHERICHIA COLI .	3112574	1	~CAT	TTA~	607	990	Reverse
266.	Unknown	3112646	1	ATG	TGA	353	460	Forward
267.	D-alanine permease (dagA) homolog - Haemophilus influenzae (strain Rd KW20)	3112686	1	ATG	TAA	393	1235	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
268.	Unknown	3112810	1	-CAT	TTA~	328	468	Reverse
269.	Unknown	3112934	1	ATG	TAG	107	739	Forward
270.	3-OXOACYL- [ACYL- CARRIER PROTEIN] REDUCTASE PRECURSOR (EC 1.1.1.100) (3-KETOACYL- ACYL CARRIER PROTEIN REDUCTASE). - CUPHEA LANCEOLATA	3112956	1	ATG	TGA	586	1146	Forward
271.	HIGH- AFFINITY BRANCHED- CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN LIVG (LIV -I PROTEIN-G). - SALMONELLA TYPHIMURIU M.	3112994	1	ATG	TAA	307	648	Forward
272.	Unknown	3113026	1	ATG	TGA	235	483	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
273.	Unknown	3113098	1	-CAT	TTA~	28	360	Reverse
274.	CELL DIVISION PROTEIN FTSH. - BACILLUS SUBTILIS.	3113274	1	ATG	TGA	125	700	Forward
275.	Unknown	3113306	1	-CAT	CTA~	255	509	Reverse
276.	PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE II BC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII -FRU). - XANTHOMONAS CAMPESTRIS (PV. CAMPESTRIS).	3113406	1	-CAT	TCA~	237	725	Reverse
277.	Unknown	3113432	1	-CAT	CTA~	17	310	Reverse
278.	Unknown	3113436	1	CTG	TAA	1	441	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
279.	HOLLIDAY JUNCTION DNA HELICASE RUVB. - ESCHERICHIA COLI.	3113510	1	ATG	TGA	187	411	Forward
280.	Unknown	3113514	1	ATG	TGA	361	495	Forward
281.	Unknown	3113546	1	TTG	TAA	2	241	Forward
282.	CELL DIVISION PROTEIN FTSA. - BACILLUS SUBTILIS.	3113610	1	TTG	TGA	3	665	Forward
283.	Unknown	3113692	1	ATG	TAG	304	594	Forward
284.	GALACTOSE- 6-PHOSPHATE ISOMERASE LACB SUBUNIT (EC 5.-.-.-). - LACTOCOCCU S LACTIS (SUBSP. LACTIS) (STREPTOCOC CUS LACTIS).	3113696	1	ATG	TGA	176	661	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
285.	3- ISOPROPYLM ALATE DEHYDROGE NASE (EC 1.1.1.85) (BETA-IPM DEHYDROGE NASE) (IMDH). - LACTOCOCCU S LACTIS (SUBSP. LACTIS) (STREPTOCOC CUS LACTIS).	3113762	1	~CAG	TTA~	275	508	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
286.	PHOSPHO-2- DEHYDRO-3- DEOXYHEPTO NATE ALDOLASE (EC 4.1.2.15) (PHOSPHO- 2- KETO-3-DE OXYHEPTON ATE ALDOLASE) (DAH P SYNTHETASE) (3-DEOXY- D- ARABINO- HEPTULOSON ATE 7- PHOSPHATE SYNTHASE). - CORYNEBACT ERIUM GLUTAMICU M.	3113794	1	ATG	TAG	40	219	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
287.	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, PHE-SENSITIVE (EC 4.1.2.15) (PHOSP HO-2-KETO-3-DEOXYHEPTONATE ALDOLASE) (DAHPSYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE). - ESCHERICHIA COLI.	3113794	2	ATG	TGA	283	453	Forward
288.	PYRUVATE KINASE (EC 2.7.1.40). - LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).	3113802	1	ATG	TGA	69	260	Forward
289.	Unknown	3113990	1	-CAT	TTA~	6	164	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
290.	ADAPTIVE- RESPONSE SENSORY- KINASE SASA (EC 2.7.-.-). - SYNECHOCOC CUS SP. (STRAIN PCC 7942) (ANACYSTIS NIDULANS R2).	3114082	1	ATG	TAG	22	189	Forward
291.	FOLYLPOLYG LUTAMATE SYNTHASE (EC 6.3.2.17) (FOLYLPOLY- GAMMA- GLUTAMATE SYNTHETASE) (FPGS). - LACTOBACIL LUS CASEI.	3114096	1	CTG	TGA	1	243	Forward
292.	50S RIBOSOMAL PROTEIN L6 (BL10). - BACILLUS STEAROTHER MOPHILUS.	3174146	1	-CAT	TCA-	581	949	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
293.	grpE protein - Lactococcus lactis	3174148	1	-CAT	TTA~	256	780	Reverse
294.	Unknown	3174150	1	-CAT	TCA~	347	472	Reverse
295.	ribosomal protein S14 (rpS14) homolog - Haemophilus influenzae (strain Rd KW20)	3174152	1	-CAT	TTA~	137	391	Reverse
296.	50S RIBOSOMAL PROTEIN L3. - BACILLUS STEAROTHER MOPHILUS.	3174154	1	ATG	TAA	441	1067	Forward
297.	PHOSPHATE TRANSPORT SYSTEM REGULATORY PROTEIN. - ESCHERICHIA COLI.	3174166	1	-CAT	TTA~	101	751	Reverse
298.	PROBABLE TRANSKETOL ASE (EC 2.2.1.1) (TK). - STREPTOCOC CUS PNEUMONIAE	3174184	2	-CAT	TTA~	895	1350	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
299.	ntpJ protein - Enterococcus hirae	3174206	1	TTG	TAG	2	763	Forward
300.	Unknown	3174208	1	ATG	TAA	311	1054	Forward
301.	Unknown	3174210	1	~CAT	TTA~	290	2305	Reverse
302.	ACYL CARRIER PROTEIN. - CRYPTOMON AS PHI.	3174220	1	ATG	TAG	788	1021	Forward
303.	ISL2 protein - Lactobacillus helveticus	3174224	1	~CAT	TTA~	447	737	Reverse
304.	ISL2 protein - Lactobacillus helveticus	3174226	1	ATG	TAG	850	1164	Forward
305.	Unknown	3174228	1	CTG	TAA	1	240	Forward
306.	Unknown	3174228	2	ATG	TAG	278	580	Forward
307.	Possible Ca ²⁺ - transporting ATPase	3174236	1	~CAT	TTA~	53	241	Reverse
308.	Possible Ca ²⁺ - transporting ATPase	3174238	1	~CAT	TTA~	53	529	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
309.	CATION- TRANSPORTI NG ATPASE PACL (EC 3.6.1.-). - SYNECHOCOC CUS SP. (STRAIN PCC 7 942) (ANACYSTIS NIDULANS R2).	3174238	2	-CAT	TCA~	549	1298	Reverse
310.	PROLYL- TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-- TRNA LIGASE) (PRORS) (GLOBAL RNA SYNTHESIS FACTOR). - ESCHERICHIA COLI.	3174270	1	-CAT	TTA~	150	1646	Reverse
311.	Unknown	3174278	1	ATG	TGA	733	867	Forward
312.	Unknown	3174278	2	ATG	TAA	1680	1880	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
313.	PROLYL- TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-- TRNA LIGASE) (PRORS) (GLOBAL RNA SYNTHESIS FACTOR). - ESCHERICHIA COLI.	3174284	1	ATG	TAA	1009	2103	Forward
314.	BSCELABCD NCBI gi: 8957 - Bacillus subtilis.	3174288	1	ATG	TAA	78	464	Forward
315.	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ. - ESCHERICHIA COLI.	3174294	1	ATG	TGA	370	981	Forward
316.	Unknown	3174294	2	ATG	TAA	1044	1217	Forward
317.	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ. - BACILLUS STEAROTHER MOPHILUS.	3174298	1	ATG	TAA	431	976	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
318.	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ. - BACILLUS STEARTHER MOPHILUS.	3174298	2	ATG	TAA	922	1179	Forward
319.	Unknown	3174302	1	-CAT	TTA~	322	1320	Reverse
320.	Unknown	3174302	2	-CAT	CTA~	1486	1857	Reverse
321.	Unknown	3174314	1	ATG	TGA	523	891	Forward
322.	Unknown	3174314	2	ATG	TAG	888	1370	Forward
323.	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9). - BACILLUS SUBTILIS.	3174328	1	-CAT	CTA~	213	653	Reverse
324.	5,10- METHYLENET ETRAHYDROF OLATE REDUCTASE (EC 1.7.99.5). - SALMONELLA TYPHIMURIU M.	3174342	1	ATG	TAA	372	1238	Forward
325.	Unknown	3174356	1	-CAA	TCA~	584	1342	Reverse
326.	LSSAKACNP NCBI gi: 695615 - Lactobacillus sake.	3174368	1	ATG	TAA	219	539	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
327.	agrB protein - Staphylococcus aureus	3174368	2	ATG	TGA	730	1056	Forward
328.	RESD PROTEIN. - BACILLUS SUBTILIS.	3174372	1	CTG	TGA	1	315	Forward
329.	PROBABLE TRANSCRIPTI ONAL REGULATORY PROTEIN ENDR. - BACILLUS POLYMYXA.	3174384	1	-CAT	TCA~	239	418	Reverse
330.	Unknown	3174384	2	-CAT	CTA~	514	1074	Reverse
331.	30S RIBOSOMAL PROTEIN S2. - ESCHERICHIA COLI.	3174390	1	ATG	TAA	597	1457	Forward
332.	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ. - ESCHERICHIA COLI.	3174402	1	ATG	TGA	372	980	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
333.	GTP-BINDING PROTEIN ERA HOMOLOG. - STREPTOCOC CUS MUTANS.	3174420	1	-CAT	TTA~	592	1086	Reverse
334.	GTP-BINDING PROTEIN ERA HOMOLOG. - STREPTOCOC CUS MUTANS.	3174420	2	-CAT	TTA~	1022	1492	Reverse
335.	SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA. - SYNECHOCOC CUS SP. (STRAIN PCC 794 2) (ANACYSTIS NIDULANS R2).	3174426	1	ATG	TGA	812	1270	Forward
336.	NITRATE TRANSPORT PROTEIN NASD. KLEBSIELLA PNEUMONIAE	3174426	2	ATG	TAG	1298	1543	Forward

				Codon		Position		
SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Start	Stop	Start	Stop	Direction
337.	PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99.-). - SALMONELLA TYPHIMURIUM.	3174428	1	-CAT	TTA~	35	835	Reverse
338.	Unknown	3174444	1	ATG	TAA	164	895	Forward
339.	CYSTEINYL-TRNA SYNTHETASE (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYSRS). - BACILLUS SUBTILIS.	3174454	1	-CAT	TCA~	504	1079	Reverse
340.	Unknown	3174460	1	ATG	TAG	529	1275	Forward
341.	PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y). - ESCHERICHIA COLI.	3174462	1	TTG	TGA	2	721	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
342.	30S RIBOSOMAL PROTEIN S11 (BS11). - BACILLUS SUBTILIS.	3174466	1	-CAT	TTA~	1019	1303	Reverse
343.	Unknown	3174474	1	-CAT	TTA~	238	423	Reverse
344.	Unknown	3174476	1	-CAT	TTA~	241	1446	Reverse
345.	PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3). - BACTEROIDE S NODOSUS (DICHELOBAC TER NOD OSUS).	3174490	1	-CAT	CTA~	668	1291	Reverse
346.	mesI protein - Leuconostoc mesenteroides	3174496	1	ATG	TAG	812	1666	Forward
347.	Unknown	3174506	1	ATG	TGA	179	352	Forward
348.	GALACTOKIN ASE (EC 2.7.1.6). - LACTOBACIL LUS HELVETICUS.	3174514	1	-CAT	TCA~	209	340	Reverse
349.	GALACTOKIN ASE (EC 2.7.1.6). - BACILLUS SUBTILIS.	3174514	2	-CAT	TTA~	1177	1359	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
350.	FORMATE ACETYLTRAN SFERASE 1 (EC 2.3.1.54) (PYRUVATE FORMATE- LYASE 1). - ESCHERI CHIA COLI.	3174524	1	-CAT	TTA~	19	867	Reverse
351.	Unknown	3174546	1	-CAT	CTA~	912	1127	Reverse
352.	CACSPC NCBI gi: 899232 - Clostridium acetobutylicum.	3174550	1	ATG	TAG	645	956	Forward
353.	Unknown	3174562	1	CTG	TAG	1	504	Forward
354.	KETOACYL REDUCTASE HETN (EC 1.3.1.-). - ANABAENA SP. (STRAIN PCC 7120).	3174562	2	ATG	TAA	525	1280	Forward
355.	Unknown	3174570	1	ATG	TAG	249	593	Forward
356.	ATP- DEPENDENT DNA HELICASE RECG (EC 3.6.1.-). - ESCHERICHIA COLI.	3174570	2	ATG	TGA	604	1695	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
357.	PROTEIN DLTD PRECURSOR. - BACILLUS SUBTILIS.	3174580	1	ATG	TGA	3	611	Forward
358.	ALANYL- TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-- TRNA LIGASE) (ALARS). - ESCHERICH IA COLI.	3174582	1	ATG	TGA	537	875	Forward
359.	PTS SYSTEM, MANNOSE- SPECIFIC IIC COMPONENT (EIIC-MAN) (MANNOSE- PERMEASE IIC CO MPONENT) (PHOSPHOTR ANSFERASE ENZYME II, C COMPONENT) (EII-P-MAN). - ESCHERICH IA COLI.	3174586	1	ATG	TGA	533	865	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
360.	PTS SYSTEM, FRUCTOSE- SPECIFIC IIC COMPONENT (EIIC-FRU) (FRUCTOSE- PERMEASE IIC COMPONENT) (PHOSPHOTR ANSFERASE ENZYME II, C COMPONENT) (P28). - BACILLUS SUBT ILIS.	3174586	2	ATG	TAA	747	1172	Forward
361.	URIDYLATE KINASE (EC 2.7.4.-) (UK) (URIDINE MONOPHOSP HATE KINASE) (UMP KINASE) (SMBA PROTEIN). - ESCHERICHIA COLI	3174594	1	-CAT	TTA~	319	579	Reverse
362.	Unknown	3174606	1	CTG	TAA	1	153	Forward
363.	Unknown	3174608	1	ATG	TAA	336	863	Forward
364.	Unknown	3174634	1	-CAT	CTA~	99	308	Reverse
365.	Unknown	3174634	2	-CAT	TCA~	305	826	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
366.	5-METHYLTETRAHYDROPTEROYLTRIGLYCINAMATE-HOMOCYSTEINEMETHYLTRANSFERASE (EC 2.1.1.14) (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME). - ESCHERICHIA COLI.	3174642	1	-CAT	TCA~	250	1620	Reverse
367.	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN BRAF. - PSEUDOMONAS AERUGINOSA.	3174644	1	ATG	TGA	283	765	Forward
368.	Unknown	3174652	1	ATG	TGA	913	1134	Forward
369.	Unknown	3174654	1	ATG	TGA	158	319	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
370.	ADENYLOSUC CINATE LYASE (EC 4.3.2.2) (ADENYLOSU CCINASE) (ASL). - BACILLUS SUBTIL IS.	3174658	1	~CAT	TTA~	941	1477	Reverse
371.	Unknown	3174660	1	ATG	TGA	454	594	Forward
372.	Unknown	3174662	1	~CAT	TCA~	103	768	Reverse
373.	50S RIBOSOMAL PROTEIN L16. - MYCOPLASM A CAPRICOLUM.	3174664	1	ATG	TAA	33	446	Forward
374.	STAGE V SPORULATIO N PROTEIN E. - BACILLUS SUBTILIS.	3174666	1	ATG	TAG	151	816	Forward
375.	Unknown	3174676	1	~CAT	CTA~	24	359	Reverse
376.	Unknown	3174678	1	~CAT	TCA~	1	207	Reverse
377.	Unknown	3174714	1	ATG	TAA	839	1363	Forward

				Codon		Position		
SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Start	Stop	Start	Stop	Direction
378.	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX. - ESCHERICHIA COLI.	3174736	1	CTG	TGA	3	317	Forward
379.	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX. - ESCHERICHIA COLI.	3174736	2	ATG	TAG	411	797	Forward
380.	Unknown	3174738	1	ATG	TAA	184	558	Forward
381.	Unknown	3174744	1	ATG	TAA	507	1082	Forward
382.	PYRROLIDON E-CARBOXYLATE PEPTIDASE (EC 3.4.19.3) (5-OXOPROLYL-PEPTIDASE). - STR EPTOCOCCUS PYOGENES.	3174748	1	ATG	TAA	218	691	Forward
383.	Unknown	3174748	2	ATG	TGA	693	875	Forward
384.	Unknown	3174760	1	ATG	TGA	280	495	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
385.	Unknown	3174770	1	ATG	TGA	226	402	Forward
386.	RECOMBINAT ION PROTEIN. - BACILLUS SUBTILIS.	3174772	1	ATG	TAA	898	1527	Forward
387.	ALPHA- ACETOLACTA TE DECARBOXYL ASE (EC 4.1.1.5). - ENTEROBACT ER AEROGENES (AEROBA CTER AEROGENES).	3174774	1	ATG	TAG	155	550	Forward
388.	3- ISOPROPYLM ALATE DEHYDRATAS E (EC 4.2.1.33) (ISOPROPYLM ALATE ISOMERASE) (ALPHA- IPM ISOMERASE). - LACTOCOCCU S LACTIS (SUBSP. LACTIS) (STREPTOCOC CUS LACTIS).	3174784	1	ATG	TAG	291	650	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
389.	peptide chain release factor 1 - Bacillus subtilis	3174802	1	ATG	TAA	293	1372	Forward
390.	ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL - Lactococcus lactis subs p. lactis plasmid pUCL22	3174806	1	-CAT	CTA~	592	1194	Reverse
391.	Unknown	3174812	1	ATG	TAA	55	933	Forward
392.	FAD synthase (EC 6.3.-.-) - Corynebacteriu m ammoniagenes	3174818	1	-CAT	TTA~	4	921	Reverse
393.	CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDR OLASE) (CDA). - BACILLUS SUB TILIS.	3174826	1	ATG	TAG	25	414	Forward
394.	Unknown	3174832	1	-CAT	TTA~	23	382	Reverse
395.	Unknown	3174838	1	ATG	TAA	184	540	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
380.	SARPLRPO NCBI gi: 677848NCBI gi: 473748 - Staphylococcus aureus.	3174842	1	-CAT	TCA~	299	574	Reverse
381.	Unknown	3174852	1	-CAT	TCA~	181	540	Reverse
382.	TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKA HOMOLOG. - METHANOSA RCINA MAZEI.	3174858	1	CTG	TGA	1	1077	Forward
383.	Unknown	3174870	1	-CAT	CTA~	228	953	Reverse
384.	6-PHOSPHO- BETA- GALACTOSID ASE (EC 3.2.1.85) (BETA-D- PHOSPHOGAL ACTOSIDE GALACTOXY DROLASE). - LACTOCOCCU S LACTIS (SUBSP. LACTIS) (STREPTOCOC CUS LACTIS).	3174878	1	-CAT	TCA~	227	667	Reverse
385.	hemolytic factor - Bacillus cereus	3174926	1	-CAT	TCA~	591	1142	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
386.	DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (X-PROLYL DIPEPTIDYL AMINOPEPTIDASE IV) (X-PDAP). - LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).	3174936	1	ATG	TAA	189	479	Forward
387.	ARGININE HYDROXIMATE RESISTANCE PROTEIN. - BACILLUS SUBTILIS.	3174936	2	ATG	TGA	496	846	Forward
388.	Unknown	3174938	1	ATG	TGA	366	587	Forward
389.	Unknown	3174946	1	~CAT	CTA~	111	380	Reverse
390.	Unknown	3174952	1	~CAT	TTA~	37	819	Reverse
391.	DnaK protein - Lactococcus lactis	3174970	1	CTG	TGA	3	380	Forward
392.	Unknown	3174990	1	ATG	TAA	141	1058	Forward

				Codon		Position		
SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Start	Stop	Start	Stop	Direction
409.	LACALS NCBI gi: 473900 - Lactococcus lactis (strain DSM 20384, sub_species lactis) DNA.	3175000	1	ATG	TAA	794	1015	Forward
410.	Unknown	3175006	1	ATG	TGA	56	631	Forward
411.	cellobiose phosphotransferase system celA - Bacillus stearothermophilus	3175006	2	ATG	TAA	646	963	Forward
412.	Unknown	3175010	1	-CAT	TTA-	13	231	Reverse
413.	Unknown	3175014	1	ATG	TGA	58	219	Forward
414.	Unknown	3175016	1	ATG	TAA	120	503	Forward
415.	Unknown	3175032	1	ATG	TAA	364	669	Forward
416.	Unknown	3175046	1	ATG	TGA	105	401	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
417.	GLYCYL- TRNA SYNTHETASE ALPHA CHAIN (EC 6.1.1.14) (GLYCINE-- TRNA LIGASE ALPHA CH AIN) (GLYRS). - ESCHERICHIA COLI.	3175074	1	~CAT	CTA~	107	787	Reverse
418.	GLYCYL- TRNA SYNTHETASE ALPHA CHAIN (EC 6.1.1.14) (GLYCINE-- TRNA LIGASE ALPHA CH AIN) (GLYRS). - ESCHERICHIA COLI.	3175074	2	~CAT	TCA~	787	936	Reverse
419.	endopeptidase PepO (EC 3.4.-.-) - Lactococcus lactis subsp. lactis	3175092	1	~CAT	TTA~	47	490	Reverse
420.	BSCELABCD NCBI gi: 895746 - Bacillus subtilis.	3175094	1	~CAT	CTA~	303	1019	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
421.	DNA LIGASE (EC 6.5.1.2) (POLYDEOXY RIBONUCLEO TIDE SYNTHASE (NAD+)). - ESCHERICHIA COLI.	3175098	1	ATG	TAA	134	265	Forward
422.	Unknown	3175098	2	ATG	TAA	210	446	Forward
423.	TAGATOSE 1,6- DIPHOSPHAT E ALDOLASE (EC 4.1.-.-). - LACTOCOCCUS LACTIS (SUBSP. LA CTIS) (STREPTOCOC CUS LACTIS).	3175102	1	ATG	TGA	495	950	Forward
424.	Unknown	3175104	1	CTG	TAA	1	525	Forward
425.	Unknown	3175114	1	~CAT	TTA~	59	508	Reverse
426.	Unknown	3175126	1	ATG	TAA	3	203	Forward
427.	Unknown	3175136	1	ATG	TGA	370	582	Forward
428.	Unknown	3175138	1	~CAG	TCA~	1134	1448	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
429.	2- ISOPROPYLM ALATE SYNTHASE (EC 4.1.3.12) (ALPHA- ISOPROPYLM ALATE SYNTHASE) (ALPH A-IPM SYNTHETASE) .- LACTOCOCCU S LACTIS (SUBSP. LACTIS) (STREPTOCOC CUS LACTIS).	3175140	1	ATG	TAA	963	1382	Forward
430.	LPLC PROTEIN. - BACILLUS SUBTILIS.	3175150	1	-CAT	TCA~	246	827	Reverse
431.	Unknown	3175158	1	-CAT	TTA~	114	407	Reverse
432.	PROTEASE SYNTHASE AND SPORULATIO N NEGATIVE REGULATORY PROTEIN PAI 1. - BACILLUS SUBTILIS.	3175164	1	-CAT	TTA~	245	754	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
433.	PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTG. - ESCHERICHIA COLI.	3175172	1	ATG	TAG	380	844	Forward
434.	TRIOSEPHOSP HATE ISOMERASE (EC 5.3.1.1) (TIM). - BACILLUS SUBTILIS.	3175174	1	~CAT	TTA~	270	818	Reverse
435.	Unknown	3175188	1	~CAT	TTA~	429	935	Reverse
436.	PNUC PROTEIN. - SALMONELLA TYPHIMURIU M.	3175192	1	ATG	TAG	111	536	Forward
437.	recF protein - Streptococcus pyogenes	3175228	1	~CAT	TTA~	144	356	Reverse
438.	3- DEHYDROQUI NATE SYNTHASE (EC 4.6.1.3). - ESCHERICHIA COLI.	3175240	1	~CAT	TTA~	410	1123	Reverse
439.	Unknown	3175256	1	~CAT	TTA~	77	283	Reverse
440.	Unknown	3175262	1	ATG	TAA	84	377	Forward
441.	Unknown	3175266	1	~CAT	TTA~	50	481	Reverse
442.	Unknown	3175288	1	ATG	TGA	430	522	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
443.	NAD-DEPENDENT METHANOL DEHYDROGENASE (EC 1.1.1.244) (MEDH). - BACILLUS METHANOLICUS.	3175298	1	-CAT	TTA-	440	658	Reverse
444.	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34). - ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS).	3175306	1	ATG	TGA	478	639	Forward
445.	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27) (GLUTAMINE AMIDOTRANSFERASE) . - LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).	3175310	1	ATG	TGA	117	683	Forward
446.	Unknown	3175322	1	CTG	TAA	3	413	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
447.	ALANYL- TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-- TRNA LIGASE) (ALARS). - ESCHERICH IA COLI.	3175332	1	ATG	TAA	432	1250	Forward
448.	dihydrolipoamid e dehydrogenase (EC 1.8.1.4) - Pelobacter carbinolicus	3175356	1	~CAT	TTA~	486	1241	Reverse
449.	Unknown	3175366	1	CTG	TGA	1	405	Forward
450.	Unknown	3175380	1	~CAT	TCA~	168	413	Reverse
451.	ASPARTATE-- AMMONIA LIGASE (EC 6.3.1.1) (ASPARAGINE SYNTHETASE) .- ESCHERICHIA C OLI.	3175380	2	~CAT	TTA~	422	913	Reverse
452.	aldose 1- epimerase precursor (mutarotase) (mro) homolog - Haemophilus influenza e (strain Rd KW20)	3175406	1	~CAA	TTA~	6	701	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
453.	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) (DHODEHASE) - BACILLUS SUBTILIS.	3175442	1	ATG	TAA	198	551	Forward
454.	SINGLE- STRAND BINDING PROTEIN (SSB) (HELIX- DESTABILIZING PROTEIN). - BACILLUS SUBTILIS.	3175444	1	-CAT	TCA-	12	242	Reverse
455.	3-OXOACYL- [ACYL- CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3- KETOACYL- ACYL CAR- RIER PROTEIN REDUCTASE). - ESCHERICHIA COLI.	3175444	2	-CAT	TTA-	319	717	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
456.	Unknown	3175446	1	-CAT	TCA~	432	971	Reverse
457.	Unknown	3175450	1	ATG	TAG	75	584	Forward
458.	LPLB PROTEIN. - BACILLUS SUBTILIS.	3175478	1	ATG	TAA	63	278	Forward
459.	Unknown	3175494	1	ATG	TGA	514	759	Forward
460.	Unknown	3175500	1	ATG	TGA	310	537	Forward
461.	30S RIBOSOMAL PROTEIN S9 (BS10). - BACILLUS STEARTHER MOPHILUS.	3175504	1	-CAT	TTA~	537	866	Reverse
462.	AMINO ACID PERMEASE ROCE. - BACILLUS SUBTILIS.	3175512	1	ATG	TAA	319	816	Forward
463.	ARGININE HYDROXIMATE RESISTANCE PROTEIN. - BACILLUS SUBTILIS.	3175526	1	-CAT	CTA~	1	381	Reverse
464.	Unknown	3175532	1	ATG	TAA	309	644	Forward
465.	P115 protéin - Mycoplasma hyorhinae (SGC3)	3175536	1	ATG	TGA	132	899	Forward
466.	Unknown	3175538	1	ATG	TGA	427	507	Forward
467.	Unknown	3175552	1	ATG	TAA	76	381	Forward
468.	Unknown	3175556	1	-CAT	TTA~	175	597	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
469.	Unknown	3175564	1	ATG	TAA	3	164	Forward
470.	30S RIBOSOMAL PROTEIN S17 (BS16). - BACILLUS SUBTILIS.	3175566	1	-CAT	TTA~	388	648	Reverse
471.	Unknown	3175600	1	-CAT	CTA~	366	626	Reverse
472.	LICD PROTEIN. - HAEMOPHILU S INFLUENZAE.	3175612	1	ATG	TGA	134	535	Forward
473.	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7). - BACILLUS SUBTILIS.	3175632	1	TTG	TAA	3	506	Forward
474.	ASPARTATE CARBAMOYL TRANSFERAS E (EC 2.1.3.2) (ATCASE). - BACILLUS SUBTILIS.	3175638	1	ATG	TGA	269	526	Forward
475.	SPOOB- ASSOCIATED GTP-BINDING PROTEIN. - BACILLUS SUBTILIS.	3175640	1	-CAT	TCA~	21	476	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
476.	URACIL PERMEASE. - BACILLUS CALDOLYTICUS.	3175644	1	~CAT	TTA~	42	287	Reverse
477.	Unknown	3175650	1	ATG	TAA	158	676	Forward
478.	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS). - BACILLUS SUBTILIS.	3175652	1	~CAT	TTA~	179	514	Reverse
479.	Unknown	3175664	1	ATG	TGA	596	979	Forward
480.	DIACYLGLYCEROL KINASE (EC 2.7.1.107) (DAGK) (DIGLYCERIDE KINASE) (DGK). - STREPTOCOCCUS MUTANS.	3175670	1	~CAT	TTA~	77	367	Reverse
481.	DnaK protein - Lactococcus lactis	3175688	1	~CAA	TTA~	170	1093	Reverse
482.	serine transporter (sdaC) homolog - Haemophilus influenzae (strain Rd KW20)	3175698	1	ATG	TGA	289	528	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
483.	phage infection protein precursor - Lactococcus lactis subsp. lactis (strain C2)	3175726	1	-CAG	TTA-	152	892	Reverse
484.	SCU19250 NCBI gi: 625076 - Streptomyces coelicolor.	3175744	1	ATG	TGA	3	431	Forward
485.	livH protein - Escherichia coli	3175754	1	ATG	TAA	3	677	Forward
486.	URACIL PERMEASE. - BACILLUS SUBTILIS.	3175758	1	-CAT	TTA-	49	555	Reverse
487.	Unknown	3175770	1	ATG	TAG	28	171	Forward
488.	Unknown	3175770	2	ATG	TAA	141	311	Forward
489.	Unknown	3175774	1	CTG	TAA	1	408	Forward
490.	METHIONYL- TRNA SYNTHETASE (EC 6.1.1.10) - (METHIONINE --TRNA LIGASE) (METRS). - BA CILLUS SUBTILIS.	3175778	1	ATG	TGA	384	767	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
491.	STAGE III SPORULATION PROTEIN E. - BACILLUS SUBTILIS.	3175786	1	-CAT	TTA-	8	202	Reverse
492.	L-FUCOSE ISOMERASE (EC 5.3.1.-). - ESCHERICHIA COLI.	3175790	1	ATG	TGA	328	534	Forward
493.	L-FUCOSE ISOMERASE (EC 5.3.1.-). - ESCHERICHIA COLI.	3175790	2	ATG	TGA	440	784	Forward
494.	50S RIBOSOMAL PROTEIN L15. - BACILLUS STEAROTHER MOPHILUS.	3175792	1	ATG	TAA	230	670	Forward
495.	Unknown	3175794	1	-CAT	TCA-	190	381	Reverse
496.	COME OPERON PROTEIN2. - BACILLUS SUBTILIS.	3175800	1	-CAT	TTA-	182	649	Reverse
497.	Unknown	3175804	1	CTG	TAA	1	567	Forward
498.	Unknown	3175806	1	-CAT	TCA-	283	657	Reverse
499.	Unknown	3175812	1	-CAT	TCA-	78	596	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
500.	FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS). - BACILLUS SUBTILIS.	3175836	1	ATG	TAG	60	590	Forward
501.	Unknown	3175848	1	~CAT	TCA~	72	620	Reverse
502.	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) (PSP) (O-PHOSPHOSERINE PHOSPHOHYDROLASE) - ESCHERICHIA COLI.	3175854	1	ATG	TAA	347	841	Forward
503.	Unknown	3175866	1	~CAT	CTA~	175	534	Reverse
504.	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5). - BACILLUS SUBTILIS.	3175882	1	~CAA	TTA~	254	520	Reverse
505.	Unknown	3175896	1	~CAT	TTA~	64	636	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
506.	Unknown	3175916	1	ATG	TGA	177	437	Forward
507.	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) (TRANSCRIPT ASE BETA CHAIN). - BACILLUS SUBTILIS.	3175948	1	TTG	TAG	2	187	Forward
508.	Unknown	3175960	1	ATG	TGA	534	758	Forward
509.	DNA topoisomerase (ATP- hydrolyzing) (EC 5.99.1.3) chain B - Staphylococcus aure us	3175984	1	~CAT	TTA~	125	604	Reverse
510.	GLUTAMYL ENDOPEPTID ASE PRECURSOR (EC 3.4.21.19) (GLUTAMATE SPECIFIC ENDOPEPTID A SE) (GSE). - BACILLUS LICHENIFOR MIS.	3175998	1	~CAT	TCA~	43	540	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
511.	6-phosphofructokinase (EC 2.7.1.11) - <i>Lactococcus lactis</i>	3176002	1	ATG	TAA	662	829	Forward
512.	Unknown	3176010	1	CTG	TAA	1	546	Forward
513.	ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS). - <i>THERMUS AQUATICUS</i> (SUBSP. <i>THERMOPHILUS</i>).	3176030	1	-CAT	TCA~	140	625	Reverse
514.	Unknown	3176046	1	-CAT	TTA~	242	454	Reverse
515.	GLYCOGEN BIOSYNTHESIS PROTEIN GLGD. - <i>BACILLUS SUBTILIS</i> .	3176048	1	ATG	TAG	411	704	Forward
516.	S71704 NCBI gi: 560722 - <i>Legionella pneumophila Philadelphia-1</i> .	3176050	1	ATG	TGA	205	492	Forward
517.	PFS PROTEIN (P46). - <i>ESCHERICHIA COLI</i> .	3176076	1	-CAT	TCA~	40	234	Reverse
518.	Unknown	3176082	1	ATG	TAA	48	491	Forward

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
519.	SGHRDT NCBI gi: 510450 - Streptomyces griseus.	3176086	1	-CAG	TCA-	23	535	Reverse
520.	Unknown	3176108	1	-CAT	TTA-	4	501	Reverse
521.	trsB protein - Yersinia enterocolitica	3176112	1	ATG	TGA	127	408	Forward
522.	Unknown	3176116	1	ATG	TAA	198	515	Forward
523.	Unknown	3176120	1	-CAA	TTA-	295	729	Reverse
524.	SIGNAL PEPTIDASE I (EC 3.4.21.89) (SPASE I) (LEADER PEPTIDASE I). - BACILLUS CA LDOLYTICUS.	3176124	1	-CAT	TCA-	298	570	Reverse
525.	ligoendopeptidas e F - Lactococcus lactis	3176132	1	-CAT	TCA-	51	380	Reverse
526.	Unknown	3176134	1	-CAT	TTA-	299	436	Reverse
527.	Unknown	3176136	1	CTG	TAA	1	273	Forward
528.	Unknown	3176152	1	-CAT	TCA-	260	688	Reverse
529.	Unknown	3176158	1	ATG	TGA	273	386	Forward
530.	purine- nucleoside phosphorylase (EC 2.4.2.1) - Bacillus subtilis (fragment)	3176172	1	-CAT	TTA-	89	331	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
531.	Unknown	3176178	1	-CAA	CTA~	101	532	Reverse
532.	PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (EIIBC-LAC) (LACTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-L AC). - LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).	3176182	1	-CAT	TCA~	43	246	Reverse
533.	Unknown	3176184	1	ATG	TGA	61	336	Forward
534.	Unknown	3176188	1	ATG	TAG	42	248	Forward
535.	Unknown	3176208	1	ATG	TAA	41	238	Forward
536.	Unknown	3176216	1	-CAT	TTA~	135	335	Reverse
537.	Unknown	3176248	1	-CAT	TTA~	141	386	Reverse
538.	Unknown	3176260	1	ATG	TGA	158	343	Forward
539.	Unknown	3176272	1	-CAT	TTA~	331	465	Reverse

SEQ ID NO:	IDENTITY	Assembly ID	ORF #	Codon		Position		Direction
				Start	Stop	Start	Stop	
540.	REGULATORY PROTEIN MTRR. - NEISSERIA GONORRHOEAE.	3176280	1	ATG	TAA	287	502	Forward
541.	Unknown	3176288	1	~CAA	TCA~	5	520	Reverse
542.	Unknown	3176304	1	~CAT	TCA~	41	433	Reverse
543.	Unknown	3176330	1	CTG	TGA	2	298	Forward
544.	Unknown	3176330	2	ATG	TAG	271	381	Forward
545.	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86). - ESCHERICHIA COLI.	3176338	1	~CAT	TCA~	5	130	Reverse
546.	Unknown	3176394	1	~CAT	TTA~	17	223	Reverse
547.	Unknown	3176398	1	~CAT	TTA~	41	310	Reverse
548.	Unknown	3176420	1	~CAA	TTA~	382	678	Reverse
549.	possible acid phosphatase	3176446	1	ATG	TGA	113	475	Forward
550.	Unknown	3176480	1	ATG	TAG	151	417	Forward
551.	Unknown	3176542	1	ATG	TAA	129	446	Forward
552.	Unknown	3176560	1	~CAT	TTA~	102	374	Reverse

Table 2 shows the correlation between the SEQ ID NO of each DNA sequence of the invention with the SEQ ID NO(S) of polypeptide or polypeptides that its open reading frame(s) encodes. For example, the DNA of SEQ ID NO:1 encodes one polypeptide, that of SEQ ID NO:24. Whereas, the DNA of SEQ ID NO:2 encodes two polypeptides, the polypeptides of SEQ ID NO:286 and SEQ ID NO:287.

TABLE 2

DNA	Protein (open reading frame)
1	263
2	264
3	265
4	266
5	267
6	268
7	269
8	270
9	271
10	272
11	273
12	274
13	275
14	276
15	277
16	278
17	279
18	280
19	281
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21	283
22	284
23	285
24	286,287
25	288
26	289
27	290
28	291
29	292
30	293
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32	295
33	296

DNA	Protein (open reading frame)
34	297
35	298
36	299
37	300
38	301
39	302
40	303
41	304
42	305,306
43	307
44	308,309
45	310
46	311,312
47	313
48	314
49	315,316
50	317,318
51	319,320
52	321,322
53	323
54	324
55	325
56	326,327
57	328
58	329,330
59	331
60	332
61	333,334
62	335,336
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67	341
68	342
69	343
70	344
71	345
72	346
73	347
74	348,349

DNA	Protein (open reading frame)
75	350
76	351
77	352
78	353,354
79	355,356
80	357
81	358
82	359,360
83	361
84	362
85	363
86	364,365
87	366
88	367
89	368
90	369
91	370
92	371
93	372
94	373
95	374
96	375
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98	377
99	378,379
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102	382,383
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106	387
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108	389
109	390
110	391
111	392
112	393
113	394
114	395
115	396

DNA	Protein (open reading frame)
116	397
117	398
118	399
119	400
120	401
121	402,403
122	404
123	405
124	406
125	407
126	408
127	409
128	410,411
129	412
130	413
131	414
132	415
133	416
134	417,418
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136	420
137	421,422
138	423
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DNA	Protein (open reading frame)
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164	449
165	450,451
166	452
167	453
168	454,455
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174	461
175	462
176	463
177	464
178	465
179	466
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187	474
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189	476
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191	478
192	479
193	480
194	481
195	482
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DNA	Protein (open reading frame)
198	485
199	486
200	487,488
201	489
202	490
203	491
204	492,493
205	494
206	495
207	496
208	497
209	498
210	499
211	500
212	501
213	502
214	503
215	504
216	505
217	506
218	507
219	508
220	509
221	510
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234	523
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237	526
238	527

DNA	Protein (open reading frame)
239	528
240	529
241	530
242	531
243	532
244	533
245	534
246	535
247	536
248	537
249	538
250	539
251	540
252	541
253	542
254	543,544
255	545
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258	548
259	549
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261	551
262	552

Examples

In order to facilitate understanding of the following example certain frequently occurring methods and/or terms will be described.

5 "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

10 "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a 15 larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37° C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

20 Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, (1980) *Nucleic Acids Res.*, 8:4057.

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another 25 oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., *et al.*, *supra*, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 30 10 units to T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

Example 1**Isolation of DNA coding for a virulence gene in *Streptococcus pneumoniae***

As mentioned above each of the DNAs disclosed herein by virtue of the fact that it includes an intact open reading frame is useful to a greater or lesser extent as a screen for identifying antimicrobial compounds. A useful approach for selecting the preferred DNA sequences for screen development is evaluation by insertion-duplication mutagenesis. This system disclosed by Morrison et al., J. Bacteriol. 159:870 (1984), is applied as follows.

Briefly, random fragments of *Streptococcus pneumoniae*, strain 0100993 DNA are generated enzymatically (by restriction endonuclease digestion) or physically (by sonication based shearing) followed by gel fractionation and end repair employing T4 DNA polymerase. It is preferred that the DNA fragments so produced are in the range of 200-400 base pairs, a size sufficient to ensure homologous recombination and to insure a representative library in *E.coli*. The fragments are then inserted into appropriately tagged plasmids as described in Hensel et al., Science 269: 400-403(1995). Although a number of plasmids can be used for this purpose, a particularly useful plasmid is pJDC9 described by Pearce et al., Mol. Microbiol. 9:1037 (1993) which carries the *erm* gene facilitating erythromycin selection in either *E. coli* or *S. pneumoniae* previously modified by incorporation of DNA sequence tags into one of the polylinker cloning sites. The tagged plasmids are introduced into the appropriate *S. pneumoniae* strain selected, inter alia, on the basis of serotype and virulence in a murine model of pneumococcal pneumonia.

It is appreciated that a seventeen amino acid competence factor exists (Havastein et al., Proc. Nat'l. Acad. Sci. USA 92:11140-44 (1995)) and may be usefully employed in this protocol to increase the transformation frequencies. A proportion of transformants are analysed to verify homologous integration and as a check on stability. Unwanted levels of reversion are minimized because the duplicated regions will be short (200-400 bp), however if significant reversion rates are encountered they may be modulated by maintaining antibiotic selection during the growth of the transformants in culture and/or during growth in the animal.

The *S. pneumoniae* transformants are pooled for inoculation into mice, eg., Swiss and/or C57B1/6. Preliminary experiments are conducted to establish the optimum complexity of the pools and level of inoculum. A particularly useful model has been described by Veber et al. (J. Antimicrobiol. Chemother. 32:432 (1993) in which 10^5 cfu inocula sizes are introduced by mouth to the trachea. Strain differences are observed with respect to onset of disease e.g., 3-4 days for Swiss mice and 8-10 days for C57B1/6.

Infection yields in the lungs approach 10^8 cfu/lung. IP administration is also possible when genes mediating blood stream infection are evaluated. Following optimization of parameters of the infection model, the mutant bank normally comprising several thousand strains is subjected to the virulence test. Mutants with attenuated virulence are identified by

5 hybridization analysis using the labelled tags from the "input" and "recovered" pools as probes as described in Hensel *et al.*, Science 269: 400-403(1995). *S. pneumoniae* DNA is colony blotted or dot blotted, DNA flanking the integrated plasmid is cloned by plasmid rescue in *E. coli* (Morrison *et al.*, J. Bacteriol. 159:870 (1984)) and sequenced. Following

10 sequencing, the DNA is compared to the nucleotide sequences given herein and the appropriate ORF is identified and function confirmed for example by knock-out studies. Expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. Alternatively, genomic DNA libraries are probed with restriction fragments flanking the integrated plasmid to isolate full-length cloned virulence genes whose function can be confirmed by

15 "knock-out" studies or other methods, which are then expressed and incorporated into a screen as described above.

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Black, Michael
Hodgson, John
Knowles, David
Nicholas, Richard
Stodola, Robert
- (ii) TITLE OF THE INVENTION: Novel Compounds
- (iii) NUMBER OF SEQUENCES: 552
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SmithKline Beecham Corporation
 - (B) STREET: 709 Swedeland Road
 - (C) CITY: King of Prussia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19406-0939
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 14-MAY-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/017670
 - (B) FILING DATE: 14-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: King, William T.
 - (B) REGISTRATION NUMBER: 30,954

(C) REFERENCE/DOCKET NUMBER: P50475

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-5015

(B) TELEFAX: 610-270-5090

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTANACAAAC CAGATAAGGA CCAAGAGCTT AAAGCTGAAA TTCAATCCAT TTTTATCGAA	60
CACAAGGGAA ATTATGCTTA TCGCTGTATT CATTTAGAAC TAAGAAATTC GTGCTTATCT	120
GGTAAATCAT AAAAGAGTTC AAGGCTTGAT GAAAGTACTC AATTTACAAG CTAAAATGCG	180
ACAGAAACGA AAATAAAGGA GACGTTGGTA AGAAGGCAGA GAATCTCATT CAAGGCCAAT	240
TTGAAGGCTC TAAAACAATG GAAAAGTGCT ACACAGATGT GACAGAATTT GCCATTCCAG	300
CAAGTACTCA AAAGCTTTAC TTATCACCAG TTTTAGATGG CTTTAATAGC GAAATTATCG	360
CCTATAATCT TTCAACTTCA CCCAACTTAG AACAAGTACA AACAATGTTG GAACAGGCAT	420
TCACAGAGAA GCACTACGAG AATACGATTC TCCATAGTGA CCAAGGCTGG CAATACCAAC	480
ACGATTCTTA TCATCGGTTC CTAGAGAGTA AGGGAATTCA AGCATCCATG TCACGCAAGG	540
GAAACAGCCA AGATAACGGT ATGATGGAAT CTTTCTTTGG GATTCTGAAA TCGGAAATGT	600
TTTACGGTTA TGAGAAGTCG TTTCAAGTCG TTAAGCAATT GGAACAAGCC ATTATAGACT	660
ATATTGATTA CTACAACAAT AAGAGAATTA AGGTAAACT AAAAGGACTT AGCCCTGTGC	720
AATACAGAAC TAAATCCTTC GGATAAATTA ATTGTCTAAC TTTTGGGGGG CAGTACATTT	780
TTGGTATATA TAAAATTTGT AGGAG	805

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 764 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCGATCTGG	TTACCGTTGC	TGATAGTAAT	GAAATACCTA	CTAACAATTC	ACCTAAAGCA	60
TCAATTTGAA	AAGTTTCTAC	TAGAATATGA	AATAAAGGAT	TAATGGGTCT	TGTCAGGTAT	120
TTATCAAATT	CGCCCTTACG	AACCAGGCGT	TGCCCTAGAG	CCCATAAATT	ATCAAAAAAG	180
AGATGATCAA	TTCCCTTGGG	AATTAGGGAA	AAGCCATAGA	TAAAGGCAAT	CTGCTGAAAA	240
CTCCACCCAT	CAAGTGATGG	GATGTTTTGA	AATATAATAT	TAAGAAATAA	CAGGTTTAAC	300
CCTTGCGTTA	AAAAACGCCT	AAAACGCCAA	CAACGAAGTC	AACCTTATAC	TCCACAATTT	360
GCTTGAGGTA	TTGTCTGATA	AAAATCAAGT	GCATACGTTG	ATATTTCTTC	ATACTAACCT	420
CCTTGAATAG	TAATGTGGGA	CTGTACACGT	TTCCAAATAA	TTTGGGACAA	AGCAATCATA	480
ACAAGCAACC	AAAATAATTG	TAGCAAGACA	GCCTGAAGAA	TCTGACTGGC	ATCGTATTTT	540
CCAACAATGA	TCATAACTGG	AGTATAAATC	AAGGATGAAA	AAGGCAAAAG	GAGAGGATAT	600
CTGAGACAAC	CTTTGGAGAG	GATGCCAAGG	GAATCAAAC	CCCCGACATT	AAAGCCACTA	660
TGGAAGTCTT	AAGTAGGTTG	GAACCCCAAA	GATTTTAAAA	CACAAAGGCT	GTAAATCCCA	720
AGCAAATATT	AAAGAAAAAG	TTAATCAGAT	AGGCGAGCGT	TAAG		764

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAAGACAGG	AGTCCGAATG	TCAATACGGA	TTTCAGAACG	TTCATGATTG	ATCATGAGAC	60
CTGCGACATT	AAAGGATAGG	TGACCAGAAG	GTTTCATCTGC	TATATCACCA	AAGATTTGTC	120
TTCTGTGCC	GTCTTGACCT	GCTTGTGTTG	CAAGAAACT	GAGAGCAGGG	TGTTCTTGGA	180
GAGGAGCAAG	AATGGTAGCT	AGTCGGATGA	CAGCATTGAT	ACCTTGACTA	GCATCCTTAG	240
CATGCTTTGG	CACTCCGAGA	ACCGTTACGG	TTTGTTCACT	GGATTGGTAA	TCATAACCAG	300
CTTCTTTGAG	ACCGTTACAA	ACCTGTTTCA	AGAGGGGACC	TTGGTAGTTG	GCCTTGCTCTG	360
GTACAACGTT	AAAGGCGCCT	CCTACTTCAA	GCTCTAGTTG	ATCCGATCCA	GAGCCATAAA	420
GTTTGACCTG	TAGAAGCCCT	TTTTCAGCAT	AGGTCAGAAG	AAAAGATGAG	TCAGGTGCNA	480
AGCCCATACT	GGCCTGTTCT	TCGATGGTAT	TGTAGCGTGC	CATGCAGCGC	CAGAGGGTTT	540
CCTCATCGGT	ACCAAAGATA	AAGCGTACGC	GCTTTTTGAA	CTGAATACCT	TGGTCCAGCA	600
AGCTTTTAC	TGCATAGAGA	GCTGCGAGCG	GAGGGCCTTT	ATCATCTTGG	ACACCACGTC	660
CGATACCCAG	CCGTCTTTGA	TAGTTGCTTC	AAATGGCGGT	GTCTGCCAAT	CTGCTTCATC	720
ACCTGATGGA	ACAACATCCA	AATGACAGAG	AATGGCCAGA	AGCTCTGCTC	CCTGACCGAT	780
TTCTGCATAT	CCGTAATAAC	CTTTAGGGTC	AAGATAGGTA	GTGAAACCTA	TGTCTCGACA	840

AATCTCTAAA	TTTTTTCTA	GGACATCTTG	GATTGCTTGT	CCAAAAGGTG	TTCCATTTTC	900
TCCTTCATTG	AGTACTGAAG	GATAGGAAAT	CAAGGTTTTT	AATGATATAA	GAAATTCATC	960
TTTAACTTGA	TTTGTTATAT	CTATTTTCAT	GGAATCACCT	CACTCACCAT	TTTATAGGAA	1020
TGGAAGGAAG	GTTCCAAGGA	GAAGAAGGGC	GATGGTCACT	ACAATAATAG	CGACTACGAG	1080
TTTGCCCATG	AATTTCCACC	AAGTACCAAT	GTTGATACGT	CCAAGTGCAA	GAG	1133

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGATAAGTAT	GAGACTCGAA	GCATTGAACA	TTAAACTTCC	AGATTTCAGA	TATATGGTGG	60
ACCTTCAAAT	CATCATACTT	ATTTTGGAGA	TAAAAAACGA	TATTTACAAG	CAATTAAGAA	120
TTGAGCAAGA	GCTATTTACA	GTAGCTTAAT	GAAAGGAAAG	TATGTCAATT	ACATCATTTG	180
TAAAAAGAAT	TCAAGATATC	ACTCGAAACG	ATGCTGGTGT	TAATGGTGAT	GCTCAACGTA	240
TTGAGCAAAT	GTCTTGTTA	TTATTCTTAA	AAATTTATGA	TAGCCGTGAA	ATGGTTGGGG	300
AATTAGGAAG	AAGGACGGAG	TATGGAGTCA	ATTATTCCCA	GGAGGAATTA	AAATGGCGGA	360
AATTGGGGCT	CATGCTCAAA	ATGGGGAACG	GGTATTGACA	GGCGATGAAT	TAATTGATTT	420
TGTCATAAAC	AAGTTATTCA	AAGAGTTGAA	AGGAGCTTGA	AATAACTTCA	AATATGCCTA	480
TTCGAAAAAC	GATTATTAAA	TCAGCTTTTG	AAGATGCGAA	CAACTATATG	AAAAATGGCG	540
TCTTGTTACG	CCAAGTCATC	AATGTTATTG	ATGAAGTTGA	TTTCAATAGC	CCTGAAGATC	600
GTCATTCGTT	TAATGATATT	TACGAAAAAA	TTCTTAAAGA	TATTCAAAAT	GCTGGGAACT	660
CAGGAGAATT	TTATACGCCA	CGTGCAGCGA	CTGATTTTAT	TGCCGAAGTT	CTTGACCCAA	720
AACTTGAGAG	ATCAATGGCA	GACCTTGCTT	GCGGAACAGG	AGGCTTCTTG	ACTTCGACTC	780
TGAACCGTTT	AAGTAGTCAA	CGTAAAACTA	GTGAAGATAC	CAAAAAATAT	AATACAGCTG	840
TTTTTGGTAT	TGAAAAGAAA	GCATTTCTTC	ATCTTTTAGC	AGTTACAAAT	CTGTTTCTTC	900
ACGAAATTGA	TGACCCTAAA	ATTGTTTCATG	GAAATACTTT	GGAGAAAAAT	GTTTCGTGAAT	960
ATACCGATGA	TGAAAAATTT	GACATTATTA	TGATGAATCC	ACCTTTTGGA	GGGTCAGAAT	1020
TAGAAACAAT	AAAAATAAC	TTCCAGCAG	AATTACGGAG	TTCTGAAACA	G	1071

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTAGGATAGA CCGCTTTT	TA GCATTTATCT	AAGCATTCCA	GAGTACATGT	ATCTTGCATG	60
TGCTCTTTCT	TTTGGGGTTG	AAACGATAGG	AGAAGGAAAT	GTTAGAATTG	120
TCGATGCTTT	TGCTTGGGGA	CCGCCCCCTCT	TGATTTATTG	GTCGGAACAG	180
AACCATGCGG	CTAGGACTCT	TGCAGGTTTT	GCGTCTGCCC	AAGGCCTTTC	240
TATCCAGGAT	AAGGGACATG	GTGATGTATC	CAGTTTTACA	GCTTCTTG TG	300
TTGGGCATTC	AAACTGGTTG	GGAAACAGGG	AAATATCCAT	TAGGGAGTTG	360
TCAAGGTTGG	TGGACCAGGA	GCTCTATTTT	GGATGTGGAT	GGCGGCTTTC	420
CTACCAAGTA	TGCGGAAGGA	CTCTTGGCCA	TCAAATACCG	CACCAAGGAC	480
CAGTAGCGGG	AGGTCCCATG	CATTATATCC	TTCTAGGGAT	GGGAGAAAAG	540
TTGCTGTTTT	GTTCGAGTA	GCAGGAGTAT	TGGTTGCTCT	CTTGGAATC	600
CCCAAGTCAA	CTCGATTACA	GAATCTATCC	AAAATACAAC	GACGATTTCG	660
CAGCTCTCGT	CTTGCTGTC	TTTGTAGCGA	TTGCAGTCTT	TGGTGGACTC	720
CTAAGGTTTC	AACTACTGTT	GTTCCTTT	TA TGCCATCAT	TTATATCTTA	780
CAGTTATTTT	CTTTAATATC	GGAAAAATCC	CTGGCACAAT	CGCTTTAGTC	840
CTTTTAGTCC	CCTTGCTGCG	GTAGGTGGAT	TTGCTGGTGC	TAGCGTTCGG	900
AAAATGGTGT	GGCGCGTGGT	GTGTTTTC	AA TCGAATCTGG	TCTGGGTTCT	960
CAGTGCAGC	TGCCAAGACA	AATGAACCAG	TAGAGCAAGG	TTTGATTTCC	1020
CCTTTATTGA	TACCCTCATC	ATTTGTACTC	TA ACTGGTTT	GACCATCTTG	1080
TTTGAGTGG	TGACTTGAAT	GGGGTTGCCT	TGACTCAGTC	AGCTTTCTCA	1140
CACACTTTGG	GCCTGCCCTC	TTGACCATCT	TCCTTG TGCT	TTTTGCCTTT	1200
TAGGTTGGAA	CTATTACGGA	AGAACGCTGT	TTTGAGTTCC	TCTTTGGGGT	1260
TGGCTCTACC	GNGTGGTTTT	TGTGCTCATG	GTCTTGTTAG	GAGGATTTAT	1320
ATGGTCTGGA	TTATCGCAGA	TATCGTTAAC	GCCTTGATGG	CTCTGCCAAA	1380
CTCTTGGTCT	TGTCGCAAGT	CGTTATTGCT	GAAACTAAAA	AGTATTTTGA	1440
AATCACACAG					1450

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTCATCATCT	GTCAAAAAGC	GTTTCTTAGC	AGTCGTGATA	TCCATAAAAT	AATCTAATAT	60
CACGATTTCC	TCATCCGCAA	AGAAAGGAAG	GCTGACCAAC	TCCAGTGCCA	CATCCTTGTA	120
AACTACTTCT	TGCATATCAA	AGTAGGCAAA	GTTGAGGTCA	GCAGAATCAT	ACCCAATCTG	180
TTTCAACACT	TGACTCTTCA	TCACTTCAAA	CTGACCCTGA	TCTGTCCCTG	TAAATAGGCG	240
CAGGCTCGGT	AAATTTCGATA	AAGTCAACTT	CTGACTTTCT	TCAATGGCTA	GCATCGTCTC	300
TCCTTTCTTC	AGATTTTTCG	ATTTAATTTA	GTCAATATAG	CGCAATTTCC	CACGGAAATC	360
TTCTAAGCTC	TCGTAGCCTT	TTTCCACCAT	GATTGCTTTC	AGTTCATTGG	TAAAGCGGTC	420
AAAAGCACTG	ACGCCTTCTT	TGTGAAGGGT	CGTTCCCAAC	TGCACCATAC	TGCTCCACA	480
GAGGATGTGT	TCAAAGGCAT	CTCGACCAGT	CAGAACGCCA	CCTGTTCCGA	TAATTTGGAT	540
TTGAGGATTT	AAACGTTGAT	AAAAGGCGTG	AACATTGGCT	AGAGCAGTCG	GTTTGATGTA	600
TTATCCACCA	ATTCCACCAA	AACCATTCTT	AGGCCGAATA	ACGACAGATT	CGTCTTCTAT	660
ATAGAGGCCG	TTTCCGATAG	AGTTAACGCA	GTTGACAAAC	TTGAGCGGAT	ATTTGTTGAA	720
AATAGCTGCC	GCTTGATCAA	AGTGAACAAT	ATCAAAATAA	GGTGGCAATT	TAATTCCAAG	780
AGGTTTGGTG	AAGTAAGCAA	ACACTTCTGC	CAAAATCCGG	TCTGTTGTCT	CAAAATCATA	840
GGCAATCTGA	GGTTTACCTG	GAACATTGG	ACAGGAAAGA	TTTAG		885

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCAAAACAAG	TGGTGAGATT	CCAGAAAAAA	AAACGCGAAG	AAATTGCGTC	AGATTATCAC	60
AACTATCTTT	GAACAAAAGA	TGAATAAGCA	TAGTATTAAG	TAGAGAATGA	AAAAATATTT	120
TATTGGCGGT	TTGGGAAGCA	ATGCCTATCA	TAGCAAGGAT	TTTCTTCAAG	AACTAGATTC	180
GCAGGTCTAT	TTCTTAAATC	CATATGAAAA	GCATCTTCGA	GATGAAACAG	AATTGAAATC	240
ATGTTTTAAA	AATGAGATTG	TAGAGGAAGA	ATCTATCTGT	CTGATAGGTC	ATTCTATTGG	300
AGGCGATTTA	GCTCGTTATT	TCGCATCGGA	ATTTGAAGAA	GTAAAGAAAC	TGATTCTTTT	360
GGATGGTGGC	TATCTAGATT	TAGATAAGAT	TTTACCTTTG	GATACAGAGT	TAGAGGAAAC	420
TAAAAATTAT	ATCAAATCTC	AAATTATTTT	GGACTTAGAT	GTTCTTACTT	CTAAAGAAAA	480
ATCTGAAGCA	AAGCATTGGT	CAGAAAATAT	GGAGAAAGCT	GTAAGACAGT	CCTATCACTG	540
GAATGTTGAG	TATAATAGAT	ATGAGTTGGC	TATAAATTAT	GAAAATATAG	AAGCGATACT	600
CCGCTACGG	AGAAAAATAC	AAGCTTTTAA	GAGAGAAGTG	GGAGATACCT	TGTTTATTAG	660
TCCTCGCTAT	CCTAATGAAG	CTACATGGAG	AGAGGAAGCC	CTAAAAGAAT	TGCCAGACTA	720
TTTTGATACT	ATTTTTTAGA	AACTTTGGCC	ATGAGCCTTT	ATACTCAGCA	CCTA	774

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCTGAACTT	GGCAAGATGG	TAGCAGTTCT	CAATACGCCA	GTAAGAGTCA	TTGAAGAAGC	60
CTGTCAAAAA	GCTTCTGGAA	CTTGGAGTGG	TTACTCCAGC	CAACTATAAC	ACACCTGCAC	120
AAATCGTCAT	TGCTGGAGAA	GTGGTTGCAG	TTGATCGAGC	GGTTGAACTT	TTGCAAGAAG	180
CAGGTGCCAA	ACGCTTGATT	CCTCTTAAGG	TGTCAGGTCC	CTTTCACACC	GCTCTCCTTG	240
AGCCTGCTAG	CCAGAACTA	GCTGAAACTC	TAGCTCAGGT	AAGTTTTTCA	GATTTTACTT	300
GTCCCCTAGT	CGGCAATACA	GAAGCTGCTG	TGATGCAAAA	AGAGGACATT	GCTCAGCTCT	360
TGACGCGTCA	GGTCAAGGAA	CCCGTTCGTT	TCTATGAAAG	TATTGGGGTC	ATGCAAGAAG	420
CAGGCATAAG	CAACTTTATT	CGAGATTGGA	CCGGGGAAAG	TCTTGTCAGG	TTTTGTTAAA	480
AAAATTGATC	AAACTGCTCA	CTTAGCTCAT	GTGGAAGATC	AAGCGAGTTT	AGTAGCACTT	540
TTAGAAAAAT	AGACTAAAAT	AAGTAGAAGT	TTTGAAAGGA	AAAAAATGAA	ACTAGAACAT	600
AAAAATATCT	TTATTACAGG	TTGAGTCGT	GGAATTGGTC	TTGCCATCGC	CCACAAGTTT	660
GCTCAAGCAG	GAGCCAACAT	TGTCTTAAAC	AGTCGTGGGG	CAATCTCAGA	AGAATTGCTC	720
GCTGAGTTTT	CAAACATATG	TATCAAGGTG	GTTCCCATTT	CAGGAGATGT	ATCAGATTTT	780
GCAGACGCTA	AGCGTATGAT	TGATCAAGCT	ATTGCAGAAC	TGGGTTTCAGT	AGATGTTTTG	840
GTCAACAATG	CAGGGATTAC	CCAAGATACT	CTTATGCTCA	AGATGACAGA	AGCAGATTTT	900
GAAAAAGTGC	TCAAGGTCAA	TCTGACTGGT	GCCTTTAATA	TGACACAATC	AGTCTTGAAA	960
CCGATGATGA	AAGCCAGAGA	AGGTGCTATC	ATTAATATGT	CTAGTGTTGT	TGGTTTGATG	1020
GGGAATATTG	GTCAAGCTAA	CTATGCTGCT	TCTAAGGCTG	GCTTGATTGG	CTTTACCAAG	1080
TCTGTGGCAC	GCGAGGTCGC	TAGTCGGAAT	ATACGAGTCA	ATGTGATTGC	TCCAGGAAAT	1140
GATTGAGTCT	GATATGACAG	CTATCTTATC	AGATAAGATT	AAGGAAGCTA	CACTAG	1196

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGGAAAAC	CACCCTTTTC	AACCTTTTGA	CCGGTGTTTA	TGAACCAAGC	GAGGGAACAG	60
TAACCCTAGA	TGGTCACCTT	TTGAATGGGA	AATCACCTTA	TAAGATTGCC	TCTTTGGGAC	120
TTGGACGTAC	TTTCCAAAAT	ATCCGTCTTT	TTAAAGATTT	AACAGTTTTA	GACAATGTTT	180
TGATTGCTTT	TGGAAACCAT	CACAAACAGC	ATGTTTTTAC	TAGTTTCTTA	CGCTTACCAG	240
CTTTTTACAA	GAGTGAAAAA	GAATTAAAGG	CTAAAGCTTT	GGAATTGTTG	AAAATCTTTG	300
ATTTAGATGG	TGATGCAGAG	ACTCTTGCTA	AAAATCTTTC	CTACGGACAA	CAACGTCGTT	360
TGGAAATTGT	TCGTGCCCTT	GCTACGGAAC	CCTAAAATTC	TCTTCTTAGA	TGAACCAGCA	420
GCAGGTATGA	ACCCACAGGA	AACAGCCGAA	TTGACTGAGT	TAATTCGTCG	TATCAAAGAT	480
GAGTTTAAGA	TTACAATCAT	GTTGATTGAA	CACGATATGA	ATCTGGTCAT	GGAAGTAACA	540
GAACGTATCT	ACGTACTTGA	ATATGGCCGT	TTAATCGCTC	AAGGAACTCC	AGACGAAATT	600
AAGACCAATA	AACGCGTTAT	CGAAGCTTAT	CTAGGAGGTG	AAGCCTAATG	TCTATGTTAA	660
AAGTTGAAAA	TCTTCTGTG	CATTACGGTA	TGATCCAAGC	AGTTCGTGAT	GTAAGCTTTG	720
AAGTTAATGA	AGGAGAAGTT	GTTTCCCTTA	TCGGTGCCAA	CGGTGCAGGT	AAGACAATA	780
TTCTTCGCAC	CTTGTCAGGT	TTGGTTCGAC	CAAGTTCAGG	AAAGATTGAA	TTTTTAGGTC	840
AAGAAATCCA	AAAAATGCCA	G				861

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTATGAGAGA	GAATGACCTT	CTCTTGATTA	CTGCGGACCA	TGGAAATGAC	CCAACGTATG	60
CAGGAACGGA	TCACACTCGG	GAATATATTC	CATTGTTGGC	CTATAGCCCT	GCCTTTAAAG	120
GAAATGGTCT	CATTCCAGTA	GGACATTTTG	CAGATATTTT	AGCGACTGTT	GCCGATAACT	180
TTGGTGTGGA	AACTGCTATG	ATTGGGGAAA	GTTTCTTAGA	TAAATTGGTA	TAAGATGACG	240
CGCTATGCTT	TGCTGGTGAG	AGGTATCAAT	GTTGGTGGTA	AGAATAAGGT	CGTCATGGCG	300
GAGCTTCGTC	AAGAATTGAC	AACTTGGA	CTGGAAGG	TTGAGAGCTA	CATCAATAGT	360
GGCAATATTT	TCTTTACTTC	GATAGATTCC	AAAGCCCAAT	TGGTTGAAAA	GCTAGAGACT	420
TTCTTTGCAG	TCCATTATCC	ATTATTCCA	GAGCTTTTCT	TACTGAGTC	TAGAGGACTT	480
TGAGGCGGAA	CTTGAAAATC	TACCAGCTTG	GTGGAGCACA	GACTTGGCAC	GAAAAGATTT	540
TCTCTTTTAC	ACTGAGGGTT	TGGATGTGGA	CCAACGTCAT	CG		582

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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CTGATTTTTT ACAATACCTG CGAAATCTTA GATTTCCTGT GCGGACATGG AAGAGTCGGC      60
CAACGGACGT TGATTGTAC CATCTGTAAT ATGAACAAAA CCTGGTACAG TTGGGATTCC      120
ATAGCGTGAG CGGAATGCTT GCAAATCATT GAGTTGGCTT GGTCTTCAC TATTGATGAA      180
GTAAATGTGA GCTTTGGTTT CAGCTACGAC ACCTGACAAT GTACCTGCAA ATTTACGGCA      240
GTAAGGGCAA GTTTTGGCAG CGATAAAGAA GGTTGCAGTT TCTTTTTTAT CAAGAGCTTC      300
TTGCGCACGC ACAACTGTAG TGACTTCAAG GTCTTTGATG TTATCTAAAA ATTGTTCCAT      360
GAGATTACCT CGCTTTCATT GATAAGTCTA GTATGCCATA AAGTTTCTAA AATTGCTTAG      420
ATTTGATACG AAAAAAATG AGGTTGGTTG GTCTCATCTT TTATAGGTCT TTATTTTACA      480
AATGCATTGA TTTCTGCTTC GATGTTAGCA ATCTTAGCTT GTGATTCTTC GTTGGTTTCC      540
CCTACAACCTG CAATGTAGAA CTTGATTTTT GGTCTGTGAC CTGAAGGGCG AACGGCAATC      600
CATGAACCGT CAGCAAGTTG TGTATTTCAA CACATCACTT GGAGGAGTTG TCAAGTTTGT      660
AACAGTACCG TCAGCAACAG TAGCAGTTTG TGCCTTGA                                698

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

TCAAGNGGAT TCGTTTCGGC GGAGNTATGA CGACGGGAAA AACCTTGAAC CAATTTTTGA      60
TTGAGATGGA TGGTTTTGAG GGAAATGAAG GGATTATTCG TCATCGCTGC GACAAACCGT      120
TCAGATGTAC TTGATCCTGC CCTTTTGCCT TCCAGGAAGT TTTGATAGAA AAGTATTGGT      180
TGGCCGTCCT GATGTTAAAG GTCGTGAAGC AATCTTGAAA GTTCACGCTA AGAACAAGCC      240
TTTAGCAGAA GATGTTGATT TGAAATTAGT GGCTCAACAA ACTCCAGGCT TTGTTGGTGC      300
TGATTTAGAG AATGTCTTGA ATGAAGCAGC TTTAGTTGCT GCTCGTCGCA ATAAATCGAT      360
AATTGATGCT TCAGATATTG ATGAAGCAGA AGATAGAGTT ATTGCTGGAC CTTCTAAGAA      420
AGATAAGACA GTTTCACAAA AAGAACGAGA ATTGGTTGCT TACCATGAGG CAGGACATAC      480

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CATTGTTGGT CTAGTCTTGT CGAATGCTCG CGTTGTCCAT AAGGTTACAA TTGTACCACG	540
CGGCCGTGCA GGCGGATACA TNATTGCACT TCCTAAAGAG GATCAAATGC TTCTATCTAA	600
AGAAGATATG AAAGAGCAAT TGGCTGGCTT AATGGGTGGA CGTGTAGCTG AAAAAATTAT	660
CTCTAATGTC CAAACTACCA GGAGCTTCAA ACGACTTTGA ACAAGCC	707

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCAATCAAT TCTTCATTAG TAGTTGATTG ATGCAGTTGA CTTTCGATTT GTTCACTCTT	60
GCGGTCGATT GAACGAAGGG CTGTTAGGTA AAGTCTGCAT TGCGATAAAG AATTTGAAAG	120
ATAAAACGTG AACGCATGAA GGTATAGAAA TTACGCAATC GACGGTTGAT AAAGACATCA	180
AGGACAGGTA GTGGTTCCAA ACACGTAGTG ATAATGGTTT CCTCAGTGAT GATAATACCA	240
AGCGGGATGG TTACCTAGTA GGTGCGGTTA TTTCTTTCTT CCGTGACCGG CACGTCTACG	300
ATAATCAGGG TATACTCGTC CTCAATGGTA ATACGACACA TTTCTTCCGC ATCGAGCGGT	360
GCTCGAAGGT CGGCAATATC AATATCGAAG GTGTTGGCGA TTTCGAGTGA TTCATTTTGA	420
GTCGGATTGA CGAGATTGAT CCAAGTACCC GGTTCAGCG TATCGATCTC TTTAAATTCA	480
GTGTTGTAG AGAGAAAAAC TTGTTTCATA GCCCTTAGCC TTTCTCATTC TTCAGATTTT	540
TTCACACTGT ACTATTATAC TACAAAATCG G	571

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTGNGGAGAG ACTTNAGTAT TTTGTGGCAG ACAGACCTCG ATAATCACCA CAGGCACTAG	60
GAACCACTGG AACTGTCAGA GTGAGTGCTT CACCACTGCG CATAGATTTA CCAAGCAACT	120
TCTTTGCAAT AGCACCAGCC ACGAACCTGC TACCAAACCTG TTTTTCAGCA TAGAGTAGGC	180

AAACATAAAC CCGCAAAGGA CTGGAAGCAT CAAACCAAAG GCAGCTCCAC CAATTTTCAT	240
GGAACATAGA AGCTAAACTC ATGGTAAGAA CCAAGATTGC CAAGGTTTTC ATTTGGAACA	300
CTCAAAGCAC CGTCAATCAA GAAGGCAAGG GCAATCATGA TACCACCACC GATAACGAAT	360
GGTAACATTT GAGATACACC ACTCATCAAG TGTTTGTAGA AGGCACCACC AAGGCTTTGT	420
TTTTTCGTTAG AGGCTGTTGC GACTTTGGCA CCATTAGCGG CACGGTAGAC TTCCGCATCT	480
CCTGAAATAG CCAAGTTGAT CAATTCCTCT GTCTTACGGA TACCGTCAGC AACTGGACGA	540
TTGATCAAAG GTTTGCCATC GAAACGATCC ATTTCAACGG CCTTGTCTGC TGCAATGATA	600
ATAGCTTTAG CCTTACGGAT ATCTTCTGCA GTTAGTTGAT TTCCAACACC GCTAGCACC	660
TTGGTTTCGA CCTTGATACC AACCCCCATT TCAGCAGCTA CTTTTTGAAG GGCTTCTTGG	720
GCCATGTAAG TGTGGGCAAT ACCTGTTGTA CAAGCTGTAA C	761

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCTAAACG AATTCTCTAC AAGCACCGCA AGGGCATGGC TGAACCTCCA CCATAAGGTG	60
GTTTGTCTCG AAAGGCTAAT ACTTCNTTAA CCTTAGTTTG TCCTGAAAAT TGGTACATAT	120
TGAAGAGGGC CGCCCGTTC TCGCAGAGAT GGAAACACC ACAGGTTCCC TCCATACAGA	180
ATCCTGTAAT TATTTGTCCA TCTCCTGCTT CTAATGCAGC TACAACATGA TTGGCATAAA	240
CAAAGTCTGA TACTTCATGT GGATTGTATA GTTTCTGTGC TTCTTCGTAC ATCTTTTCCC	300
AGATGTCCAT TATTGTATCC TCTTTATTTA GAGATTTCTT TTAGAATGTT TTCGATATGC	360
TGAATTGATT TTTCACGTCC AAGCAAGAAA ATTGTATCTG GTAATTCTGG CCCATGCATT	420
TCGCCTGAAA CTGCGATACG AATAGGCATG AAAAGATTTT TCCCTTTAAT ACCTGTTTCT	480
TTTTGGACTG CTTTAATTG CGGGAAGATA TTTTCTGTCA CAAATTCATC ATCTGTCATC	540
CGCTTCAAGT TTTGCTTTGA ATGCTTCAAG AACTGTTGGA ACTGTTTCAC CCGTCATGAC	600
TTGCGCTCT GCTTCTGTCA ATTCCTGGGA AATCTGAGAA GAAAGATCTG TCCATGGGAT	660
ATCTCATCTA CTGATTCATT GTGGTTTATA GAG	693

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGTATCTAG TGGCAACGCC GATTGGCAAT CTAGATGATA TGACTTTTCG TGCTATCCAG	60
ACCTTGAAAG AAGTGGACTG GATTGCTGCT GAGGATACGC GCAATACAGG GCTTTTGCTC	120
AAGCATTTTG ACATTTCAC CAAGCAGATC AGTTTTCATG AGCACAATGC CAAGGAAAAA	180
ACTCCTGATT TGATTGGTTT CTTGAAAGCA GGGCAAAGTA TTGCTCAGGT CTCTGATGCC	240
GGTTTGCTTA GCATTTCAGA CCCTGGTCAT GGATTGCGT TAAGGCAGCT ATTGGAGGGA	300
AGAAATTGCA GTTGTTACAG TTCCAGGTGC CTCTGCAGGA ATTTCTGCCT TGATTGCCAG	360
TGGTTTAGCG CCACAGCCAC ATATCTTTTA CGGTTTTTTA CCGAGAAAAT CAGGTCAACA	420
GAAGCAATTT TTTGGCTCTA AAAAAGATTA TCCTGAAACA CAGATTTTTT ATGAATCACC	480
TCATCGTGTA GCAGACACGT TGGAAAATAT GTTAGAAGTC TACGGTGACC GCTCCGTGT	540
CTTGGTCAGG GAATTGACCA AAATCTATGA AGAATACCAA AGAGGTACAA TTTCTGAATT	600
GCTGGAAGC ATCTCTGAAA CGTCTCTCAA GGGTGAATGT CTTCTGATTG TTGAAGGTGC	660
CAGCAAAGGT GTGGAAGAAA AAGATGAGGA AGACTTGTTT TTAGAAATCC AAG	713

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTTAAGGAA AATCAAATCT CTCATGCTGA TACCTCTCCT CATTAAATTA AATAGTAAAA	60
AAGATTCTAT CTCACTCCCT GATTATTACA AAACCATTGA AATATCACA CTAATAGGCT	120
AGAATGGACA TAGTAAGATN TAGTAGATGA GTCATTCTAC TCAAATCCAC GTTAGAAAGG	180
ACTGCTATGC CAGACAATCT CGCGCTTCGC ATGCGCCCTA AAACCATCGA CCAGGTCATC	240
GGTCAGGAGC NTCTGGTCGG ACCTGGAAAA ATCATCCGCC GCATGGTGGA AGCCAACCGC	300
CTGTCCTCCA TGATTCTATA TGGCCCTCCT GGAATCGGCA AAACAGTAT TGCCTCTGCC	360
ATCGCTGGAA CGACCAAGTA TGCCTTGCGA GACCCCAAC GCGACAGTTG ATAGTTAAAA	420
AGCGACTGCA AAAAATCTCG GAAGAAGCTA AATTTTCTGG TGGTCTCGTC CTATTGCTAG	480
ACGAAATCCA CCGACTAGAT AAGACCAAGC AAGACTTCCT CTGGCCTCTC TTGGAAAGTG	540
GACTGGTCAT CATGATTGGA GCAACGACTG AAAATCCTTT CTTCTCTGTC ACTCCTGCCA	600
TTCGTAGCCG AGTTCAAATT TCCGAGTTGG AACCTCTGTC TAACCAAAAC GTCAAAGGAG	660
GCCCCGCAA	670

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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CTCTTAGTAT CNTGATTATG GCGACTTATG AAACCTTCNC GGCGGTCTAT GATGCGGTCA      60
TGGACGAATA GTTTATGCGA CAAATGGACG AATTTTCTC ATGCGTCATT TGCCTAAGAC      120
CGAAGGAGAG AAAGAACTC TTGAATTGG CTTGTGGGAC AGGAATTCAA TCAGTCCGCT      180
TCTCTCAGGC TGGTTTGTAT GTGACTGGAC TTGACTTGAG TCGGATATG TTGAAGATTG      240
CGGAGAAGAG GAGCAACTTC AGCCAAGCAA AAGATTGCTT TTATAGAAGG TAATATGCTA      300
AATTTGTCCA AGGCAGGGAA ATACGATTTT GTCACGTGTT ATTCCGACTC TATCTGCTAT      360
ATGCAGGATG AGGTGGAAGT AGGGGACGTC TTTAAGGACG TGTACAATGC GCTGAATGAA      420
GAAGGAGTTT TCATCTTTGA CGTGCACTCG ACCTACCAGA CAGATGAAGT ATTGCCCTGG      480
CTATTCCTAC CATGAAAATC TCGGAAGATT TTGCCATGCT TTGGGATACA TATGAGGGCG      540
GAGCTCCTCA CTCCATCGTG CATGAGATCG AGCCT                                575

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

CTTGCTTTTA ATTGATAATG ATCCTTTTAA AGATGATGAA GATTTCGTGT CAACCTATGA      60
CCTTGATAAA TCTTTTATTT CTATGGTATC TGTGATGTA TCAGAATACC TAGGAAGTCA      120
GGAACCCATT AAAAAGACTT TGACCATACC AAAATGGGCA GATAAGTTGG GACGAGAAAT      180
GGGACTTAAC TTTTCTCAGA CTTTGACAGA CGCTATTGCA GATAAGAAAG TTCAAGCCTA      240
AGATTAAGCG TGGTATCGTG GTAATAGTCA ATAAAAAAGC ACGTCCACTT GTGCTAGTTA      300
CTCGCCTATT GATTTTATAG ATTTATTAGC CCTTTCGAGG GCTTTTATA TTGATTTTAA      360
TGAGAAATAA AGAAATCAGA CTTTTAAGAA AATCATTGAT ACCAAGGGTT TAAATGAGGT      420
AATATGGTAT AATTAGGACA TAAAATAATT TTGTGGTAAG ATGGTAGTAT CTATTTTAGC      480

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ATATTTCCGA GCAACGGGGC GATTAAA

507

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

CTTTGACAAA GAGTATGACA CCTGACCGTG AAGTCATTAC CTTTATTCCT GAAAAATTTA    60
TTGTGGATGG TTTCCAAGGG ATTCGTGACC CACGTGGCAT GATGGGGGTT CGCCTTGAAA    120
TGCGTGGTTT GCTTTATACA GGACCTCGTA CTATCTTGCA CAATTTGCGT AAGACGGTTG    180
AGCGTGCAGG TGTTCAGGTT GAAAATGTTA TCATTTCACC ACTAGCAATG GTTCAGTCTG    240
TTTTGAACGA AGGGGAACGT GAATTTGGTG CTACAGTGAT TGATATGGGG GCAGGTCAAA    300
CGACTGTCGC TACAATCCGT AATCAAGAAC TCCAGTTCAC ACATATTCTC CAAGAAGGTG    360
GAGATTATGT AACTAAAGAT ATCTCCAAGG TTTTGAAAAC CTCTCGCAA TTAGCGGAAG    420
GCTTGAAACT GAATTACGGG GAAGCCTATC CGCCTCTTGC AAGCAAAGAA ACCTTCCAAG    480
TAAAGGTTAT TGGAGAAGTA GAACCAGTCA AAGTGACGGA AGCCTACTTG TCAGAAATTA    540
TTTCTGCACG AATCAAGCAC ATCCTTGAAC AAATCAAGCA AGAATTAGAT AGAAGGCGTC    600
TGGTTGGACC TCCCTGGTGG TATTGTCTTA ATCGGTGGGA ATGCCATTTT ACCAGGTATG    660
GTTGAG

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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CTCGTACAAA CGGTATGGGA TTTGCACGTG ACAAGATGGT TATTACCACT GTAAACAAAA    60
ACCTAGAATT GACAGCTAAA TGGATTGATG CACAATACGC TCCACTCCAA TCTGTGCAAA    120
ATAACTGGGG AACTTACGGA GATGACAAAC AACAAAACAT CTTTGAATTG GATCAAGCGT    180
CAAAATAGTCT AAAACACTTA CCACTAAACG GAACTGCACC AGCAGAACTT CGTCAAAAGA    240

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CTGAAGTAGG AGGACCACTA GCTATCCTAG ATTCATACTA TGGTAAAGTA ACAACCATGC	300
CTGATGATGC CAGAATGGCG TTTGGATCTT ATCAAAGAAT ATTATGTTCC TTACATGAGC	360
AATGACAATA ACTATCCAAG AGTCTTTATG ACACAGGAAG ATTTGGACAA GATTGCCCAT	420
ATCGAGGCAG ATATGAATGA CTATATCTAC CGTAAACGTG CTGAATGGAT TGTAATGGC	480
AATATTGATA CTGAGTGGGA TGATTACAAG AAAGAACTTG AAAAATACGG ACTTTCTGAT	540
TACCTCGCTA TTAAACAAAA ATACTACGAC CAATACCAAG CAAACAAAA CTAGAGGTTG	600
ATTATGGGAG ATAAGAAATA CACAGTAGAA AAAGCCAATA GTTTTATAGC AGAAAATAAA	660
CATCTCGTTA ATACTCAATA TAAGCCTGAA GGACATTTT CAG	703

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCACAACAAC TCTCGTNTGA TCACTATGGG GGCACAACCT GTTGGTGATG AATTGGCTAA	60
AAACATCGCT AAAGGATTTG TTAATGGTAA ATACGACCGT CNACATCATC AAATCCGGGT	120
TGACATGTTG AACAAAATGG GCTAATTAGA TTACAGTAAG AAAGGTAAGT TAAAAATGAG	180
AATTGCAATT GGATGCGACC ACTTCGTAAC AGATGAAAAA ATGGCGGTTT CAGAATTTTT	240
GAAATCAAAA GGATATGAAG TCATTGACTT TGGTACATAT GACCATACAC GGACTCACTA	300
CCCAATCTTT GGTAAAAAAG TACGGGAAGC TGTAACATC GGCCAACCTG ATCTTGGAGT	360
ATGTACCTGT GGTACTGGTG TTGGTATCAA CAACCCTGTA AATAAAGTCC CACGTGTTCC	420
CTCTGCCTTG GTTCGTGATA TGACAACAGC CCTTTATGCT AAAGAACAAT TGAACGCCAA	480
CGTTATCGGT TTTGGTGGTA AGATTACTGG TGAATTGCTC ATGTGCGATA TCATCGAAGC	540
TTTCATCCAT GCTGAATACA AACCATCTGA AGAAAACAAA AAATTGATTG CGAAAATTGA	600
ACATGTTGAA ACAACAAATG CTCAACAAAC AGATGCAAAC TTCTTCACTG AATTNCCTTG	660
AAAAATGGGA TCG	673

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTACTTTCCG CCAGAGTTTT GAGGTCGCTA GAACATTTTG CTTATCGATA CTAGTAACGA	60
TTTTTCTGCG ATTTCTTGCA ATTTCAAAGG CTTGCGAAT AATCCGCTCC ACTTCCTCAT	120
AGCTATAGTC GTTGATATCA CGCGCTTTGC GCTCTTCAAG AATATGATCT CCAAAGTAAA	180
TCTCGCCTAA TCAATTAACG CACCACGACA AAGTATACAC CAGAAATTCG TTCCGGTTTG	240
AGTGGTGACA AATACTTGAG ACTGTCAAAG ATTTTACAG GACGAATATT AGCGTAAAGA	300
TTGAGTTCTT ACGGAGAGCC ATCAGGCCTT GTTCAGGGCG AACCGCTACT CCATCATACT	360
GAGGACTACC GATAGCTACT AGTAGGATAG CATCTGCTTC CCTACTTGCC TTAAGGGTTT	420
CATCAGGTAA GGGAGGTCCT GCTGCATCAA TATCTGCACC TCCGAACGGT CGTCTGTCAA	480
TCTNCATAGT CAAAACCTGT TTTTTCAG	508

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCTTGTCAG AGAAATTTAC AAAACGTTAG GAGAATAAGA TGGCATTAT TGAAAAAGGT	60
CAAGAAATCG ATATGGAAGT CATCAAGGCT GAAACCCAAT TGTCTGCAGA AGCCTTGAGA	120
CTCAAGGAAA GCCGTGACAG GGAATTGGCA GATATTATTT CAGGGGAAGA TGACCGTATT	180
CTCTTGGTGA TTGGTCCTTG CTCTTCTGAT AATGATTAGG CGGTCTTGGA ATATGCTCGC	240
CGTTTATCCG CCTTGCAAAA GAAGGTAGCG GATAAGATTT TCATGGTCAT GCGCGTGTAT	300
ACTGCTAAGC CTCGTACCAA TGGAGACGGC TATAAAGGGT TGGTTCACCA GCCAGATACT	360
TCTAAGGCTC CAACCTGAT TAACGGCTTG CAGGCTGTGC GCCATTTGCA CTACCGCTTT	420
GATTACAGAT ACTGGTTTGA CAACGGCAGA TGAGATGCTT TATCCGTCAA ATCTGATCTT	480
GGTGGATGAC TTTGGTCAC	499

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTTGTCATAA TTTACAATTT AGTTAATAAG ACCAAAAAGG TCATATATAT AAAGGAGTCA	60
CAAAAATCAT GAACAAACGT GTAAAAATCG TTGCAACTTT GGGTCCTGCG GTAGAAATCC	120
GTGGTGGTAA AAAATTCCGT GAGGACGGAT ACTGGGGTGA AAAACTTGAT GTTGAAGCTT	180
CAGCTAAAAA CATTGCTAAA TTGATTGAAG CTGGTGCTAA CACATTCCGA TTCAACTTCT	240
CACACGGCGA CCACCAATGA ACAAGGTGNA GCGTATGGCA ACTGTTAAAC TTGCGGAAAA	300
AATTGCAGGT AAAAAAGTTG GTTTCCTTCT TGATACAAAA GGACCTGAAA TCCN	354

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTTCTTTACT GAGATGGATT TTCCTTTTTTA GTTCGTGCCA ATCTCAAGGC ACGATTGGA	60
TTGAGACGAT TAAATAGTTC TTCCAATTTT TTTTCATTCC AAACGTCTGC GGCGGAAACA	120
AAATTACCAT CCGCATCTCG GAAAGATATC GGTTTATCTC CCATACCACT CTCCTAGTCT	180
ACAAATTCAA ACTCAAATTT ACCAATGCGG ACCAAATCCC CATCTTTAGC TCCACGCGCA	240
CGAAGGGCTT CATCAACCCC CATACCACGA AGCTGACGGG CAAATTTTCAT GACAGATTCA	300
TCACGATCAA AGTTGGTCAT ATTAAAGAGT TTCATGAGTT TTTCACCAGA AAGTACCCAT	360
GTCGCATCGT CATCAGCACT AATTTCAAAG GCTTTTTTCTT CTTGTCAAA TCCATAGTAA	420
GCTTCTTCTT CCATATCAGA CTCGTCGTAG AGCAAAAATT CTGGTGTCTT GTCTAACAAT	480
TCAGCTGTAG CATCTAAAAG TGTGCCCAGA CTTGCTTGGT CAATCCAGAA ATTGGGAAGA	540

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACTAAAGGT GCAGGTGCCA GATGATCGTC ACCAACGTAT CAGATAGTCA ATTACTTTCC	60
CAAATCTTAC TCAATCTTTT ATCCAATGCC ATCCGTTACA CTGAACAAGG GGGAAAAATT	120
GAGGTCAAGA CCCAAAAGGT GAACGAAGGC ATTAAGATTT CTGTATCAGA TACAGGGCAT	180
TGGTATTAGT CAATTAAAGC ATGATCGTAC CCCTGACCGT CACTACCGAG TTACCAAAGG	240
TCGAAACTGA GATTCCGGTT AGCCACGGTG GTGGCCTTGC CATTGTCAA GAACTCAGTC	300
AATTTATTAG GTGGCCGNAG TCACGGTGAC GAC	333

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTGAACATAG GCTTAGAAGG AGTCTACCAG CAGGAGAATG CAGCCTTGGC GTTGCAAAC	60
TTTCTTCTCT TTATGGGAGA AGGANNGGAA GCTGTCGATG AACAGGCTGT AAGAAAGGCC	120
TTGGAACACA CCCATTGGGC TGGTCGCTTG GAGCGTATTC GCCCACAGAT TTACTTGGAT	180
GGTGCTCATA ACCTCCCTGC CTTGACTCGC TTGGTTGACT TCATCANCCA ANAANTATCA	240
TGAGGGTCAT CGTCCTCAA TCCTTTTTTG GA	272

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGCATCAGC CAAAGCTTTC ACACGTCCGT GATATAGATA TCCACCGCGG TCGAACACCA	60
CTTCTGAAAT ACCTTTAGCG TTTGCACGTT CTGCAACGAG TTTACCGACA GCAACGGCTT	120
GTTCAGTTTT AGTTCCTTTT GAAACTTCTT TATCAAGAGT TGAAGCACTT GCGAGCGTTA	180

CACCCGCTAC	GTCATCAATC	ACTTGAGCGT	AGATGCCTGT	ATTAGAACGG	AATACGTTCA	240
AACGTGGGCG	ATCAGCAGTT	CCAGAGAGTT	TTCCGCGAAC	GCGACGGTGG	CGTTTTTGGC	300
GGAGTTTGTT	TTTATCTGGT	TTTGAAATCA	CAGTTTTTCAC	CTCTTTAGTT	TTAAATCGTG	360
TGCTATGCAC	AAAGTTGGAA	AATAGGTTGG	TGGTTGATGA	TCAACCACTC	AACATTATTT	420
ACCTGTTTTA	CCTTCTTTAC	GGCGAACGAA	TTCACCAACG	TAACGGATAC	CTTTACCTTT	480
ATATGGTTCT	GGTGAACGAA	GGCTACGTAC	GTAAGCAGCT	GTTTGACCAA	CTACTTCTTT	540
TGAAATTCCG	CTAACAACGA	TTGTTGTTGG	GTTTGGAAGT	TCAAAAAGTAA	TTCTTTACAG	600
CTTCAACTTC	GTCTGGATGA	GATTTACCAA	CAGCCAAAAC	AAGTTTAGAT	CCTTGAAGCT	660
GTGCACGGTA	ACCAACCCCA	CGCATTTCAA	GTTCTTTTCT	GAATCCTTCT	GATACACCAA	720
CAACCATGTT	GTTCAAAAGG	GCACGAGTAG	TTCCGTGGAT	AGTTTTTATT	TCTTTTGAAT	780
CGTTTGGACG	GTGAAAAGTT	ATTTCACTAC	CTTCCACACG	GATTTCAATA	TCTTTTGAAG	840
ACTCACGAGT	AAGTTCTCCT	TTAGGTCCTT	TTACAGTTAC	AACGTTGTCA	TTGTTAGCGA	900
GTTCAACACC	AGCAGGCAAC	ACGATAACTT	TATTACCAAT	ACGTGACATG	TTTATTTTCT	960
CCTGTTAAAT	TGTCAGGCCA	GAACGGCCAG	TTTTCACGGG	GTTCAAATAC	TTATTTAGTT	1020
CAAGAGCCAT	CCAACTCTC	CCAGCAGACG	ATGACCACCC	AGTAGATACC	ATCGCCCAAG	1080
TCTTTCAAAA	AGGCTACAAA	CTCCATGAAC	GCATCCCTAC	GCCCAGCCAA	TGGTAGTGGT	1140
GTTATAACTA	AGAATACAA					1159

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGATCGGACA	AGAATCTATT	CTGTAAATTG	CGACACGAGG	AGTCGAAATC	GATTTTACTT	60
CGACGACGAG	TTAGTAAGGA	AGCTAGACAA	ACGCCATAGC	GATTGCCGTT	TTCTGACGAG	120
TTGCTTTAGC	TACCGTCAGA	ATTGCCGAAT	CGAACACGCC	CTAAGCTCTG	AGTAAAAAAG	180
ATAGATTTTC	TTGTGTTTCAT	CGAACAATTC	GTCAATCTCC	TATTTTACT	GCGAGCTTTT	240
TACGGGCTTT	GTATCTTAGT	TATACACCAC	TACCATTGCT	GGGCGTAGGA	TGCGGTCATG	300
GAGTTTGTAG	CCTTTTGTAA	AGACTTGGGC	GATGGTATCT	ACTGGGTGGT	CATCGTCTGC	360
TGGGAGAGTT	TGGATGGCCA	TATGGTAGTT	ATGGTCAAAT	TCGCCATCTG	CTGCGATTTC	420
TTCAATTCCCT	TCTTCTTTCA	AAGCGTGAAT	CAAGCTTTCT	TGCACCATCC	CCAAGCCCTT	480
CTTCACATCA	TCTGTCAAAC	CTTCAACTGC	AAGTGCACGC	TCAAGGTTGT	CAAGAGATGG	540
TAAGATTGCT	TTTGCCAAGT	CCTGGCTACG	ATAACGTTGC	AAGTTTGTAC	GTTCTTCATT	600
GGCACGGCGT	TGGATATTTT	GCATTTCTGC	ATGAGCGCGA	AGATATTTGT	TTTCGAATC	660
ATCTGCACGT	TCATTTGCCA	AGTCCAATC	AGACTTTTCA	GGAGTTGTTT	CTTCAGCTGT	720
TTCCACAAC	TCCTCTTCTT	GAAGTTCTTC	TACTTCTCCA	TTTTTTATAT	CTTGGGCCAT	780

GTTCGCCTCC CTTTAATGAT TTCAATCTTA ATGTACTTCA TAACGATTAC TGCTGAGGTA 840
 GCGGTAAAAA TCTGTCNNCN TCATAGTCAA AACACGGTGA ACACATTGAC TNGATTGATA 900
 A 901

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTNNTGTCAA AAGTATTGCT ATCCTTATTC ATAGAATAAA GAATACGGCG CTGAACCGGC 60
 TTCAACCCAT CACGAATATC TGGCAAAGCC CGGTCTTGAA TAATGTACTT GGAGTAGCGA 120
 CCAAAGCGCT CTCCCATGAT GTCCTCCAGG GACATGTTTT GAATGTTAGA CATAAGATAC 180
 AAAGCCCAT AATACCAAG TGAAAATAGA AAATTCTTGA AGTAAGCAAA CTCACAAGAG 240
 AATTATCTT TTTCACACAG TATCTAGGGC GTGTTCAACT CCTTCAAAG AATGTAGAGT 300
 AGGTTTTTAT GCAGTAAAAG ATATTTTACG GGAATTCGTC CCGTGTTTCA TTACGATAAG 360
 TAACCAAAT ATCTGTTTG TATTTTCAA TATGAAAATA TGGTTTTCCA AAATTAGTCT 420
 TAGTTTGTGT CTTAGCCGCT CCCTTAAACG CCTCTTTGAG ATAAGCACTC ATAGCAGATT 480
 CTTCATTAAT AATCCTGCAA TTTTTCAAA CCAAGATTTT CAACTGCTT TTTCACATAG 540
 TCATTACAT CCGACTCTAA TTTCCAGTTT ACTAACATAT TATTTTCTTT CATTAACAACA 600
 CTGTCGCTTC TTCTAGCGTA AACTTGACAT TATCTTCAAT CCATTTACGG CGTGGTTCTA 660
 CCTATCTCC CATGAGAACA TTGACGCGGC GTTCGGCGCG CGCTAAATCT TCAATTGTGA 720
 CACGGATGAG GGTACGTGTT TCTGGGTTCA TGGTTGTTTC CCAGAG 766

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGTTCA AATTGGCAAG CCAATTGAA CCCGGGCTAA ACTCTGTGTG AAAAAGATAA 60

ACTTTCCTAG AAACCTTAGT TTCTTCGTCA AGTTCCTAT TTTACTTGG AGTTTTGACG	120
CTCTTGATAT CTTAAATTAC CAAGATGCTT TTGTTACACC AGGAATTTGA CCTTTATGCG	180
CAAGTTCGCG AAAAGCGATA CGACTCAGAC CAAATTTGCG GTAAACTGAA TGTGGGCGCC	240
CCGTAACCTCT ACAACGATTA TGTAACGAG TCGGTGAGGC GTTGCAGAGT AATTTAGATA	300
AACCTTCGTA GTCCCCTGCC GCCTTTAATG CAGCACGTTT TTCAGCATAA CGGTCAACAA	360
TTTTTTGGCG TTTAGCCTCT CTAGCTACCA TTGATTTTCT AGCAATTAGA TTTACCTCCT	420
ATATTATTTT GCAAAAGGCA TTCCAAGGCC TTGTAAGCAA TGCACGTGAC TCTTCGTCAG	480
TGTTAGCAGT TGTTACGATA ACGATGTCAA GACCACGAGT TTTGTCAACG TCATCGAAGT	540
TGATTTCTGG GAAGATTAAT TGTNCTTTCA CACCAAGTGT GTAGTTCCCG CGTCCATCAA	600
ATGATTTTGT TGGAACACCG TGGAAGTCAC GTACACGTGG AAGTGAAACT GATACCAATT	660
NACCCAAGAN TTCGTACATA CGTTCACCAC GAAGGGTAAC TTTTGCACCG ATCGCNACAC	720
CTTCACGAAG ACGGAAGCCG GCGATTGATT TTTAGCTCT AGTGATNAGT GGTTTTGTAC	780
CNGAGATAAG TGCCAATTCT CCAGCAGCTT TTTCAGGCTT TTAGCGTTTG A	831

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTACTCGTAC AGGTGCACAA GTTGC GG GTC CAATCCCACT TCCAAC TGAA CGTAGCCTCT	60
ACACAATCAT TCGTGCGACT CACAAATACA AAGACTCTCG CGAACAA TTT GAAATGCGTA	120
CACACAAACG TTTGATCGAT ATCGTTAACC CAACTCAAAA AACAGTTGAT GCCTTGATGA	180
AATTGGATCT TCCAAGTGGT GTAAACGTAG AAATCAAACT TTAATCTAAA ATATAAAAGA	240
GCAGAGGCTG GTGTTTCAAT CTAATTGAAC ACGGACTAAA CTCGGTGTGA AAAAGATAAA	300
CTTCCTATTG TCCGTTAGAC ACTGCGTTAG TTTCTATTT TCAC TTTGAG TTTGACGCCC	360
TTTGTATCTT AGACTTGAGC ATAAAAACG CTCGTAAAAA ACTTTT TGAA TAAAAAATAT	420
AGAAAAGGAA CTATTTTCTC ATGACAAAAG GAATCTTAGG GAAAAAAGTG GGAATGACTC	480
AAATCTTCAC TGAAGCTGGC GAATTGATCC CTGTAACAGT TATTGAAGCA ACTCCAAACG	540
TTGTTCTTCA AGTTAAAACT GTTGAAACAG ACGGATACAA CGCTATCCAA GTTGGTTTCG	600
ATGACAAACG CGAAGTATTG AGCAACAAAC CTGCTAAAGG ACATGTAGCG AAAGCTAACA	660
CGGCTCCTAA GCGCTTCATT CGTGAATTCA AAAACGTTGA AGGCTTGAA GTTGGCGCTG	720
AAATCACAGT TGAAACATTC GCAGCTGGAG ATGTTGTTGA TGTAAC TGGT ACTTCTAAAG	780
GTAAAGGTTT CCAAGGTGTT ATCAAACGCC ACGGACAATC ACGTGGACCA ATGGCTCACG	840
GTTCTCGTTA CCACCGTCGT CCAGGTCTTA TGGGGCCTGT TGCACCTAAC CGCGTATTCA	900
AAGGTAAAAA CCTTGCAGGA CGTATGGGTG GTGACCGCGT AACAA TCAA AATCTTGAAG	960
TTGTACAAGT TGTTCCAGAA AAGAACGTTA TCCTTATCAA AGGTAACGTA CCAGGTGCTA	1020

AGAAATCTCT TATCACTATC AAATCAGCAG TTAAAGCTGG TAAATAATAA AGAAAGGGGA 1080
 AATCAGTCAC AATGGCAAAC GTAACATTAT TTGACCAAAC TGGTAAAGAA GCTGGCCAAG 1140
 TTGTTCTTAA CGATGCAGTA TTTGGTATCG AACCAAATGA ATCAGTTGTG TTG 1194

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCCTCACTA TCTACACTGC TTAAATTGGT CAAATGAACT TTTTACAAC CATAAAAAAG 60
 AGCACTTAAT CGTACTCTTC TCTTTAAGG ATTAGTTGAA TTAATTCAA TCCACTAGTT 120
 CTCCTGTTTC TAGGTAGACT AGGCGTTCAC AAATGTTAGC AATGTAATCA GCGAAGCGTT 180
 CCAGATGCCC TATGATATAA AGGTATTGTG TTCCATTGGG AATTGAGGTT TCTTGGTCTT 240
 TCATAAGTCC AATGATTTC TTTGATAAGG CATAATAATA TTGGTCAATC TGTTTCATCTT 300
 TTTGAGCAAT ACTAATAGCT TTTGAGGCTT GGTGCAAAGG AAAGGCAACC AATAAATCGG 360
 CTAGCATGCT GAGGGATAAT TTACCCATTT GGTGTAAGT TTCTTCGCCA GGGGCTAGTT 420
 GATTTTCTTT TAGTTGCAA ACAGCTTTGG CAATGCCTGC CATATGGTCT CCCATACGTT 480
 CAAGGTCTGA ACAAGAAGAC ATGATGCTAA TCACAAATCG AAGGTCAGAC ACTTGTGGCT 540
 GCTGCAAGGC TAACAAACGG GCACAGGTCA ATTCGATAGC GCTTTGACCT TGGTTGATAG 600
 CATGATCCTT ATTGATAATT AGCTTTGCCA TCTCCTTGTC TTTGGAGGCT AAGGCCAGTA 660
 AGGCTTTTGA AGCTGTTTCA AGGACAAGTT GCCCTAGTCC TAAAAAGGAT TGTTCTAATT 720
 CATGCAATTC TAAGTCAAAT TGATTTCTCA TAGGTTTTC CTTCCTTATC CGAACCGTCC 780
 TGAAATATAG TCTTCTGTGC GCTGATCTTT TGGATTGGTA AACACGTCAA CGGTATCTCC 840
 AAATTCGCAA ATTTCTCCTG TTAAGAAAA AGCAGTTTTA TCTGAAATAC GTGAAGCTTG 900
 TTGCATGTTA TGGGTAACAA TGATAATCGT ATAATCCTTT TTTAGTTGCT GAATGAGGTC 960
 TTCAATTTTT AAAGTGGAGA TAGGGTCTAA GGCTGAAGTC GGCTCATCCA TTAACAGAAT 1020
 ATCAGGTTCT ACTGCTAAAG CTCGCGCAAT GCAAAGGCGT TGCTGCTGAC CGCCAGATAA 1080
 GGACATGGCA CTCTTTTAA GATCATCTTT GACTTCTTCC CAAATGGCTG CCCCTTTTAA 1140
 AGATTTCTCC ACTAAGGCAT CTAATTGTTT TTTGTCTCGA ATACCATGTG TCCTTGACC 1200
 ATAAGCCACG TTATCATAGA TAGACATGGC AAAGGGATTA GGCTGTTGAA AAACCATCCC 1260
 TACACGCTTG CGTAGCTGAT TAAGGTTGAA TTTGCTACTA TAAATATCTT GCTCATCTAA 1320
 GAGGACTTGG CCTTCAATAT GGCAAGAAGG AACCAAATCG TTCATCCGAT TAAGGGTTTT 1380
 TAGAAAAGTT GATTTGCCAC AACCAGATGG GCCTATCAAG GCAGTAATCT GTCTTTCTGG 1440
 TAATTGAATC GAAATATTTT TTAAGGCTTG AAAATCCCCG TAAAATAAGT CTAGGTGTCT 1500
 GACTGAAAT GTTCCCATAC TAGAAG 1526

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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CTGGGGCAGA CGCACC GAAG ATGTCAATAC CGATGNCCGC GCCATCCAAA CCAACATACT      60
TGTACCAACT TTGGGTCGCT GCCATTTC AA TGGCCACACG ACGACGAGTC TTAGATGGTA      120
AAATGTCTTC CTTGTAGGTA GCATCTTGAG CATCAAATAG TTCGGTTGAG GGCATAGATA      180
CCACACGTAC TTTACCACCT TGTA AAAACCA ATTCCTTAGC AGCTTTGATA GCTAGATTGA      240
CCTCAGATCC TGTAGCAATG ATAATAGTAT CAAATCCCGG GGTATCATAC ACGACGTAGG      300
CTCCTTTAGC GACCTTACCA AAGTCTGTCC CTTCTTCAAC TACCAAGTTT TGACGGGTTA      360
AGACAATGAC AGTTGGAGTG GTGGTACTGG TCAAGGCATG ATGCCAAGTC GCTTGAGTTT      420
CACGGGCATC CGCTGGACGG ATAACAGTCA AGTTTGGCAT TGAGCGTAAA CCTGCCAAAT      480
GTTCAACTGG TTCATGAGTT GGACCATCTT CACCAACGGC AATTGAATCA TGGGTAAAGA      540
CATAAGTTAC AGGCAACTCC TGAATGGCTG ATAGCCGAAT AGCAGCTTTG ACGTAGTCAG      600
AGAAAACAAA GAAGGTTC CG CCATAAACTC GTAAACCACC ATGAAGAGCC ATTCCATTGA      660
GGATTGTTCC CATGACAAAT TCACGTACCC CAAACTGAAT ATTGCGGTTT AATGGATTAT      720
ATTTATCTTG TAAGCCATCT GCCTTGATGT AGGTCATGTT GGAGTGAGCT AAGTCTGCCG      780
ATCCACCTAA GAAGGTGGT AAAACTGCTG CTGTATTAAAT AGCATCTTGG GACGAATTAC      840
GAGTTGCTTG AGAGAAGCCA TTCTCATAGA CAGGGAAGTC TTTTTCAGTA ATGGTTACAG      900
GGGATTTTCC AGTACAATAG CGTCAATCTC ACTAGCAACT TCGGGATAAG CAACCTTGTA      960
ATCAGACACC AAATAGCCC AAGCATCGTA TGCCCTCCTGA CCACGATCCG CTACATTTGT      1020
CTTGAAATCA GAATATACTT CCTCTGGTAC TTCAAATGGA TCGTAATCCC ATCCCCAAAA      1080
CTTACGAGTT GCTCCTGTTT CTTCTGTCTC TAGTGGTGCA CCATGAACAG CATTTGTACC      1140
ACTTTTATTG GGTGAGCCGT AACC AATTAC CGTTTTCACT TCAATCAAAC ATCGGCTTGC      1200
CTGAAACTTT JGCTGTTTCG ATAGCAGCAT GGATGGCTTC CAAGTCTGTT CCATTTTCAA      1260
CCAAGGCAGT ATGCCAACCG TAGGCATTGT AACGGTCACG AACACTTTCT GTAAAGGAAT      1320
CCTTTGTCTC ACCATCCAAG TTGATATCAT TTGAATCATA AAGAACAACC AACTTATCAA      1380
GTTTTTGCAA GCCTGCGTAT GAAGCTGCCT CGCTTGAGAC ACCTTCCATC AAGTCTCCGT      1440
CTCCACAGAT AACGTAAGTA TAGTGGTCAA AGATATTGTA GCCTTCACGG TTATATTGCG      1500
TGCCAAGAA ACGTTCTGCT TGGGCAAAAC CAGTAGCAGT TGAAATCCCT TGCCCTAGAG      1560
GACCTGTCTG AGCATCAATC CCTGCCGTAT GACCAAATTC TGGGTGACCT GGTGTTTTTG      1620
AACCCCATTG ACGGAAGCTC CTTAATCTCA TCCATGCTGA CATCTTCAA AACCAGAAAG      1680
GTGAAGAAGA GCATAAAGGA GCATTGAACC ATGACCTGCT GAAAGAATAA AGCGGTCG      1738

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(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

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CTTGGGAGCT ATTTTGCTTA GTTTTGCGCT TATTCCTCAA CTGGGCTGGG GACGTGGTCT    60
TTTtagttcc ATTTTCTAG CGATCTCAGC CTTCTGTAAT GCCGGTTTTG ATAATTTAGG    120
GAGCACTAGT TTATTTGCTT TTCAGACAGA TTTACTGGTC AATCTGGTGA TTGCAGGCTT    180
GATTATTACA GCGGGCCTTG GTTTTATGGT CTGGTTTGAT TTGGCTGGTC ATGTAGGAAG    240
AAAGAAAAAA GGACGTCTGC ACTTTCATAC GAAGCTTGTA CTATTATTGA CTATAGGTTT    300
GTTGTTATTT GGAACGGCAA CTACTCTCTT TCTTGAGTGG AACAATGCTG GAACGATTGG    360
CAATCTCCCT GTTGCCGATA AGGTTTTAGT TAGCTTTTTT CAAACAGTGA CGATGCGAAC    420
AGCTGGCTTT TCTACGATAG ATTATACTCA GGCTCATCCT GTGACTCTTT TGATTTATAT    480
CTTACAGATG TTTCTAGGTG GGGCACCTGG AGGAACAGCT GGGGGACTCA AGATTACGAC    540
ATTTTTTGTC CTCTTGGTCT TTGCACAAAG TGAGCTTTTA GGCTTGCCCTC ATGCCAATGT    600
TGCGAGACGA ACGATTGCGC CGCGAACGGT TCAAAAATCC TTTAGTGTCT TTATTATCTT    660
TTTGATGAGC TTCCTTGATA GGATTGATTC TGCTAGGGAT AACAGCCAAA GGCAATCCTC    720
CCTTTATCCA CCTCCATATT TGAAACCATT TCCAGCTCCT TAGTACAGTT GGTGTTAACG    780
GCAAACTCTGA CTCCCTGACC TTGGGAAATT                                810

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(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

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CTCAACCCTG GCATGGAAAA TATCCATGTA GCGGCTGGAG ATTTGCTTAA GGGTGTGGAA    60
ATTGAGGCAG ATGTGATTGT GGCTAATATC TTGGCGGATA TCCTCATTCA TCTAATAGAC    120
GATGCCTATC GTTTGGTTAA GGACGAAGGC TACCTGATCA TGAGTGGCAT TATCAAGGAT    180
AAGTGGGACA TGGTGC GCGA GTCGGCTGAA TCAGCTGGAT TTTTCCTCGA AACTCACATG    240
GTTCAAGGGG AATGGAATAC CTGTGTCTTT AAGAAAACCA AGGATATCTC TGGTGTGATT    300

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GGAGGCTAGC	ATGCAGCAGT	ATTTTGTA	AGGCAGTGCT	ATCTCTCCTG	TCACTATCGA	360
GGACAAGGAA	ACCAAGTAAGC	ATATGTTTCA	GGTTATGCGC	TTGAAAGAAG	AGGATGAGGT	420
TACCTTAGTC	TTTGATGATG	GCATCAAGCG	CTTGCGCGCG	GTGCTGGATA	TGGAAAATCG	480
TCAGTTTGAG	TTGGTCCAAG	AATTAAATGA	CAATGTGGAA	CTACCAGTCC	AAGTGACCAT	540
CGCATCTGGA	TTTCCCAAGG	GAGACAAGCT	GGAGTTCATC	GCTCAAAAAG	TAACCGAACT	600
GGGTGCTAGC	CAAATCTGGG	CCTTTCCTGC	AGACTGGTCA	GTTGCCAAGT	GGGATGGCAA	660
GAAATTGGGT	AAAAAAGTTG	AAAAACTAGA	AAAAATTGCC	CTTGAGCAG	CCGAGCAAAG	720
CAAGCGTAAT	ATTGTACCAA	GTATTAAACT	TTTCGAGAAA	AAAGCAGATT	TTCTAGCTCA	780
GCTGGACCAG	TTTGATTCTA	TCATAGTAGC	CTATGAAGAA	TCAGCTAAAG	AAGGAGAAGC	840
CGCTGCGCTT	CTGCAAGCAG	TCACTGGTCT	TGAAACAGGA	GCCAAACTGC	TCTTTATCTT	900
TGGTCCAGAA	GGTGGTCTGT	CACCTGCAGA	AATCGAAAGT	TTTGAAGCTA	AAGGAGCAGT	960
TTTGGCAGGC	CTAGGTTCTC	GTATTTTGCG	AGCAGAAACA	GCACCGCTTT	ACGCCTTATC	1020
AGCCCTTAGT	GTTTTAGTAG	AATTAGAGAA	ATAAGAGGAA	GAAAATGGAA	CAAAAACACC	1080
GTTCAGAATT	TCCAGAGAAG	GAACCTCTGGG	ACTTAACAGC	CCTATACCAA	GACCGTGAGG	1140
ATTTCTTGCG	TGCAATCGAG	AAAGCTCGTG	AAGACATCAA	CCAGTTTAGC	CGTGATTACA	1200
AGGGCAATCT	TCACACTTTT	GAGGATTTCTG	AGAAGGCCTT	TGCGGAATTG	GAACAGATCT	1260
ACATTCAGAT	GAGCCATATT	GGCAACTATG	CTTTTATGCC	TCAGACGACG	GACTATAGCA	1320
ATGACGAATT	TGCCAATATT	GCCCAAGCTG	GGATGGAATT	TGAAACAGAT	GCCAGCGTAG	1380
CCTTGACCTT	CTTTGACGAT	GCCTTGGTGG	TAGCAGACGA	GGAAGTCTTG	GACCGTTTGG	1440
GTGAATTGCC	TCACCTTGACG	GCAGCTATTC	GTCAGGCCAA	AATCAAAAAA	GCCCACTATC	1500
TAGGGGCTGA	TGTGGAGAAG	GCCTTGACCA	ATCTCGGTGA	AGTTTTCTAT	AGTCCGCAGG	1560
ACATTTATAC	TAAGATGCGA	GCTGGGGATT	TTGAAATGGC	TGACTTTGAA	GCCCCATGGCA	1620
AGACCTATAA	AAACAGCTTT	GTCACCTATG	AGAATTCTAC	CAAAATCACG	AGGATGCTGA	1680
GGTTCGGGAG	AAATCCTTCC	GTTCTTCTC	AGAGGGACTT	CGGTAAGCAC	CAAAATACGG	1740
CTGCAGCAGC	CTATCTGGCT	CAGGTCAAGT	CTGAAAAACT	CTTGCTGAT	ATGAAGGGAT	1800
ACGACTCTGT	CTTTGATTAT	CTTCTAGCTG	AACAAGAAGT	GGACCGTGTC	ATGTTTGACC	1860
GCCAGATTGA	CCTCATCATG	AAGGACTTTG	CACCAGTCGC	TCAGAGATAC	CTCAAGCATG	1920
TTGCCAAGGT	AAATGGTCTT	GAAAAGATGA	CCTTTCGAGA	CTGGAAATTG	GACTTGAGACA	1980
GCGCCCTGAA	TCCTGAAGTG	ACTATTGACG	ATGCCCTATGA	TTTGGTCATG	AAGTCGGTAG	2040
AACCTTTGGG	GCAAGAATAT	TGTCAGGAAG	TTGCTCGTTA	CCAAGAAGAG	CGCTGGGTGG	2100
ACTTTGCTGC	TAACAGTGGC	AAGGATTCCG	GTGGTTATGC	GGCGGACCCA	TATCGCGTAC	2160
ACCCTTATGT	ACTCATGAG					2179

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTTAAGGTTT	TCTTCNATAC	TTTGGTTTTC	AATTAACCCA	NAGTTCCTGA	AGAGGTAGCC	60
CAATTCNTGA	CGGAGAAAAT	CNCTCGAGTT	ATNATTGGCC	AAGTCTTTAC	CTCGGTAANA	120
AATCGTCCCA	GCATAAGGTT	CTAATTTCCC	AATCATGTTT	ATCAAGGTGT	TTTCCGCTAT	180
CACCTGAACC	AATTAAGGCA	TAGATTTTCC	AGCCTCAAAT	GTCATTGAAA	GATTCGAAAA	240
TAATCTCTCGT	TCTCCAAAAG	ATTTACTCAC	CTGTTTAAAGT	TCAATCATAT	TAACCTCCCT	300
TCAAAACAAG	AATGGACATC	TTGTTTTCTT	TCTGCATTTG	GACATGTAAC	TGTAAGAGAG	360
ATAGACCAGT	AAAGAGTAAC	AAGACTAAGA	AAGCAACTCC	TATCTCTACC	TGAAGAAATA	420
CACCTGCAAC	AAATCCCAGT	AAAAACACAC	CCAGTTGAGC	AAAGAGATAA	GTGCGATGGA	480
TTTCTAAGAA	CCTGAGACCT	GCAATGCGTT	TGATAAAAAT	GGCAGCTCTA	AATTCTTCAA	540
AGTAGAGCCT	ATTCATAGTG	TTAAACAACA	AGATTGAAGT	TGCAATCCCA	AGCACAGCTC	600
CTGCTAGCAT	TACCCAACGT	TCCCTCTGGA	TATTATCCAA	TAATGTGATG	TAGTTGTGGT	660
AACCTGTTTG	CATTTCTGAG	ACCCAATTTT	CAATGCCTTG	TCTCTGGATA	AGCTCCTGGG	720
CATCAGACAA	TTGATTAAAG	AGAACGTAGT	TCTGTACTGC	GTCTATCCAA	AACAAAATGG	780
ACTGTGGACC	AGTTGATTGG	GGTGTATATA	CAATGATGAT	TGGATCTTTC	AAAAACTGCT	840
GGTAAGAAAT	AGGGGTCGTA	TTATACACAA	AACGATCCTG	ACCTGATTCT	AAATAACCTA	900
CCGTAGCAGT	CATTTGCTGT	CGTTCATCTT	GACTAGACAT	GCGACTGGTT	AAGTCGTCTT	960
CAAAAACAGA	TTTATAATGT	TCTTCCTCTG	AACGGAGGTG	TTCAGGCAGC	AATAAGACAA	1020
ACTCCCCTAC	ATCAAGGTGA	TTCATCTTTT	GCTCAATAGT	TGTATCTACA	GGAATGTTTT	1080
GACGCTCCAA	GTATTGCGGT	GTGACGATAA	GGACATTGCC	ATTCGGGTTG	TAATCGTGCC	1140
ATTCTGTAGA	GGTTATCAAG	TTTTTGGAGG	AAGCCATGCC	ATTTTGCAAA	GTACGGTCAA	1200
TTAACTGGTG	TCTAGATAAG	AAAGCCTTTT	GTTCTGAAAC	AGCCAGATCC	ATCAATTGAT	1260
ACCAAGTTCT	GAGTTTCCTT	TGAGCTTGTT	CATCAAAACC	AGGACTCGTT	CCTTCACGGC	1320
TGATTGATAG	GGTAATCAGT	TGCCCTTCCCT	GACTCCAAAAC	CTCTTGTTCCA	ATCCGATGCT	1380
GTTGCCAGGC	TTGGGAATAC	TTTAAGCTAC	TCCCTATTCC	CAGCGTTACA	ATAATAATCG	1440
CTAATAGTTG	ACCGATTAAA	ATCAAACTAA	TGATTCTCTT	GACAGGCACT	TGCCCTTTTA	1500
TAATCTGCAT	CAGGTGTATC	TTTTTTATCC	CAACTGCGAA	GAGTTGAGCG	AAAAACAGGG	1560
AGATCGACAA	CAAGATGAGA	TTATAACTGA	GCAAGCCTGC	TCCTATGGTC	ATTAGGGATT	1620
GCGTTGGAAG	CGACAGAATT	TTTTGCATAA	GAATGGCGAG	CACGCCAGCT	AAACTGAAAC	1680
CAACAGCTAT	CCCTTTCAAA	TCCTCACCAA	CTGGTCTAAG	GAAAAATGGAC	CACCGTTTCT	1740
CTCCTGAAAT	GAGGCCAATG	CCCGACGACC	GTAATTGGCT	AATTTGACTA	ATTAAAGTCA	1800
GTGCTACAAA	GGTTAAGATG	AAAATCAATA	GACTGATTAA	CTGAAATCCG	TTACTAAAGA	1860
TAGCCATTAA	CGTAGATAGT	TTAGATGGAA	TTGTCAGGTT	CATATTAGTC	AAGCCAAGTT	1920
GACTTAGCTC	CTCCCTTAGC	AAGTGAATAT	CTAGGTGTCC	ATCGAATACA	AAATAGTTTG	1980
TTTCAACACT	ACTACTTTGA	GCATCTTCTA	GTTTTTTTTC	CTGAAGCCCA	TCAGGCAACT	2040
TTCCGTCCCC	AAAGGTTGTA	TAAGAAAAAA	CTGTAGTACC	TTCTGAGTTA	GGATCTTGTT	2100
GTTGAATCGC	AATAAAGCTA	TCTGTTTCTT	CTGCTAGTTT	TTCCAAGCGT	GTAGCAACAT	2160
GCTGAAAAGT	TGTTTCAGGG	GAAGAATCAT	GTACAACAAC	GTTGGGGTAA	TAATAGGAGA	2220
CATATGTATC	AGTCCAAATG	GTAAATACCC	AAACAAAGAA	CAAACTAGCA	AGCAGGTTGG	2280
ATATGAGTAT	AAATAATTTT	TTCATAGTGC	ATTCCTTATT	CTAAAACAGA	GGGCAGAAAT	2340
ACGCCACCC	TCTATAAACT	AACAAGTTTA	CTAAACTATT	GATAAAAGAA	TCTTCTTCAA	2400
TTATTCTTTA	CCATCCCGCA	TCAAATGTAA	ATTTTAAACAT	ATTATTTACT	CCTCTGAAAT	2460

GAAATTTATG AAAATGAAGC GAAAATGGCA ACTACATATT TTAATCAGAA AATCTCAGTC 2520
TGAATTATAG TATCCTATTT TTCCCCTCCT TTCCTAACCT GGCACGTTCC TTTCT 2575

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTATTCGGAA TAAGAAAAAT GCCAGTATGG TATTGGCAGC CAAGGCTGTC AAAGATGGTG 60
AAGCAGACGC TGTCCTTTTCG GCTGGGAATA CAGGTGCTTT GTTGGCTGCT GGATTCTTCA 120
TCGTGGGTCG TATCAAGAAT ATCGACCGTC CTGGACTTAT GTCAACATTG CCGACTGTAG 180
ATGGGAAAGG TTTTGACATG CTTGACCTCG GTGCTAATGC AGAAAATACA GCCCAGCACC 240
TCCATCAATA CGCTGTCCTA GGTTCCTTCT ATGCCAAGAA TGTTCTGTCG ATTGCGCAAC 300
CACGTGTTGG TTTGCTCAAC AACGGAACAG AGAGTAGCAA GGGCGACCCG CTTCTGTAAG 360
AAACTTATGA ATTACTGGCG GCTGATGAAA GTTTGAACTT TATCGGAAAC GTGGAAGCGC 420
GTGATTTGAT GAATGGCGTT GCAGATGTTG TTGTGGCAGA TGGTTTCACG GGAAACGCTG 480
TGCTCAAAATC CATCGAAGGG ACAGCTATGG GAATCATGGG CTTGCTCAAG ACAGCTATTA 540
CAGGTGGTGG TCTTCGAGCG AAAC TAGGTG CCCTCCTTCT CAAGGACAGC CTCAGAGGTT 600
TGAAAAACA GCTCAATCAT TCAGATGTTG GTGGAGCGGT CTTGTCTGGT GTCAAGGCAC 660
CTGTTGTCAA GACTCATGGC TCAAGCGATG CCAAGGCTGT TTATAGTACG ATTCGCCAGA 720
TTCGTACCAT GCTAGAAACA GAAGTAGTTG CCCAGACTGC GCGTGAATTT TCAGGAGAAT 780
AAAAGAGATG AAAGAAAAAG AAATTTTGA CAGTATTGTG ACCATTATCC AAGAGCGACA 840
GGGAGAGGAC TTTGTCGTGA CAGAATCCTT GAGTCTGAAA GACGACTTGG ATGCTGACTC 900
AGTTGATTG ATGGAGTTA TCTTGACGCT GGAGGATGAA TTAGTATCG AAATCAGCGA 960
TGAGGAAATT GACCAACTCC AAAGTGTAGG AGATGTGGTT AAAATCATTG AAGGAAAATA 1020
GCAATCGGAG TTCCAAGTCA ACGGAAGTAG ATGGTTTTTA GAAATGAGAA ATATCGGACA 1080
AGCTGGTAAA ATCTTGGCTG ACAGTGGTTA TCAAGGGCTC ATGAAGATAT ATCCTCAAGC 1140
ACAAACTTCC ACGTAAATCC AGCAAATCA AGCCGCTAAC AGTTGAAGAT AAAGCCTGTA 1200
ATCATGCGCT ATCTAAGGAG AGAAGCAAGG TTGAGAATAT CTTTGCCAAA GTAAAAACGT 1260
TTAAAATGTT TTCAACAACC TATCGAAATC ATCGTAAACG CTTCCGATTA CGAATGAATT 1320
TGATTGCTGG TATTATCAAT CATGAAGTAG GATTCTAGTT TTGCAGGAAG TCTAATAGTA 1380
AAAAAGTGAT TAGAAAACAT CTTTTTTAAA AATAGAGATG ATTTTGAAAC AAAAAAGCTA 1440
ATTCAAGACG TTTTCATGCC AATTCAAGAT TTGGATGAAA AAAATTAATA GATACTGTTA 1500
TACTAACTT GTCAAGTTG TAACAAGACA AATATTAATA ATAAAAAGA GGTATTCGTT 1560
ATGAATACAA AAAAGATGTC ACAATTTGAA ATTATGGATA CTGAGATGCT TGCTTGAGTT 1620
GAAGGTGGCG GATGCAATTG GGGAGATTTT GCCAAAGCAG GTGTTGGAGG AGGAGTAGCA 1680

CGAGGTCTTC AG

1692

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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CCACGTTGGG GTCTTAGTAC CTGCTGATGA CGGTTTCTTA TTTGTAGAGA AATTGACTTT      60
CGAAGAGCCC TACCAAGCGA TTAAATTTGC TAGTAAGGAA GATTGCTACA AGTATTTGGG      120
CACCAAGTAT GCGGATTATA CAGGCGAGGG ACTGGCTAAG CCTTTTATCA TGGATAATGA      180
TAAGTGGGTT AAACCTTTAAT AGTGTTATGA TATGACAGTA ATCTTAGGAT TTTTATTTCT      240
ATTTTGTATA AGTTGGTGGG TTATTTCAAT CGTTAATAGC CAGAAACCAC GCAAAAATGA      300
AACATTTATT GGCTATGTCC AAAGATACGA TATTGATGGG AATGCCGTGA TCAATCAATA      360
ACCGTGTCCT TCAGAACTGA GAGGAGTTCT TGAAATCGTA AAACCACTTT GAACAAGAGT      420
AACTTCAACC CATCGGCTCC GACGGATTAA GTGCTTTCGT GAATACCAA ATCAGCCGCA      480
ATTTCTTCAT AAGTGCATA TTCTCGCACA TATTGAAGAG TGGCCATAAG AAGGTCTTCT      540
AGGCTTAATT TAGGTTTTCG TCCACCTTTT GCGTGTTTAA GTTGATAAGC TGTTTTTAAT      600
ACAGCTAACA TCTCTTCAA AGTCGTGCGT TGAACACCAA CAAGACGCTT AAATCGTGCA      660
TCGGTTAGTT GTTTACTTGC TTCATCATT ATAGAACTAC TATACCATAT TTTATTTTCGC      720
AGGAAGTCTG ATCTCATCCG GTTTTGCTTG ACGGGCTTTT GCGGTTATTT CTTCAAAAGG      780
GACCCACCAG ACTGGCCCAC AGCCCTTGAG ACCGTGGCCA TTCATATCAC CTCTTCGTCT      840
AGGGAAAAGG TGCCAGTGGG GATGGGCATC GCCATTTCTT AGAAGTTCAA TATTCATTTT      900
CTCAGCAGTA AAGGCCTTGG CAACTGCCTC TTGGACTAAA CTCATTTCTT CTAGAAAATG      960
GAGTCTTG TGCTTTTCTA AAATGGTGCA ATTCGCGGAC ATGTTCTTGT GCTAAAAAAA     1020
AACTATAGCT TGCAAGCTCA ATACTGATGG TCTCCAATCA CAAGATAGCC TGTTTCCAAC     1080
TCTTTGACAA AGTAGGGATT TTCTCCCTTC TTGATGA                               1117

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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTACAGCGTA	GAGTTCAGGG	TATTCAATTG	AAATGCGTTT	AATCGTACGT	GTTGTAGCAT	60
GTTTTCTGAC	AAAAAACGGG	ATTCGCTTAA	TCAAGTCTTG	TGGGACTAGC	GCCAGAATCT	120
TCTCAGTAGT	TTCTTTGTCA	CTAATATNAG	ACATTGCAAG	CCTTTTCTTA	ATCATTTCCT	180
GTTCTTTTTT	TGTAATACT	TTTAATTCCA	TTGATTAGT	CCTCCTATTT	TCTCTAAGTT	240
AAATTATGTA	CTAATACNGA	TGAAACTACA	AAGAATAAAC	TTTAAGAAAT	CTTCTCACTG	300
ATCAAGATTT	CTTACTTTCC	AATAGACTTC	CTGCGAAACA	AAATATGGTA	TAGTAGTTCT	360
ATGAATGATG	AAGCAAGTAA	ACAACTAACT	GATGCACGAT	TTAAACGTCT	TGTTGGTGTT	420
CAGCGCACGA	CTTTTGAAGA	GATATTAGCT	GTATTAAAAA	CAGCTTATCA	ACTTAAACAC	480
GCAAAAGGTG	GACGAAAACC	TAAATTAAGC	CTAGAAGACC	TTCTTATGGC	CACTCTTCAA	540
TATGTGCGAG	AATATCGAAC	TTATGAACAA	ATTGCGGCTG	ATTTTGGTAT	CCACGAAAGC	600
AACTTAATCC	GTCGGAGCCA	ATGGGTGAA	GTAACCTTG	TTCAAAGTGG	TGTTACGATT	660
TCAAGAACTC	CTCTCAGTTC	TGAGGACACG	GTAATGATTG	ATGCGACOGA	AGTACAAATC	720
AATCGCCCTA	AAAAAGAAT	TAGCGAATCA	TTCTGGTAAA	AAGAAATTC	ACGCTATGAA	780
GGCTCAAGCG	ATTGTCACAA	GTCAAGGGAG	AATTGTTTCT	TTGGATATCG	CTGTGAACTA	840
TAGCATGATA	TGAAGTTGTT	CAAAATGAGT	TGCAGAAATA	TCGGACAAGC	TGGTAAAATC	900
TTGGCTGACA	GTGATTATCA	AGGGCTCATG	AAGATATATC	CTCAAGCACA	AACTCCACGT	960
AAATCCAGCA	AACTCAAGCC	GCTAACAGCT	GAAGATAAAG	CCTATAACCA	TGCACTATCT	1020
AAGGAGAGAA	GCAAGGTTGA	GAACATCTTT	GCCAAAGTAA	AAACGTTTAA	AATGTTTTC	1080
ACAACCTATC	GAAATCATCG	TAAACGCTTC	GGATTACGAA	TGAATTTGAT	TGCTGGCATT	1140
ATCAATCATG	AACTAGGATT	CTAGTTTTC	AGGAAAGTCTA	TTAAAAATTG	AGAAATTAAA	1200
AGAGATGATA	TTAGGGAGAA	CTGATTTAGG	CAAAGTGTCT	CCCCTAGTTA	CGACATAAAG	1260
AAGCATAAAT	CGATAATATT	TATGTTTCTT	TACTAGTGAA	ACGCCTAGCC	AAATTACCAT	1320
AGTTACGACG	TCATGGATCC	TCTAAATCGA	TTATATTTAG	GGGTCATGAC	TAGTGAAGCA	1380
GTTAG						1385

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTGAGAAAAG	TGGTGGTTGT	TCGATTAGAA	AAACCAGTAA	CTTTTCACAA	TATGATAGCT	60
CCTGATAAGG	AAGTAGAAGT	ATCCTTGCTC	TTCTTTATCA	TCAATAACTC	AAGTTCAAGT	120
CAAACAAATA	TTCTGGCTCA	GTTGATGGAC	TTTTTCACAG	GAAATGGACA	TCTTGAAGAC	180

CTATCAAAAA	TTTCCGAACC	AGAAAACTT	TATGCTTACA	TTGCTGAAGC	AACCGCTTAA	240
TCTTGTCTAT	TAAAAAATAA	AATCGGAGGA	AATCTAAATG	ATTAAAAATC	TTGCTGCCTG	300
CGGTGCAGGT	GTAACTCAA	GTACCAAAT	TAAAAGTGCT	CTAGAAGAAG	AACTTTCAAA	360
CCGTGGTTAT	GATGTTCACT	GTGATGCAGT	CATGGTGAAA	GATGTAAACG	AAGACCTTAT	420
GAAAGGTTAC	GATATCTTTA	CACCAATCGC	TGCAACAGAT	CTTGGTTTTG	AACCAGGTAT	480
CCCAGTTATC	GAAGCTGGGC	CAATCTTATT	CCGTATACCA	GCAATGAGCG	CTCCAGTATT	540
TGACAATATT	AGACTCCCTG	CGAAACAAAA	TATGGTATAG	TAGTTCTATG	AATGATGAAG	600
CAAGTAAACA	ACTAACTGAT	GCACGATTTA	AGCGTCTTGT	TGGTGTTTCT	CGTACCACTT	660
TTGAAGAGAT	GTTAGCTGTA	TTAAAAACAG				690

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTCATCCTG	CCATACGGTC	GGTAATTGAC	CTGCTGACAT	CCGAAACCTC	CCTTAAATCG	60
CATTCTTGTC	AAAACCGAGT	TTGCGTTGAA	TAAACTTAGC	GATTTTCGACG	ATGATAATCA	120
TTGAGAAGCT	TCCAGCCATA	ACAATTCCCC	ATTGTGACAA	GTCTAGTTTG	GTTACGTGGA	180
AAATTCCTTC	AAGCGGTTCT	ACAACGATTG	TCGCCATGAG	AAGGATAAAG	GATACCACCA	240
TGGACCAGTT	AAAGGTCCTA	TACTTGAATG	GGCTAGTGAT	GGACTTAGAA	TAGGTGATTT	300
GGAGCGTCCT	ATTGGCTAGG	AAATGCTGAT	CATAGTCCTT	TGCTGAGGCT	AGGGTGTTTC	360
AACATTCAAC	ACTCAACTGG	TTGATCTAGT	TGATAGGAAG	GGAATTACTA	TAAAATACTC	420
AGGCTTCCAT	CATATTTTTT	GAAACGATTG	TGTAATCAAA	ATGTACCAAT	ATTGTAGTAT	480
TAGTACAGAA	GATGTTGTGA	ATGGATAAAT	ATATCATAAC	TGCTGTCTCA	AAAAGATTTT	540
ATATGTCTGT	GCATATATAA	TAGACTTCCT	GCAAAACTAG	AATCCTAGTT	CATGATTGAT	600
AATACCAGCA	ATCAAAATTC	TTCGTAATCC	AAAGCGTTTA	CGATGATTTT	GATAGGTTGT	660
TGAAAACATT	TTAAACGTTT	TTACTTTGGC	AAAGATGTTT	TCAACCTTGC	TTCTTTTCCTT	720
GGATAGCGCA	TGGTTACAGG	CTTTATCTTC	AGCTGTTAGC	GGCTTGAGTT	TGCTGGATTT	780
ACGTGGAGTT	TGTGCTTGAG	GATATATCTT	CATGGGCCCT	TGATAATCAC	TGTCAGCCAA	840
GATTTTACCA	GATCTNNTTT	TTTAAAAGGG	GCCT			874

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

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CTTCATCCTG CCATACGGTC GGTAATTGAT ATGCTGACAT CCGAAACCTC CCTTAAATCG      60
CATTCTTGTC AAAACCGAGT TTGCGTTGAA TAAACTTAAC GATTTGACG ATGATAATCA      120
TTGAGAAGCT TCCAGCCATA ACAATTCCCC ATTGTGACAA GTCTAGTTTG GTTACGTGGA      180
AGATTCCTTC AAGCGGTTCT ACAACGATTG TTGCCATGAG AAGGATAAAG GATACCAAGA      240
TGGACCAGTT AAAGGTCTTA GACTTGAATG GGCCAACTGT CAAGATGGAT TGGTAGACAG      300
ACTTGACATT GTAGGCATGG AAGAGCTGAA TCAAACCAAG GGTGCAAAG GCCATCGTTA      360
GGGCATCTGC ATGAATAGCA TGATTGTCAC CCACATGAAC TGGGTAAGCA ATCGCAAGGC      420
CATAAACACT CATAACAAGA GCTGCTTGA GTACACCTTG ATAAATGATA GAACTCAAAA      480
CACCACCTGA GAAGAAGCTT GCCTTGCGTC CACGTGGTTT ATGATTCATG ACACCAGGTT      540
CTGCAGGTTT AACACCACAG AACGATAGCT GGAAGGTAT CCGTTACCAA GTTGATCCAC      600
AAAAGATGAA CCGGCTGTAA GACATCCCAA CCAAACAAGG TTGATAGGAA GATGGTTAAT      660
ACTTCAGCAG TATTAGCAGA AAGTAGGTAC TGAATAGTCT TTTGAATGTT TGAGAAGACC      720
TTACGTCCTT CTTCCACTGC GACGATAATA GTCGCAAAGT TATCATCTGC AAGAATCATA      780
TCAGAAGCCC CCTTAGAAAC CTCTGTACCA GTGATTCCCA TACCGATACC GATATCGGCT      840
GTTTTCAGAG CTGGCGCGTC ATTGACACCG TCACCTGTCA TGGCAACGAC TTTACCTTGT      900
TTTTGCCAAG CCTTGACGAT ACGAACCTTG TGTTCTGGAG ACACACGGGC ATAAACAGAG      960
TATTGACCAA CGACTTTTTC AAATTCTTCA TCTGACAGTT CATTGAGTTC AGCACCAGTT     1020
AAAACGTGAC CTTCTGTATC GTTTGCGTCA ATGATTCCCA AACGTTTGGC AATGGCTTCC     1080
GCTGTGTCTT GGTGGTCACC TGTAATCATA ATTGGACGGA TTCCCGCTTC CTTAGCCACA     1140
CGAACAGCCT CAGCGGCTTC AGGACGTTCA GGGTCAATCA TCCCAATCAA ACCAGTAAAA     1200
ATTAAATCAT TTTCAAGCTC TTCAGAAGTG AGATTTTCTG GAATACTATC GATAATCTTA     1260
TAAGCACCTG CAAGGACACG CAAGGCTTGA TGAGCCATTT CAGAATTGTT TGTATGAATG     1320
AGATTTGTAA CCTTCTCATC AATCGGAGCA ATATCCCCAG CCTTATCAGC AAAGAAGACA     1380
ACGTTTTAAG AGTTGGTCTG GCGCACCTT GACTGCTACA AGGAAACGAC CATCTGGCAA     1440
TGGGTGAACT GTTGACATGA G

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(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2445 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTCCCATCAA	GCTTGCTTCA	AGTTTTTCTG	TCAAGGCTTG	CGCTTCTTCA	TCCTTGACAT	60
TAACAGTAAT	CAAATGCACA	TCAAATGGTG	CCAATTCTTT	AGGGAAATTG	ATTCCCCAAG	120
CGTAACGGTA	TTCACCTTTT	GGCGTTTTGT	TAAACAAAGA	GGCGAGCGTG	TTGCTCCATC	180
ACTGCTGAAA	GAAGACGGCT	GACACCGATA	CCGTAACATC	CCATGATGAT	TGGCACAGCA	240
CGACCATTTT	CATCCAAGAC	ATCTGCTCCC	ATGCTTGCTG	AATAGCGAGT	TCCGAGTTTG	300
AAAATATGAC	CGATCTCAAT	ACCACGCGCA	AAGTTAAGGA	CACCTTGTC	ATCTGGGGAA	360
ATTCACCCCT	CACGAACTTC	ACGGATATCC	ACATATTCTG	CAGTAAAATC	ACGGCCTGGG	420
TTCACACCAG	TCAAGTGGA	GCCATCTTCG	TTAGCACCGA	CAACTGCATT	GCGAACATCT	480
TGCACCTTAC	GATCTGCAAT	AATTTTAATA	TTCTCTGGCA	AACCAACTGG	TCCAAGTGAA	540
CCAAATCCTG	CTTGAACAAC	ATTGCGCACT	TCTTCTTCGC	TAGCAACGTC	AAAGAAATTT	600
GCTCCCAAGT	GATTTTTC	CTTGACTTCG	TTGAGTTGGT	CATTTCCAAC	TAGAAGGGCT	660
GCAACAAGCT	CACCATCTGC	AATGTAGAAG	AGGGTTTAA	TCGTTTGTTT	TTCTGGAACA	720
TTGAGGAAGG	CTGCAACTTC	ATCAATTGAT	TTAACATCTG	GCGTTTCAAC	ACGAGTAACT	780
TCTTCTTCAG	CGACAACACG	GTTGCTTGGT	TTGTACTCGT	TTGTTGCCAT	TTCTAAGTTA	840
GCTGCATAGC	TAGACTCACT	TGAGTAAGCA	ATGGTATCTT	CACCAGAGAC	TATCCATTTG	900
AGCAATTCTG	CCTTGATTTT	TTCTTGCACT	TCTGCAGGAA	TTTCGTCAAA	TGAGGCAACT	960
GACTTGTC	AGACAACCCA	GCGGTCAAGG	TCTGTACGAG	CAGATGTAAT	GGCCATAAAT	1020
TCTTGCTAT	CCTTACCACC	CATGGCTCCA	CCGTCACCAA	TAATAGCCTT	GAAGTCTAAA	1080
CCACTACGAG	TGAAAATACG	CTCATAGGCT	GCTTTGTACT	CATCATAAAC	ACTATCCAAA	1140
CTATCATAGT	TAGCGTGGAA	ACTATAAGCA	TCCTTCATGA	TAAACTCACG	TGTACGAAGA	1200
AGTCCATTAC	GTGGGCGTTT	TTTCATCACGA	TACTTGGGCT	GAATTTGATA	AAGGTTGAGT	1260
GGCAATTGCT	TGTAAGATTT	AACAGAATCA	CGGACAATAG	CTGTAAAGGT	TTCTTCGTGA	1320
GTTGGACCTA	AGATAAAGTC	TGATTTTTC	CGGTTTTTCA	GTTTGTAAG	GTCTTCACCA	1380
TAGGTTTCGT	AACGACCTGA	TTACGCCAC	AATTCTGCAC	TAAGAAGGGC	TGGAGCCAAC	1440
ATCTCAACAG	CACCAATCTT	TTCAATTCT	TGGCGCATGA	TGTTTTTAGC	TTTTTCAATC	1500
ACACGGTTGG	CAAGTGGTAG	ATAAGAATAA	ACACCTGCTG	AAACTTGGCG	AACATAACCA	1560
GCACGCAACA	TAAGAGCATG	GCTGATAACT	TGAGCATCGC	TTGGCATTTC	GCGAAGCGTT	1620
GGGATAGGCA	TTTACTTTG	TTTCATAATA	TTCTCGATT	ATCTAAAAAA	GAGTCGCATA	1680
ATGTCATTCC	AAGTCACAGC	AATCATCAAG	ACAACCATGA	TGACCACTCC	GGCCAAGGTG	1740
ACATAGGTTT	CAATTCTTG	TTCAATGGT	TGCGGCGGA	TGGCTTCTAG	GATATTGAGC	1800
ACAATCTTAC	CACCATCCAA	GGCTGGAATC	GGAATAAGAT	TAAAAATCCC	AATATTGATG	1860
GAAATCATTG	CCAAGAAGTA	CAAGAATATT	CTCAATTCCA	TTTTTAGCAG	CATCACTACT	1920
TGCCTTAAAG	ATAGCAACAG	GTCCACCCAA	CTTGTTCAAA	TCCGGTTGGA	AAATCAGATT	1980
TTTCAGAGAC	TGAAAAAATT	CCGAAGAGCT	GAGTTCAGCA	GCAGTTGTAA	AACCACCTAC	2040
AAACATGGAT	AGAAAATCTG	ACTTAACCCC	CGGTTGAACA	CCTAGAAGGT	AACGACCTTG	2100
ACTATCTTCG	GGTGTAACAG	TGACTTGTTT	GTCACCTCCC	TTTTCAGAAA	TAGTCACATC	2160
CAAAGTCGGT	GCCGTCTTAT	CTTTGGTTTC	TGTTTCCACA	GCTTGGATCA	AGCTTTCCCA	2220
GTCGCCAACC	TCATGTGAGC	CAACCTTGGC	AATTTGTGCC	GTTTCTGGTA	CTCCTACCTT	2280
GGGCCAAGGG	CACCCTTGGG	GGGCATGGAT	TATGGAACCT	GGATTGGTAT	CTAACCATCT	2340
CTGACACCAC	CCTGCATAAA	GATTAAAACC	CAAAAAACAA	CAACACCTAA	GATAAAATTG	2400
TTCATAGGAC	CTGAAAATT	GGTAATCAGT	TTGCCCCAGA	TAAAG		2445

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

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NCAGGCTANC TCTCGTCTGA ATGAAGATGG AACCTTTGCT GACAAGATTG TCATGGGACG      60
TCACCAAGGG GTCAACCAAG AGTATCCAGC TAATATTGTT GACTACATGG ACGTTTCACC      120
AAAACAGGTA GTTGCCGTTG CGACAGCATG TATTCCCTTTC TTGGAAAACG ATGACTCCAA      180
CCGTGCCCTC ATGGGAGCCA ATATGCAACG TCAGGCTGTG CCATTGATTA ATCCTCAGGC      240
ACCTTACGTT GGTACTGGTA TGAATACCA AGCAGCCCAC GATTCTGGTG CGGCTGTGAT      300
TGCTCAGTAT GATGGTAAAG TTAATTACGC AGATGCTGAC AAGGTAGAAG TTCGTCGTGA      360
AGATGGTTCA TTGGATGTTT ACCACATCCA AAAATTCCGT CGTTCAAAC T CAGGTACTGC      420
TTACAACCAA CGCACTCTCG TAAAAGTTGG TGATGTCGTT GAAAAAGGCG ATTTTCATCGC      480
TGACGGACCT TCTATGAAA ATGGAGAAAT GCGCCTTGA CAAAACCCAA TCGTTGCCTA      540
CATGACTTGG GAAGGTTACA ACTTCGAGGA TGCCGTTATC ATGAGCGAAC GCTTGGTGAA      600
GGACGATGTC TACACATCTG TTCACCTTGA AGAATACGAA TCAGAAACGC GCGATACAAA      660
GCTTGGGCCT GAAGAAATCA CTCGATCGAA ATTCCAAACG TTGGTGAAGA TGCCCTCAA      720
GACCTTGACG AAATGGGGAT TATCCGTATT GGTGCTGAGG TTAAAGAAGG TGATATTCTT      780
GTAGGTAAAG TAACACCTAA GGGTGAGAAA GATCTTTCAG CTGGAAGAAC GTCTCTTGCA      840
CGCTATCTTT GGAGACAAGT CTCGTGAAGT GCGTGATACT TCTCTTCGTG TACCACACGG      900
TGCCGATGGT GTCGTTCTGT ATGTTAAGAT CTTTACACGT GTAAATGGAG ATGAGTTGCA      960
ATCAGGTGTT AACATGTTGG TTCGTGTTTA CATCGCTCAA AAACGTAAGA TTAAGGTCGG      1020
AGATAAAATG GCCGGACGTC ACGGAAACAA AGGGGTTGTC TCTCGTATCG TTCCTGTAGA      1080
AGACATGCCT TACCTTCCAG ACGGAACTCC AGTCGACATC ATGTTGAACC CACTTGGGGT      1140
GCCATCACGT ATGAATATCG GTCAGGTTAT GGAGCCTCAC CTTGGTATGG CAGCTCGTAC      1200
TCTTGGTATT CACATTGCCA CACCAGTCTT TGATGGAGCA AGTCCTGAAG ATCTTTGGTC      1260
AACTGTTAAA GAAGCAGGTA TGGATAGCGA TGCCAAGACA ATCCTTTACG ATGGACGTAC      1320
AGGTGAACCA TTGATAACC GTGTTTCTGT TGGAGTCATG TACATGATCA AACTCCACCA      1380
CATGGTTGAC NATAAATTGC ACGCGCGTTC AGTCGGACCT TATTCAACTG TTACCCAACA      1440
ACCACTCGGA GGTAAAGCTC AGTTTGGTGG ACAACGTTTC GGTGAGATGG AGGTTTGGGC      1500
TCTTGAAGCC TACGGTGCGT CAAATGTCCT TCAAGAAATC TTGACTTACA AGTCTGACNA      1560
TATCAACGGG ACGTTTGAAA GCCTATGAAG CTATTACAAA AGGCAAAACCA ATTCCAAAAC      1620
CAGGTGTTCC AGAATCCTTC CGAGTTCTTG TCAAAGAATT GCAATCTCTT GGTCTTGACA      1680
TGCGTGTCCT AGACGAAGAT GACCAAGAAG TGGAACTTCG CGACTTGGAT GAAGGAATGG      1740
ACGAAGATGT CATCCACGTA GATGACCTTG AAAAAAGCCG CGAAAAAGCA GCCCAAGAGG      1800

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CTAAAGCAGC	CTTTGAAGCT	GAAGAAGCTG	AGAAAGCAAC	AAAAGCGGAA	GCAACAGAAG	1860
AAGCTGCTGA	ACAAGAATAA	GCAGTTCAC	TAGAATAGAA	AGGGAAGAAA	TAGTGGTTGA	1920
TGTAAATCGT	TTTAAAAGTA	TGCAAATCAC	CCTAGCTTCT	CCAAGTAAAG	TCCGTTTCATG	1980
GTCTTATGGA	GAAGTCAAAA	AACCTGAAAC	AATCAATTAC	CGTACCTTGA	AACCAGAACG	2040
TGAAGGACTC	TTTGATGAAG	TGATCTTTGG	TCCTACAAAA	GA CTGGGAAT	GTGCTTGTGG	2100
TAAGTACAAA	CGCATTTCGT	ACAGAGGAAT	TGTTTGTGAC	CGCTGTGGGG	TTGAAGTAAC	2160
CGGTACGAAA	GTTCGTCGTG	AGCGTATGGG	ACATATCGAA	TTGAAAG		2207

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGACTGAAAT	GGGTGAATTG	TACTCTTGGC	TTGGTTTGTG	AGTAGGGATT	AACTTGGCTA	60
CCAAATCTCC	AATGGAGAAA	AAAGAAGCCT	ATGAGTGTGA	TATTACTTAC	TCAACTAACT	120
CAGAAATCGG	ATTTGACTAC	CTTCGTGACA	ATATGGTCGT	TCGCGCTGAA	AACATGGTAC	180
AACGTCCGCT	TAACATATGCC	TTGGTCGATG	AGGTTGACTC	TATCTTGATT	GACGAGGCTC	240
GTACACCTTT	GATTGTATCA	GGTGCCAATG	CGGTTGAAAC	CAGTCAGTTG	TATCACATGG	300
CAGACCACTA	TGTAAAATCT	TTGAACAAAG	ATGACTACAT	CATCGATGTG	CAGTCTAAGA	360
CTATTGGTTT	GTCTGATTCA	GGGATTGACA	GGGCTGAAAG	CTACTTCAAA	CTTGAAAACC	420
TCTATGACAT	CGAAAACGTG	GCTTTGACCC	ACTTTATCGA	TAACGCCCTT	CGTGCCAACT	480
ACATCATGCT	TCTCGATATT	GACTATGTGG	TGAGCGAAGA	GCAAGAAATC	TTGATTGTCTG	540
ACCAATTTAC	AGGTCGTACC	ATGGAAGGTC	GTCGTTATTC	TGATGGATTG	CACCAAGCTA	600
TTGAAGCCAA	AGAAGGTGTG	CCAATCCAGG	ATGAAACCAA	GACATCTGCC	TCAATCACGT	660
ACCAAAACCT	TTTCCGTATG	TACAAAAAAT	TGTCTGGTAT	GACGGGTACA	GGTAAGACTG	720
AGGAAGAAGA	ATTTCGTGAA	ATCTACAACA	TTCGTGTTAT	TCCAATCCCA	ACAAACCGTC	780
CTGTTCAACG	TATTGACCAC	TCAGACCTTC	TTTATGCAAG	TATCGAATCT	AAGTTTAAAG	840
CGGTTGTCGA	AGACGTTAAG	GCTCGTTACC	AAAAGGGTCA	ACCTGTCTTG	GTTGGTACAG	900
TAGCGGTTGA	AACTAGTGAC	TACATTTCTA	AGAAATTGGT	TGCAGCTGGT	GTTCTCTCACG	960
AAGTCTTGAA	TGCCAAAAAC	CACTATAGAG	AAGCCCAAAT	CATCATGAAT	GCTGGTCAAC	1020
GTGGTGCCGT	TACCATCGCA	ACCAACATGG	CGGGTCGTGG	TACCGACATC	AAGCTTGGTG	1080
AAGGTGTTCTG	TGAACCTGGA	GGACTTTGTG	TTATTGGTAC	CAGAACGTCA	TGAAAGTCGT	1140
CGTATCGATA	ACCAGCTTCG	TGGACGTTCA	GGTCGTCAAG	GAGATCCAGG	TGAGTCACAA	1200
TTCTACCTAT	CTCTTGAAGA	TGATTTGATG	AAACGTTTGT	GTTCTGAACG	CTTGAAGGGA	1260
ATCTTTGAAC	GCTTGAACAT	GTCTGAAGAG	GCCATTGAGT	CTCGCATGTT	GACGCGTCAG	1320
GTTGAAGCAG	CTCAGAAACG	TGTCGAAGGA	AATAACTACG	ATACCCGTAA	ACAAGTCCTT	1380

CAATACGATG ATGTCATGCG TGAACAACGT GAGATTATCT ATGCTCAACG TTACGATGTC	1440
ATCACTGCAG ATCGTGACTT GGCACCTGAA ATTCAGTCTA TGATTAAGCG CACGATTGAA	1500
CGTGTCTGTTG ATGGTCATGC GCGTGCCAAA CAAGATGAAA AACTAGAGGC AATTTTGAAC	1560
TTTGCTAAGT ACAACTTGCT TCCTGAAGAT TCTATTACGA TGAAGACTT GTCAGGCTTG	1620
TCTGATAAGG CCATCAAGGA AGAGCTTTTC CAACGTGCCT TGAAGGTTTA CGATAGTCAG	1680
GTTTCAAAAC TACGCGATGA AGAAGCAGTT AAAGAATTCC AAAAAGTTT GATTCTACGA	1740
GTGGTGGATA ACAAGTGGAC AGATCATATC GATGCCCTTG ATCAATTGCG TAACGCGGTT	1800
GGACTTCGTG GCTATGCTCA GAACAACCTT GTTGTGAGT ATCAGGCAGA AGGTTTCCGT	1860
ATGTTTAATG ATATGATTGG TTCGATTGAG TTTGATGTGA CACGCTTGAT GATGAAAGCA	1920
CAAATTCATG AACAAGAAAG ACCACAGGCA GAACGTCATA TCAGTACAAC AGCGACTCGC	1980
AATATCGCTG CTCACCAAGC AAGTATGCTA GAAGATTTGG ATTTGAGCCA GATTGGACGC	2040
AATGAACTTT GCCCATGTGG TTCTGGTAAG AAATTTAAAA ACTGTCACGG TAAAAGACAA	2100
TAAAATGAGA TAGTTTAGAG GCGGATATCT TGTGAAAAGT AAATTTTAC TGGGTATCCG	2160
TTTGCTTTAT AAGGAGATGA GTTATGGTAT TTACAGCAAA AAGCTCTAAA ATAAATATAG	2220
AAGAAGTTCG TGCCTTGTC AAATTAGAAG GTCAGGCTTT GGAGAGGAAA TCACAGCGAG	2280
ATCAAGAGCT AGAAGCCATT ATACGTGGAG AAGACCAGCG AATTCTCTTG GTAATCGGG	2339

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TTAATNGGTA CTTTGGCGAG NCCTTTTAGG NAAAATGGTA TCNATGGCCN TGATCTAGTT	60
TTGGTATCGC TTA CTTTATG GCTAGACAAT ACAAAGTTGA TGGTATTCCT GCTGGTATTG	120
TGTCATTATC ATCTTTTATT ACAGTTACGC CTTTCATTAC AGGAGAGGCT GGAGCAGGAA	180
TGCCTACCGC TTTCATGGCA TCAAAAGGTT TATTTGTTGC TATGATTTTA GGATTGATTA	240
ATGGCTATAT CTACCAATGG TTTATAAATC ATAATATACA GATAAAAATG CCGGATGGTG	300
TTCCACCAGC AGTATCTAAA AGCTTTAGTG CCATTATTCC TGGTGCAGTG ACTATTGTTG	360
GTTGGTTGAT TGTTTATGCA ACTTTAGATA AATTAAGTTT ACCTAATCTT CATGAAATTG	420
CTCAAGTTAG CTTTGGGAGG TCCACTTGGA CTTT TAGGAA ATAATGTTAT TGGTCTTCTT	480
ATCTTAATTT TCCTTAATAG TAGTTTTTGG TTTGTAGGAT TACACGGAGG AAATGTTGTT	540
AATGCAGTTA TGAAACCGTT ATGGTTAGCT AATCTAGATG CAAATAAAGT ACNCGCCNC	600
CCGGGGGAAT CCCNCTATTT CNTAAACGGG CCCCCCCCCG NG	642

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

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CTTACTTTGC AGAAATTTTC CGTGGGGGAT TGACACTATT CCAAGAGGAC AGTATGAGGC      60
TGCCAAGGTC TTGAAGTTTA GCCCTTTTGA CAGAGTGC GC TATATTATCT TGCCCCAAGT      120
GACCAAGATC GTTCTTCCTA GTGTCTTTAA TGAAGTTATG AGTTTGGTCA AGGATACTTC      180
TTTGGTCTAC GCTCTCGGAA TTTCAGACCT TATCTTGGCT AGTCNAACAG CTGCTAACCG      240
CGATGCTAGT CTGGTTCCTA TGTTCTTGGC AGGAGCTATT TACTTGATTT TAATTGGGAT      300
TGTGACAATT ATTTCCAAAA AAGTTGAGAA AAAGTACAGT TATTATAGAT AGGGGGCAGG      360
ATTCGATCTA TGTTAGAATT ACGAAATATC AATAAAGTCT TTGGAGACAA ACAAATCCTG      420
TCTGATTTCA GTCTAAGTAT TCCTGAAAAG CAAATCCTGG CTATCGTTGG ACCTTCTGGT      480
GGAAGTAAGA CAACTCTTTT ACGTATGCTT GCGGGTCTTG AAACCATTGA TTCAGGGCAA      540
ATCTTTTATA ATGGACAACC TTTAGAGCTG GATGAATTGC AGAAGCGCAA CCTACTGGGA      600
TTTGTCTTCC AAGATTTTCA ACTATTTCTT CATCTATCAG TTCTGGAAAA TTTGACTTTA      660
TCGCCTGTGA AGACCATGGG AATGAAGCAG GAAGAGGCTG AGAAGAAGGC GAGTGGACTC      720
TTGGAACAGT TAGGACTAGG AGGACACGCA GAGTCCTATC CTTTCTCACT ATCTGGTGGG      780
CAAAAGCAGC GGGTGGCTTT GCGCGTGCT ATGATGATTG ACCCAGAAAT CATTGGCTAC      840
GATGAACCAA CTTCTGCCCT GGATCCAGAA TTACGTTTGG AAGTGGAGAA GCTAATCTTG      900
CAAAATAGGG AACTTGGGAT GACCCAGATT GTGGTTACCC ATGATTTGCA GTTTGCTGAA      960
AATATCGCCA TGTATTATTG AAAGTAGAAC CTAAATAGGA GGAAAAATGG ATGAAAAAAT      1020
GGATGCTTGT ATTAGTCAGT CTGATGACTG CTTTGTCTT AGTAGCTTGT GGGAAAAATT      1080
CTAGCGAAAC TAGTGGAGAT AATTGGTCAA AGTACCAGTC TAACAAGTCT ATTACTATTG      1140
GATTTGATAG TACTTTTAGT TCCCAATGGG ATTTGCTCAG AAAGATGGTT CTTATGCAGG      1200
ATTTGATATT GATTTAAAAA CANCTCTTNT TGNNAATAC GGAATCACGG TAAATTGGCA      1260
ACCGATTGAT TGGGATTTGA AAGAAGCTGA ATTGACAAAA GGAACGATTG ATCTGATTTG      1320
GGATGGCTAT TCQCTACAG ACGAACNCCG TGANAAGGTG GCTTTCAGTA ACTCATATAT      1380
GAAGAATGAG CAGGTATTGG TTACGAAGAA ATCATCTGGT ATCAGGACTN CAAAGGATAT      1440
GACTGGAAAG ACATNAGGAG

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(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTGCTATCTT CATCGTTTCA ATCAATACCG GTGCCTACAT GACTGAAATC GTCCGTGGTG	60
GTATCCTGGC AGTTGACAAG GGACAATTTG AAGCTGCGAC TGCTCTTGGT ATGACTCATA	120
ACCAAACCAT GTGTAAGATT GTCCTACCTC AGGTTGTCCG CAATATCCTA CCAGCAACTG	180
GTAATGAATT TGTCATCAAT ATCAAAGATA CATCTGTATT GAACGTTATA TCTGTTGTCTG	240
AGCTTTATTT CTCAGGAAAT ACCGTGGCGA CGCAAACCTA TCAATACTTC CAGACATTTA	300
CAATCATCGC CGTGATTAC TTTGTCTCA CCTTCACCGT AACACGTATC CTACGCTTTA	360
TCGAGCGCAG AATGGACATG GATACCTATA CTACAGGTGC TAACCAAATG CAAACGGAGG	420
ATTTGAAATA ATGACACAAG CAATCCTTGA AATTAAACAC CTCAAAAAT CCTATGGACA	480
AAACGAAGTG CTAAAAGACA TTTCTCTCAC TGTCACAAG GGAGAAGTTA TCTCTATCAT	540
CGGAAGCTCT GGAAGTGGGA AATCGACCTT CCTACGCTCC ATTAACCTAC TTGAAACGCC	600
AACTGATGGA CAAATCCTTT ATCATGGACA AAACGTCCTC GAAAAAGGCT ATGACCTCAC	660
GCAATACCGT GAAAAGTTAG GGATGGTTTT CCAATCCTTT AACCTCTTTG AAAATCTCAA	720
CGTTCTTGAA AACACAATCG TCGCTCAGAC AACTGTCTT AAACGCGAAC GCACAGAAGC	780
TGAAGAAATT GCCAAAGAAA ACCTGGAAAA GGTGGGCATG GGAGAACGCT ACTGGCAATT	840
GCCAAACCAA ATAGCAACTA TCAGGTGGTC AAAAACAACG TGTGGCCATC GCTCGTGCCC	900
TATCAATGAA TCCAGACATC TATGCTCTTT GATGAACCAA CTTCTGCCCT TGACCCTGAG	960
ATGGTTGGAG AAGTAATTAA CGTTATGAAG GAATTGGCTG AGCAAGGCAT GACCATGATT	1020
ATCGTAACCC ATGAGATGGG ATTTGCCCGC CAGGTTGCCA ACCGCGTTAT CTTTACTGCA	1080
GATGGCGAGT TCCTTGAAGA CGGAACACCT GACCAAATCT TTGATAACCC ACAACACCCT	1140
CGTCTGAAAG AGTTCTTAGA TAAGGTCTTA AACGTCTAAA CTCAAATGC AAGGATTTCC	1200
TTGCAGTTTT TCTACCTCGT ATTGGAATTT TTGATTTTTC GGAAATTAT GTTAGAATTA	1260
AGTTTATGAA ATGAGGTTTC CTCATACCTA GCAAGACTAG GAATAAAAAT AGAAATTAGG	1320
TAG	1323

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTCTTCAAAT TCTTCACGAG TACGGAAGAA ATAGTCAACA CCGTCCACTT CTCCAGGACG	60
TTGTGCGCGT GTCGTCATCG ATACAGAATA TTGAAATTGG TTTTCAGAAC TCTCAAAAAT	120

CTCTCTTCTA	ACCGTTCCTT	TTCCAACCCC	TGAAGGACCA	GAAAAAACGA	TTAGTAAGCC	180
TCGGTCTGCC	ATTGTGTCTC	CTTTTAGTCA	ATCTGTGAAA	TAACATTTCT	CTAGAATAAT	240
GGCAAAAAGC	CAGATTATCC	TTTACAGTCT	TTCTATATAG	TGTAACAAAA	AAGCAGTAAT	300
TTTTCAACTG	CTCTTTCTTA	TTTATTTAGC	ATAATCTACT	GCACGAAGCT	CGCGAATCAC	360
GGTTACCTTG	ATATTTCCCTG	GATAATCGAG	ATTGTTTTCA	ATTTTCTTAC	GAACTTTGTG	420
AGCCAAGATT	GTGACTTTGT	CGTCCTTGAT	TTTTCCCTGGA	TTGACCATGA	TACGAATTTT	480
ACGTCCTGCT	TGAAGGGCAA	AGCTAGTTTG	CACTCCTTCA	AAGCCGTTAG	CAATTTCTTC	540
CAAATCATGG	AGACGCTTGA	TGTAGCTTTC	AAGAGACTCA	CTACGAGCAC	CTGGACGGGC	600
TGCGCTCAAG	GCATCTGCTG	CAGCGACGAT	AAC TGCTATC	ACGCTCTCAG	CTTCAACATC	660
TCCGTGGTGA	CTAGCAATCG	TATTCAACAC	AAC TGGGGT	TCCTTGACT	TACGGGCCAA	720
TTCCATACCG	ATTTCAACGT	GGCTACCTTC	AACCTCATGG	TCAATGGCTT	TCCC GATATC	780
GTGAAGGAAT	CCAGCACGAC	GGGCAAGAGC	CGCATTTTCA	CCAAGTTCGC	TCGCCATGAT	840
ACCAGCCAAC	TTAGCAACCT	CAATCGAATG	GCGCAAAACA	TTTTGTCCAT	ATGAAGTACG	900
GAAC TGCAAA	CGTCCCATAA	TCTTCATCAA	GTCTGGATGA	AGGTTTGGCG	CACCAATTTT	960
ATAGGCAGCA	GCCTCACCGT	ATTCAAGAA	CTTATGTCA	ATCTCTTGAC	GGTTTTTCTC	1020
AACCAACTCT	TCGATACGAG	CTGGATGTAT	ACGACCATCT	TTGAGCAACA	TTTCCATAGT	1080
CATACGGGCA	ATCTCACGAC	GAATCGGATC	AAATCCTGAC	AAGGTACCA	CTTCTGGTGT	1140
ATCGTCGATA	ATCACATCGA	CCCCTGTCAA	ACTTTCAAAG	GTACGAATGT	TACGACCTTC	1200
ACGACCAATA	ATGCGTCCCT	TCATAGTATC	GTCTGGCAGA	TGAACTGTTG	AGTTTGTTGA	1260
CTCCGTACA	TATTCAACAG	CGATACGTTG	CATAGCTTGA	ACCAAGATGT	CCTTGGCCAT	1320
TTTGTAGAAA	CGTTCCCTGA	CCTCTTGCTC	AGCTTCGCGA	ATGCGGACTG	GCAATCTCCC	1380
TGGTCAAGGT	TTCTCTGTG	GGAGCCAAGA	TAATATCTCG	TGCTTCTGCC	TGAGACAGAG	1440
CACCAATACG	CTCTAGTTCT	GCGTCTTTTG	GTCTTTTCGAC	TTCTCTAAT	TGCTCTTCAC	1500
GCGCATCAAG	GTTTTTCGCT	CTATCAGAAA	ATACTTTGTT	CTTTTCTGTT	CAAGTGTTTG	1560
TTCTTTACTC	GTCAAATTGT	CGTCCTTACG	GTCAAAGGCTA	GTAGCTCTCT	CTGTCAAACG	1620
ACTTTTCGATT	TGTTTGAGTT	CTTGACGTTT	TGATTTGAAT	TCAGCGTCCA	CTTCTTCACG	1680
GTATTTTCTG	GCTTCTTCTT	TGGCCTCCAA	TAGTGCTTCT	TTTTTAAGAG	ACTTGCTTTC	1740
ACGTTTGGCT	TCATTAACAA	GTAAATCCGC	TTCAAGCTCA	GCTTGTCAC	GTAAATTAGT	1800
TGCTTCTTGT	TCAGCATTTA	AAAGCATCAA	CTCTGCAGCT	TCCTGAGATG	ATTTCATCTT	1860
AGCTGAGATG	CTGACATATC	CCAATGACTA	AACCAATGAT	GACGGCAAAA	ACAGCAATCG	1920
CAAGCGACAT	GATTTCCATG	TTTTTACCTC	ATTTTATTGT	TATTCCGAAT	GACATACATT	1980
CTTTTACATT	CTACCATAAA	AAAGTGATTT	TCACAAACCT	AAAATAGAAT	ATGTTTGGG	2040
GAAATTTGGAG	TTTAAATGCC	TATAATTTAT	TGGCACAATC	TCTATTTCTT	AGAAATCGTG	2100
GTTTAGTAAA	GATTTGAGAA	AAAGCCTACT	TTTCAGTAGA	CTTCCTAATA	ATCGTTAGAA	2160
TGCAAGAAAT	TTGTTTCTAA	CAACAGCAAG	ATTTCACTCA	GGTATTCTCT	GTAAATTAGA	2220
CTAGTGCTCT	GCACGAATTT	TATCCATTCC	TCGCAAAACC	TTGTCTGATA	ACTCCTTATT	2280
TTGGGCGATT	CTCAGGGTTT	CCTGAATACT	GTCCCATTCC	CTCTTTGAAA	GAAC TACAAT	2340
GTCCCTCATCT	GGATTTTAT	TGACCACCGT	CAAAGGCTCA	AATTTATCAT	TTACCTTCTT	2400
CATGTAGTCC	TTTAAATGAT	TTCGGAATGT	TGAGTAAAGG	ACTGCTTCCA	TAACCACACC	2460
TCGTTTTAG						2469

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

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CTATTCATGT AAGCATTTCGT CCCGAAGAGT TTATCAAAGA TGAATCTGGA GATATTGAAG      60
GAACTATTAG CGATAGCGTC TATCTTGGAC TAAATACGGA GTATTTTCATT GAGACAGGTT      120
TTGCCTCAAA AATTCAAGTT AGTGAAGAAT CAACTTTTGA AGAAGAACTA CAAAAGGCA      180
ATCGTATTCG TCTACGAATC AATACGCAA AATTAAACAT CTTTCTGCA GATGGTTCCC      240
AAAACCTGAT AAAAGGAGTC AACCATGGAA CGTAAAAAAC TAAATATTG GACAGCCTCC      300
TCTTCTTCA TCTTCTTAC CTATCTGTC TTTCTCGTTT ATCCTATCGT TACCGTGCTC      360
AAGTAAGCAC TTATACATGA AGGATAATTC TCACTAGCTA ATTTTGTCAC TTTCTTTAGT      420
AAAGCCTACT ACTCTGAGAC ACTAGTCAAC AGTTTCAGGG TTTCCATTAC CGCTACTGTC      480
ACTTCCTTAG TTGTAGGAAC CCTATTAGCT TATCTCTTCT CTATGTATGA CTTCAAGGGG      540
AAGAAATTTT TACAAATATT GATTATCATT GCTTCCATGT CAACTCCTTT CGTAGGAGCC      600
TACTCCTGGA TTCTCTTGCT GGGACGAAAT GAGGTCATCA CTAAATTTT GACAAATGCC      660
CTTTATCTTC CAGCTATCGA TATTTATGGA TTCAAAGGAA TTATACTTGT CTTTACACTG      720
CAACTATTCC CACTGGTATT TCTATATGTT GCTGGAACAA TGAACAGTAT TGACAAATCT      780
CTACTTGAAG CAGCTGAAAG CATGGGGTCC TTCGGATTTA AACCTATCGT AACGGTTGTT      840
TTACCTCTCC TAGTTCCAAC CTTACTAGCA GCTCCTTGCT TGTATTTATG AGAGCATTCT      900
CAGACTTTGG AACGCCTATG TTGATTGGCG AAGGATATCG GACTTTCCTT GTCCTGATTT      960
ATACCCAATT TATTAGCGAG GTTGGAGGAA ATTCTGCTTT TGCAATTATG GCGATTATCA     1020
TTGCCTTGGC AATTTTCCTT ATCCAAAAC ACATTGCAA CCGCTACAGT TTCAGCATGA     1080
ATCTGCTCCA TCCAATTGAG CCTAAAAAA CTACAAAAGG AAAAATGGCT GCCATTTATG     1140
CAACAGTCTA CGGAATTATC TTTATCTCTG TTTTACCTCA AATCTACTTA ATTTATACCT     1200
CTTTCCTAAA AACATCAGGT ATGGTATTTG TTAAAGGTTA TTCTCCAAAC AGTTACAAGG     1260
TAGCTTTCAA TCGTATGGGA TCTGCTATTT TCAATACCAT TCGTATCCCT TTGATTGCCT     1320
TAGTTCTAGT TGTTCCTATT TACGACATTT ATCTCCTACC TAGCCGTTAG AAAACGGAAT     1380
TTGTTTACAA ACTTAATTGA CAGCCTCAGT ATGGTACCTT ATATTGTACC AGGAACCGTT     1440
CTAGGGATTG CCTTCATTTC TTCCTTCAAT ACTGGTCTAT TTGGAAGTGG ATTTCTTATG     1500
ATTACAGGGA CTGCTTTCAT CTTGATTATG TCTCTATCTG TCAGAAGATT ACCGTATACT     1560
ATTCGCTCAT CTGTTGCTAG CTTACAACAA ATAGCACCAA GTATTGAAGA AGCTGCTGAA     1620
AGCTTAGGAA GTAGTCGTCT CAATACCTTT GCTAAGATTA CAACTCCAAT GATGCTATCT     1680
GGTATCATTT CTGGAGCCAT CTTATCTTGG GTCACAAATG TTTCAAACCT CTCTACTTCT     1740
ATCCTCCTCT ACAATGTCAA AACAAGAACA ATGACTGTAG ATCAAGCTTA TNGATACGGT     1800
CGACCTCGAG GGGNGCCCGG GCCCAATG
                                                                 1828

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(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTAAACTTTC	GCTCATAGGC	ATACAAATTA	ATCCTTTGGC	ATAAGTAGCC	ATAAAATTAA	60
CATTTTCTGT	TGTAGCTGCT	TGTGCAGAAC	AAATTAAGTC	TCCTTCATTT	TCTCTATCCT	120
TGTCGTCTAT	AACAAGAACA	AGTCGTCCCT	TCTGCAATGC	TTCTAATGCT	TCTTGTATTT	180
TTCGATATTC	CATTGACTGA	TTATCCTTTC	TGCTAAAATC	CATTTTGATA	TAATAGTTCC	240
TTCGATATTT	CTGATTTTGG	AGAGTTATCC	ATCAGTTTTT	GCACATATTT	ACCTAAGATA	300
TCATTTTCAA	GATTTACTGT	ACTCCCGACT	TGTTTACTCT	TAAGAATGGT	TTGTTTCAAG	360
GTATGAGGGA	TAACAGATAC	TGAAAAGTTT	ACTTTGGAGA	CTTTAGCGAC	AGTCAGACTA	420
ATGCCGTCAA	TTGTAATAGA	TCCTTTTTCA	ACTATTAAAT	CTAAAATTC	TTTTTGTGTG	480
TTGATTGAT	ACCATACAGC	ATTATCATCT	TTTTTTATG	ACGAGATTTT	TCCTGTACCA	540
TCAATGTGTC	CTGTAACGAC	GTGACCCCA	AGTCGACCGT	TGACAGATAA	GGCTCTTTCT	600
AGATTCACCT	CACTTCCATG	TTTTAATAGA	GTAAGAGAGC	TGTTGACTC	CATGTTTCAT	660
TCATTACATC	AACTGTAAAG	GATTGATGAT	TGAAATGAGT	AACTGTAAGA	CAGATACCAT	720
TTACTGCTAT	ACTATCGCCT	AAATGGATAT	CCGTTAATAT	TTTTGAGGCT	TTAATTGATA	780
GTTTACAATT	ACGAGAGTCT	TTCTGTATTC	TTTCAACTTT	TCCGATTTCT	TCAATTATTC	840
CTGTGAACAT	GGATAAATCA	CTTCACTTTC	TATGAGATAG	TCATTTCTTA	TTTGAGAAAA	900
AGCATAAGGT	TTCAATCTAA	TAGCGTCATT	TGGCAAAGAA	ATGCCCTCAC	CTCCGACAGG	960
AAACTTGGCA	CTGCCTCCAA	AAATTTTGG	TGCAATATAT	ATTTTCAGCT	CATCAACAAT	1020
TTGTTGTTCC	AAAGCACTCC	AATTCATTAG	ACTGCCCCC	TCTAGAACTA	GGCTATCAAT	1080
CTGCATGTTT	CCTAGATGTT	GCATTAAACT	CGATAAGTCT	ATATGATTGC	CTTTTTTCTT	1140
TATGGGAAGT	ATTCACAGC	CATGATTTTG	ATATAG			1176

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTATCGATAA CATGGATGCA GACGTTATTT CCTTTGAAGC TAGCCGTTCA AACCTTGAAA	60
TCTTGGACGA ACTCAAAGCG AAAAATTCC AAACAGAAGT GGGACCTGGG GTTTACGATA	120
TCCACTCACC TCGTGATACCA AATGAAGGCG AAATCGACAA CACAATCGAA GCCATCCTTG	180
CTAAAGTGCC AAGCAAGAAA GTTTGGATCA ACCCTGACTG TGGTTTGAAA ACACGTGGTA	240
TCCCAGAAAC AAAAGAAAGC TTGATCCGCC TTGTTGAAGC AGCTAAAGCT GCGCGTGAGA	300
AATTGTAAGA TTGGATTCT CTCCATACAG TGGTTGTTCA AAAAGAAATC AACTAGAAAA	360
GGTTATTACA TATGTCACGC CAAACACCGT CACTCTCATT TGAAGTGTT CCTCCAAACC	420
CAGCCGTGGG TAATGATAAC ATTATTTTCT CATTGTCAGG TATGCAGGAG TTGGCTCCCC	480
ATTTTATCAG TGTAATGCC AGCAATAATA AATTTAATAT CAAGGAAACG ACGGTTCTGT	540
TGGCTGACTT TATCCAAAT GATTTGGCGA TTCCGACCAT TGCCCACTTG CCAGCTATTT	600
ATCTAACTAA GGACAAGGT GCTGAACTA TTGCTGACTT GGACAAAGT GGGGTGCAGA	660
AAATCTTGGC TCTTCGTGGG GATATTATTC CAGACGTGGA ACCACAAAAG GATTTCCGCT	720
ATGCAACCGA CTTGATTGAG TTTATCAAGG AACAAACCCC TCACTTTGAT ATTATTGGAG	780
CTTGCTATCC AGAAGGGCAT CCAGATTCGC CAAATCAGAT TTCAGATATT CAAAATCTTA	840
AGAAGAAAGT GGATGCAGGC TGTTCGAGCC TCGTAACTCA GCTCTCTTT GACAATGAGC	900
GCTTCTATGA TTTTCAGGAC AAGTGATTTT TGGCTGGGAT TGATGTTCCC ATTCATGCAG	960
GAATTATGCC AATTCTGAAT CGAAATCAGG CTCTCCGACT CTTGAAGACT TGTGAGAATA	1020
TCCATCTTCC ACGCAAATTT AAAGCCATCT TAGACAAGTA TGAGCATGAC CTTGAGTCGC	1080
TCAGAGCAGC AGGACTTGCC TATGCACTGG ACCAAATCGT GGACTTGGTA ACTCAGGATG	1140
TTGCCGGTGT GCATCTCTAT ACGATGAATA ATGCTGATAC AGCAAAATAC ATCCATCAAG	1200
CAACCCATGC CTTGTTTAAT CACCAGTCTC TAGGATAATA AAAGCAAACC ATTCTTCTCA	1260
GGTGAGGGGA ATGGTTCCTT TTTAATGGCA AAGACCTCAC TTTTAAAGAA AAATATGATA	1320
AAATAGATTC TGTACGTACT TGATACAAAG ATGAAGGTAT TAAATAATAC AATGCATTTA	1380
AAGTGAAGA TTTAACGACA CGAGTGAGTC AAATCGATGT TATTTGACGA AAGAGTTAGT	1440
AAAGCATTT	1449

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTCGGTTTCC TTTTCACGAT TAAGCTCGTT GTAGAGTTTT TTTAGCACAC GGTTCATCTT	60
GAGATTTTCT TGCTCCACCT CACGGATATT GTCCAAGCGT TTGCGGCTTT CCAGCGTCTG	120
CTCTTCTAGT TGCTCAATGA TACGATTGAC GTCATTGTCC TGATCGATCT GCTGACTGGC	180
ATCTCCTACG ATAACCTCAG ATAGGCCTAG ACGTTTGCCA ATTTCAAAGG CATTACTTCG	240

GCCAGGAACA CCCTGCATAA AGCGATAGGT CGGGCGAAGA GTTGCAGTAT CAAACTCCAT	300
ACTGGCATT TGCACAAAGG CTGTCTCAAT ACCGTAGGCC TTGAGTTCTG GATAGTGGGT	360
CGTCGCCATG GTCTTGATT GACGCAGGCG AAGGTCCTCC AGAATAGCCA TGGCAAGGGC	420
TGCTCCCCTCT TGGGGATCAG TACCAGCCCC CAACTCATCC AAAAGTAAGA GTGAATGTTG	480
GTTGACCTTG CCAAGAATAT CCACGATATT GGTCAATATG CTAGAGAAGG TAGACAAGCT	540
CTGCTCAATA GACTGCTCAT CTCCAATATC AGCAAAGATT TCTTCAAAAA TACCAACACG	600
ACTTCCCCTTG TCTGCTAAAA TCGGCAATCC TGAAGTGGCC ATGACCTGTG TCAAGCCCAG	660
AGTTTGTGAGC ATGATGGTCT TCCCACCTGT ATTGGGACCT GTAATGACAA TAGCCTGTTA	720
AATCTTGACC AAAATAGACA TCATTTGCGA CGGCATTTTT GACCAAAGGA TGGCAGACAT	780
GGAGCAGTTG AATCTCTTGA TTTTCTGACA GCTGAGGCAC GACTGCTTGT CTTTCTTGGA	840
TAAATCGAAC CTTGGCACGA ATCAAGTCCA GATGACCGAT AATCCAAGCG TCATTAGCAA	900
TCTCAGCCGC ATGAGGGCGG ACACGCTCAG AAATTTCTTG GAGAATGCCA AGCATTTTCAT	960
AGCGCTCATC TGCTCGCAGA CTAGCAATTT CTTGCTCAG TTTGACTACC TCACGTGGTT	1020
CGATATAGAC GGTGTTTCCA CTAGCAGAAA TATCATGAAC GACACCTGCA ATCTTATTGC	1080
GGTAGGTGTT TTTGACTGGT AAAACCTGAC GGCCATTTCT GCTAGCAACA ATTCTTCCG	1140
TCAACATCTG CGCTTTTTCG TTGAGCAAGT CTTGTAAAAC ATCGCGTACC TGACTCTCGC	1200
TATCATGTAT TTTTCGACGG ATTTCGCGCA ATTCTTCACT GGCAAAATTT TCAATGAAAC	1260
CCGCATCATT AAAGGCCTGA AGATTTCTTT GTAATTGCGG AAAATCATGT AATTTCTCAA	1320
ACCAAAGGGC TAATTCTTCC AAG	1343

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CCGATCTCTT TTAAGAGAGT GTTTCCTATT TTGTGCTTCC ATTTTGGGG CAAGGAATTG	60
TAGATGGGGA TGGCAATCCT ATCTTTTAT TGATTATGAT ATTCGTTTGC TTCATAGTTT	120
TAGTCTTTTT GAAATGGTTA GACTATGATT TCACTAGATT GAGAAGGGAG TTTCTAGATA	180
CAGGTTTTCA AAAGTCTCTT ACTAAGATTA ACTGGGCAAT GGGGGCTTAT TATCTAGTGA	240
TGCAAAGTCT ATCTTACCTT GAATATGAAC AAGGTATTCA ATCAACGACT GTTCGCCATC	300
TCATCCTAGT GTTTTACCTA CTCTTTTATA TGGGGGGTAT CAAGAAATTG GATACCTATT	360
TGAAGGAAAA ACTTCAGGAG GAACTGAACC AAGAGCAGAC CTTGCGCTAC AGAGATATGG	420
AACGCTATAG TCGGCATATA GAGGAACTTT ACAAGGAAAT TCGGAGTTTT CGCCATGACT	480
ACACTAACCT CTTAACCAGT TACGTTTGGG CATTGAAGAG GAGGATATGG AGCAGATAAA	540
AGAGATCTAC GACTCGGTCT TAAGGGATT CAGTCAGAAA TTGCAGGACA ATAAATATGA	600
CCTGGGCAGA TTGGTGAATA TTCGTGACCG TGCCCTCAAG AGTCTCCTAG CTGGAATTT	660

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTGACTATCA	AAAAAGACCA	TTTCTTCTT	TTTCTCATCG	ATAATACGAG	AATATTTTCG	60
GAAATTAGAG	GTCGGCTGAA	TAATAAGGCC	GTCTACTCCC	AAGAGAAGCA	TGCTTTCAAT	120
ATACCGGTCC	TCACTCTCTT	GGCTGTAATT	ACTATTTCTT	ATCATTACCT	GGTAGCCATT	180
CTGGCTGGCG	ATATCCTCAA	TTCCCTTAAC	AATTGTTTTT	GAGAAACTGT	TGGTAATATC	240
ACCGATCAAA	ACACCGATTA	ATTTTGTTTCG	TTTGGAGTTT	TAAGCTACGC	GCAACAATGC	300
TCGGTTTGTA	ATTTGTTTCA	TGAATAACTT	TTTCAATCTT	TTACGCTGTC	TCTTGGGACA	360
TTTTTTCATA	TTTCCCGTTT	AGGTAAAATG	ACACGGTTGT	TTTCGAGGTC	TGAGCCATTT	420
CCGCAATGTC	TTTTATGGTC	AGTTTCTTCT	CCAATCTAAA	ACACCTCCTA	CTAATACTTA	480
TTATAACATA	TTCACTATTC	AAAATGCTTA	TTTCTAGCAC	TGCAAGCGAA	TCATTCTCTC	540
ATTTATTTTA	TCATATACTA	GACATTTTCC	ACGCATTTTT	GTTCCGTCAA	CGAGGCACAA	600
TTTTTCACCT	ACACCAATAT	CCTCGCTTAA	TAACAGAATC	AGCTTGCTCTG	TTTCGTCATT	660
TTTCACTTCA	AAAGCCAGAG	CATTTTCCAC	TTACGATCA	TCTGTCTGGT	AGACAGAATG	720
ACGGATGATT	TCAAAACTCT	CATGCGCAAT	GATGGTATAA	TCCAGCATCT	GATTCTCAAA	780
GAATTGGCGC	TGGTGAGTT	TGCTACTTCT	TTCAAGCTCA	TTGTATTTAG	GAGAAATGAT	840
GGTATCTTCC	AAATCAAAAT	CAACTTCACT	CCATAGTCTC	AACTGATTGA	TTTTCCCATC	900
TTGATAGGTC	ACATCCTTGT	CAAGGATAAA	CTGAGTCAAC	GCCTCATGCT	GACCTTGACA	960
CCTGATGTCA	TCTACCAAGA	GCCAGACATC	CTCTACCAAC	ATGAGGATTT	TTCTCTTGTC	1020
AAGATAAGGC	AAATCAGGTT	CTGCTGACCA	ATAAGCCCCCT	TCAATATAAT	GCATTCCCCTC	1080
CCTTCTTTTA	TGGTGACAAA	ACAGGGAGTG	AGGATAGTAT	TCATATTCCC	AGGATCCCGT	1140
GATTCTTTCC	GGAGCTTTCC	CATCTACAAT	GCAGGTCGAA	TGACTCCAAG	CACTCTTTAA	1200
GAGATAACGT	TCATATATCT	CCCGATAAGA	ATAACGCCCA	GCATCTATGA	AAATAGGTTG	1260
GCCTTGATAC	TGTAAGCAAA	AACTATTCTC	GTCATATGG	CTATGGGCAC	TTCTAGCGG	1320
ACCATTTTTC	AAAAATAGAT	AACGATGTTT	ATCCTTAATG	CAGACATGTC	CAGAGTCTTC	1380
AAAGATCATG	GACTTAGGCT	GCCAAGCTCT	CTTTTCAAAT	TCCTGCAGTC	GCTTGATCTT	1440
TTCTCGCCCC	AGGAACAAGA	GGCTAACCTA	ATCGACTTTA	ACATCCAAAC	CGTTAAGAAG	1500
GTCTCCCTTG	TTCAAAACCA	CAGCAGACAG	GCTCAAGTTA	TCTGTCTGTC	CTGTTGAATC	1560
GCTATCACCA	ATTTCCCATA	GTTCGTCC				1588

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

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NTCTTGGGCN CNGGGCGNNT CCTTTGAGGA CNACGGTATC GATGACCTTG ATCTCAAGTG      60
CAAGCAGTAT CTGAATCTGC AGCAGCACCT GTCCGTGCAA AAGTTCGTCC AACATACAGT      120
ACAAACGCTT CAAGTTATCC AATTGGAGAA TGTACATGGG GAGTAAAAAC ATTGGCACCT      180
TGGGCTGGAG ACTACTGGGG TAATGGAGCA CAGTGGGCTA CAAGTGCAGC AGCAGCAGGT      240
TTCCGTACAG GTTCAACACC TCAAGTTGGA GCAATTGCAT GTTGAATGA TGGTGGATAT      300
GGTCACGTAG CGGTTGTTAC AGCTGTTGAA TCAACAACAC GTATCCAAGT ATCAGAATCA      360
AATTATGCAG GTAATCGTAC AATTGGAAAT CACCGTGGAT GGTTCATCC AACAACAACT      420
TCTGAAGGTT TGTTACATA TATTTATGCA GATTAATTTA CAGAGGGACT CGAATAGAGC      480
CCTCTTTTCA GGTTTACCG TGACAATCCC TATTAAAAAT TATATCAAAA TCGTGAAAAT      540
ATTGGAAGG TATGGTAGAA TGAAAATTGT CGTGTGAACG ATAATACTCA TTCTTGATGA      600
ATTGTGAAGC AGTTGCCCTT GGGTCGTTTT GCGAGTTGAA GTCAAGAAGA GGAAAAAAAC      660
AAAAAGGAGA AATACTCATG GCAGTAATTT CAATGAAACA ACTTCTTGAG GCTGGTGTAC      720
ACTTTGGTCA CCAAACTCGT CGCTGGAATC CTAAGATGGC TAAGTACATC TTTACTGAAC      780
GTAACGGAAT CCACGTTATC GACTTGCAAC AAAGTGTAAA ATACGCTGAC CAAGCATACN      840
ACTTCATGCG TGATGCAGCA GCTAACGATG CAGTTGTATT GTTCGTTGGT ACTAAGAAAC      900
AAGCAGCTGA TGCAGTTGCT GAAGAAGCAG TACGTTTCAGG TCAATACTTC ATCAACCACC      960
GTTGGTTGGG TGGAACCTTT ACAAACGGG GAACAATCCA AAAACGTATC GCTCGTTTGA      1020
AAGAAATTAA ACGTATGGAA GAAGATGGAA CTTTCGAAGT TCTTCCTAAG AAAGAAGTTG      1080
CACTTCTTAA CAAACAACGT GCGCGTCTTG AAAAATTCTT GGGCGGTATC GAAGATATGC      1140
CTCGTATCCC AGATGTGATG TACGTAGTTG ACCCACATAA AGAGCAAATC GCTGTTAAAG      1200
AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA CACCAATACT GATCCAGATG      1260
ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG TGCTGTTAAA TTGATCACAG      1320
CTAAATTGGC TGAÇGCTATT ATCGAAGGAC GTCAAGGTGA GGATGCAGTA GCAGTTGAAG      1380
CAGAATTTGC AGCTCCAGAA ACTCAAGCAG ATTCAATTGA AGAAATCGTT GAAGTTGTAG      1440
AAGGTGACAA CGCTTAATTT ATACAAATAG TAATTACCTA GGAGGGCGGG GCTTAGCCCC      1500
GCTCTCCTAT TTTCAAAAAA TATAGGAGAA TTAAATGGC AGAAATTACA G      1551

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(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTATATTTCT	GACTATCCTA	AAAACAATGG	TGAAGCAACT	AGTCCAGCAG	CCGGGAATAA	60
TACAGGTTCT	AAATACCCTT	ATACTATTGA	TGTGACAGGC	GAGGTTGGTG	ATTTGAAACA	120
AGGTTTCTCT	GTCAACATTG	AGGTTAAAAG	CAAACTAAG	GCTATTCTTG	TTCCTGTTAG	180
CAGTCTAGTA	ATGGATGATA	GTAAAAATTA	TGTCTGGATT	GTGGATGAAC	AACAAAAGGC	240
TAAAAAGTT	GAGGTTTCAT	TGGGAAATGC	TGACGCAGAA	AATCAAGAAA	TCACTTCTGG	300
TTTAACGAAC	GGTGCTAAGG	TCATCAGTAA	TCCAACATCT	TCCTTGGAAG	AAGGAAAAGA	360
GGTGAAGGCT	GATGAAGCAA	CTAATTAGTC	TAAAAAATAT	CTTCAGAAGT	TACCGTAATG	420
GTGACCAAGA	ACTGCAGGTT	CTCAAAAATA	TCAATCTAGA	AGTGAATGAG	GGTGAATTTG	480
TAGCCATCAT	GGGACCATCT	GGGTCTGGTA	AGTCCACTCT	GATGAATACG	ATTGGCATGT	540
TGGATACACC	AACCAGTGGA	GAATATTATC	TTGAAGGTCA	AGAAGTGGCT	GGGCTTGGTG	600
AAAAACAAC	AGCTAAGGTC	CGTAACCAAC	AAATCGGTTT	TGTCTTTCAG	CAGTTCTTTC	660
TTCTATCGAA	GCTCAATGCT	CTGCAAAATG	TAAAAATGCC	CTTGATTTAC	GCAGGAGTTT	720
CGTCTTCAAA	ACGTCGCAAG	TTGGCTGAGG	AATATTTAGA	CAAGGTTGAA	TTGATAGAAC	780
GTAGTCACCA	TTTACCTTCA	GAATTATCTG	GTGGTCAAAA	GCAACGTGTA	GCCATTGCGC	840
GCGCCTTGGT	AAACAATCCT	TCTATTATCC	TAGCGGATGA	ACCGACAGGA	GCCTTGGATA	900
CCAAAACAGG	TAACCAAATT	ATGCAATTAT	TGGTTGATTT	GAATAAAGAA	AGGAAAAACC	960
ATTATCATGG	TAACGCATGA	AGCCTGAGAT	TGCTGCCTAT	GCCAAAC		1007

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTCGCCAGAG	AACTCATCCA	CATAGATATT	GCCAAGTCCA	GCTACCAAGG	TCTGGTCTAG	60
GAGATGGGAT	TTGATAGGCT	TTTTGGACTT	GGCAAGGGCA	GCTTGAAAGA	CCTGTAAATC	120
AAAGTCTTGT	TCGCTTGGTT	CAGGACCTAA	TTTTTTAGAA	ATAAAGTAGG	CGTCTAAAAG	180
GTCAGGCACC	AAGAGTTCCA	TGGTTCCAAA	CTTGCGTACA	TCCTCATAAA	CAAGCGTGCC	240
CCCATCTTCA	AACCGGAAGA	AAACATGGGC	ATGCTTGCGT	TCAGGCACTT	GGTCTGGATA	300
ATAAAAATAC	TTGCCCTCCA	TCCGCAATG	GGAAATCAAG	ACCTTGTCTG	TCAGGCAGAA	360
AAGCAAATAT	TTCCACGAC	GTCCCATTTGA	CTCGATAATC	TGACTAGGCA	ATTCCCTTTG	420

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AAACTCTTCC AAATCCGTCT TAATCATCTT GGGGTAGCGA ATTTCTATAC TCGAAATCTT 480
CTTTCCTATA ATCAATTTT CTAAGCTACG ACAAACGGTT TCAACCTCAG GTAATTCAGG 540
CATAAGTCCCT CCTTCTGTAA AAACAAGAAG CAGGCATGAG CCTACCTCTA CTTAGTATTC 600
TCTTTCATTA TAGCCCAAGT CAGCCAAATC TAGCTTTTTA TCGCGCCAGT TTTTCTTGAC 660
CTTGACCCAG GTTTCCTAGGA AGACCTTGTC TCCTAGCATG AGTTCGATAT CACGACGGGC 720
CATGCTACCG ATTTTCTTAA GCATAGCGCC ACCTTTACCG ATGATAATCC CTTTTTGCTT 780
ATCGCGCTCG ACCATGATGG TTGCACGGAT GTGAACCTTG TCTGTCTCTT CGTCTCGTTT 840
CATAGAGTCA ACAACTACTG CTACAGAATG CGGAATCTCT TCACGAGTTA GGTGCAAGAC 900
TTTCTCGCGA ACCATTTCTG AAACCTAAGAA ACGTTCTGGA TGGTCTGTGA TTTGATCAGA 960
CGGGAAATAT TGGAAACCTT CATCCAGATT TTTACTCAAA ATATCCACTA GACGAGACAC 1020
GTTATTTCCC CTGAAGGGCT GAGATTGGAA CAATTTCTCT AAAGTCCATT TGATTACGGA 1080
AGTCATCAAT CTGAGACAAG AGCTGGTCTG GATGGACCTT ATCGATTTTA TTCACCACCA 1140
AAATCACAGG AACCTTGGCA GCCTTGAGAC GCTCGATAAT CATATCGTCC CCCTTACCAC 1200
GCGATTATC AGCAGGCACC ATGAAAAGAA CAGTGTCCAC TTCGCGAAGG GTACTGTAGG 1260
CAGACTCAAC CATGAAATCT CCGAGAGCTG TTTTAGGTTT GTGAATCCCT GGTGTGTCGA 1320
TAAAGACAAT TTGCTCCTTA TCAGTCGTGT AAATTCCCAT GATTTTATTG CGCGTTGTCT 1380
GCGCCTTGTC ACTCATGATG GCAATCTTTT GCCCCATAAC GTGATTTAAA AAGGTTGACT 1440
TCCCAACATT GGGACGTCTT AAAATGGCTA CAAAGCCTGA TTTAAAAGTC ATAATTTCTT 1500
CTTACTGTGT AAAATAATAA ATCCCAGAAT CGTGGGCCAG AAAAATCAAA GCGCCTGTTA 1560
AGGAAGCAAA AAGAGAAACC ACTAATACCG C 1591

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(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

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GATCTGGAGT GGATGTTGAT TTGAAATTGC CACCAGAAGA AAGTTCTCCT GACTTGTTTA 60
TCAACGGAAA GGCACCATTT GCAGTGATT TCCAAGACTA CATGGCTAAG AAATTGGAAA 120
AAGGAGCAGG AATCACTGCC GTTGCAGCTA TTGTTGAACA CAATACATCA GGAATCATCT 180
CTCGTAAATC TGATAATGTA AGCAGTCCAA AAGACTTGGT TGGTAAGAAA TATGGGACAT 240
GGAATGACCC AACTGAACCT GCTATGTTGA AAACCTTGGT AGAATCTCAA GGTGGAGACT 300
TTGAGAAGGT TGA AAAAGTA CCAAATAACG ACTCAAACCT AATCACACCG ATTGCCAATG 360
GCGTCTTTGA TACTGCTTGG ATTTACTACG GTTGGGATGG TATCCTTGCT AAATCTCAAG 420
GTGTAGATGC TAACTTCATG TACTTGAAAG ACTATGTCAA GGAGTTTGAC TACTATTAC 480
CAGTTATCAT CGCAAACAAC GACTATCTGA AAGATAACAA AGAAGAAGCT CGCAAAGTCA 540
TCCAAGCCAT CAAAAAGGC TACCAATATG CCATGGAACA TCCAGAAGAA GCTGCAGATA 600

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TTCTCATCAA GAATGCACCT GAACTCAAGG AAAAACGTGA CTTTGTCTATC GAATCTCAAA	660
AATACTTGTC AAAAGAATAC GCAAGCGACA AGGAAAAATG GGGTCAATTT GACGCAGCTC	720
GCTGGAATGC TTTCTATAAA TGGGATAAAG AAAATGGTAT CCTTAAAGAA GACTTGACAG	780
ACAAAGGCTT CACCAACGAA TTTGTGAAAT AATGACAGAA ATTAGACTAG AGCACGTCAG	840
TTATGCCTAT GGTTCAGGAGA GGATTTTAGA GGATATCAAC CTACAGGTGA CTTTCAGGCGA	900
AGTGGTTTCC ATCCTAGGCC CAAGTGGTGT TGGAAAGACC ACCCTCTTTA ATCTAATCGC	960
TGGGATTTTA GAAGTTCAGT CAGGGAGAAT TGTCTTGAT GGTGAAGAAA ATCCCAAGGG	1020
GCACGTGAGT TATATGTTGC AAAAGGATCT GCTCTTGAG CACAAGACGG TGCTTGAAA	1080
TATCATTCTG CCCCTCTTGA TTCAAAGGT GGATAAGGCA GAAGCTATTT CCCGAGCGGA	1140
TAAAATTCTT GCGACCTTCC AGCTGACAGC TGTAAGAGAC AAGTATCCTC ATGAACCTAG	1200
CGGTGGGATG CGCCAGCGTG TAGCCTTACT CCGGACCTAC CTTTTGGGC ACAAGAATCG	1260
AAATCCCTGA GATGAGGCCT TTAGCGCCTT GGATGAGATG ACAAAGATGG AACTCCACGC	1320
TTGGTATCTT GAGATTCACA AGCAGTTGCA GCTAACAACC CTGATCNTCA CGCATAGTAT	1380
TGAGGAGGCC CTCANTCTCA GCGACCGCAT CTATATCTTG ANAAATCNCC CTGGGCAGAT	1440
TGTTTCAGAA ATTAACTAG ACTGGTCTGA AGATGAGGAC NANGAAGTCC NAAAGATTGC	1500
CNACAAACGT CAAATCTTGG CAGAATTAGG CTTAGATAAG TAGAAANATA GGGAGTTGGT	1560
GAAGATTATC CCTTTTACCA GCGCCCTTTT TTCTTTTAAA AATGAAGANA ATTCGGTAT	1620
AATMNTCAAN TAAGGTCAAG GTTTAAANAN AG	1652

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTAGGGCAAC AAGAATATAT GCAACTTCTA ACATTTAGTT TTCCTCCTCT GTAATATAGT	60
AAGGGGCCCTT CTTTCGATTT TGATAAATAA CGATCATTAT ACCGAGACCG ATAAAGACAA	120
CTGACAGCCA TTGGGACACT CGAAGGCCGA AGAACATGAG ACTATCTGTT CGCATACCTT	180
CGATGACCAT ACGACCGAAA CCATACCAA TCAAGTAAAA GGCCGTGATA TGACCTCGTC	240
TGAGACTCTT CCATTTCCGT CTAAAAATCA GAATCAAGGC AAAGCCAAGC AGATTCCATA	300
GAGACTCATA AAGGAAAGTC GGTTGACGGT AGCTCCCTC AATATACATC TGGTCACGGA	360
TAAAGCCAGG TAGATAATCC AGATTATCCA CTGTTGCACC ATAAGCTTCT TGGTTAAAGA	420
AATTACCCCA ACGCCCCAAA CTTTGAGCAA TCATAACGCT AGGCGCCGCA ATATCTAGAA	480
AATCCCAAGT ATTGATGAGT TTACGGTCAG CAAAGATATA GAGCACAAGA GCCCCAGTTA	540
TCAAACCAACC GTAAATGGCC AAACCACCAT TCCAAATGGC AAAAATCTCT CCTAAATCTT	600
GACTATAGTA ATCAAATCGG AAAATAACAT AGTAGAGACG AGCTCCTAAA ATAGCCAAGG	660
GAAAGGCTAC TAAGATAAAA TCTAAATAT CGTCTGGTAT GATCTTCTTT CTAGGTGCTT	720

CTTTCATGGT	CAAATAAACC	GCAAGAATCA	AGCCTGTCAC	AATACATAAG	GCATACCAAC	780
GAATGGCTAG	GGGTCCTAGT	TGAATAGCAA	TTGGATCAAG	CATTTTGCAC	CTCATTTTGA	840
GCTATGAGAC	TTGTCAGTCG	TTCGTCGAAC	AAACGGGTAG	CATCAAAGCC	CATTTTCCTG	900
GCACGATAAT	TCATGGCAGC	TGCCTCAATC	ACAACAGAGA	TATTACGACC	TGTTTTAACT	960
GGAATACGAA	TACGAGGAAT	GGCTACGCCA	GAAACTTCAA	GTTCTCTGTC	ATTGTTTCCA	1020
AGACGATCAA	AGGTCTTATG	CGTATCGTAA	TTTTCCAAAT	AGACAGCAAG	CTGAACCTGT	1080
GAAGAATCCT	TGACAGCACT	CGCACCGTAG	AGACTCATAA	CATCGATAAT	ACCAACCCCA	1140
CGAATTTCAA	TCAAGTGTTC	CAAAATTTCA	GCTGGTTTCA	CCCAGAGAGT	AATCTCATCC	1200
TTGGCAAAGA	TATCGACACG	GTCATCGGCT	ACCAAACGGT	GACCACGTTT	GACAAG	1256

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AAGAGATGGT	GCCTGCTAAC	CTAAGCCAGT	AATTTTCTTC	TAACCTTGGG	AAATTATGTA	60
ATACCAGAGA	CGGACCCTTT	GTTGCGCTTT	ACCCAGCCCA	ATGTAACAGC	TGACGAATTT	120
TAACATCAAT	GGTCAGCTAC	AAAATGAGGT	CGAGCATGCC	AAGATGAGTA	AGATTATTGA	180
CCGTTATCGT	CCAGCTGGTG	AGGGCTTTGT	CCGTATCGAT	ACTCAAAACA	ATATGCCTAC	240
GGCAGCGGGC	CTGTCCTCAA	GTTCTAGTGG	TTTGTCCGCC	CTGGTCAAGG	CTTGTAATGC	300
TTATTTCAAG	CTTGGATTGG	ATAGAAGTCA	GTTGGCACAG	GAAGCCAAAT	TTGCCTCAGG	360
CTCTTCTTCT	CGGAGTTTTT	ATGGACCACT	AGGAGCCTGG	GATAAGGATA	GTGGAGAAAT	420
TTACCCTGTA	GAGACAGACT	TGAAACTAGC	TATGATTATG	TTGGTGCTAG	AGGACAAGAA	480
AAAACCAATC	TCTAGCCGTG	ACGGGATGAA	ACTTTGTGTG	GAAACCTCGA	CGACTTTTGA	540
CGACTGGGTT	CGTCAGTCTG	AGAAGGACTA	TCAGGATATG	CTGATTTATC	TCAAGGAAAA	600
TGATTTTGCC	AAATTTGGAG	AATTAACGGA	GAAAAATGCT	CTGGCTATGC	ATGCTACGAC	660
AAAGACTGCT	AGTCCAGCCT	TTTCTTATCT	GACGGATGCC	TCTTATGAGG	CTATGGCCTT	720
TGTTCGCCAG	CTTCGTGAGA	AAGGAGAGGC	CTGCTACTTT	ACCATGGATG	CTGGTCCCAA	780
TGTTAAGGTC	TTCTGTCAGG	AGAAAGACTT	GGAGCATTTG	TCAGAAATTT	TCGGTCAGCG	840
TTATCGCTTG	ATTGTGTCAA	AAACAAAGGA	TTTGAGTCAA	GATGATTGCT	GTTAAACTTT	900
GCGGAAAACT	CTATTGGGCA	GGTGAATATG	CTATTTTAGA	GCCAGGGCAG	TTAGCTTTGA	960
TAAAGGATAT	TCCCATCTAT	ATGAGGGCTG	AGATTGCTTT	TTCTGACAGC	TACCGTATCT	1020
ATTCAGATAT	GTTTGATTTC	GCAGTGGACT	TAAGGCCCAA	TCCTGACTAC	AGCTTGATTC	1080
AAGAAACGAT	TGCTTTGATG	GGAGACTTCC	TCGCTGTTTC	CGGTCAGAAT	TTAAGACCTT	1140
TTTCCCTAAA	AATCTGTGGC	AAAATGGAAC	GAGAAGGGAA	AAAGTTTGGT	CTAGGTTCTA	1200
GTGGCAGCGT	CGTTGTCTTG	GTTGTCAAGG	CTTTACTGGC	TCTCTATAAT	CTTTCGGTTG	1260

ATCAGAATCT CTTGTTCAAG CTGACTAGCG CTGTCTTGCT CAAGCGAGGA GACAATGGTT	1320
CCATGGGCGA CCTTGCCTGT ATTGTGGCAG AGGATTGGT TCTCTACCAG TCATTGTATC	1380
GCCAGAAGGC GGCTGCTTGG TTAGAAGAAG AAAACTTGGC GACAGTTCTG GAGCGTGATT	1440
GGGGATTTTT TATCTCACAA GTGAAACCAA CTTTAGAATG TGATTCTTA GTGGGATGGA	1500
CCAAGGAAGT GGCTGTATCA AGTCACATGG CCCACCAAAT CAAGCAAAAT ATCAATCAAA	1560
ATTTTTTAAG TTCCTCAAAA GAAACGGTGG TTTCTTTGGT CGAAGCCTTG GAGCAGGGGA	1620
AAGCCGAAAA AGTTATCGAG CAAGTAGAAG TAGCCAGCAA GCTTTTAGAA GGCTTGAGTA	1680
CAGATATTTA CACGCCTTTG CTTAGACAGT TGAAAGAAGC CAGTCAAGAT TTGCAGGCCG	1740
TTGCCAAGAG TAGTGGTGCT GGTGGTGGTG ACTGTGGCAT CGCCCTGAGT TTTGATGCGC	1800
AATCAACCGA AACCTTAAAA AATCGTTGGG CCGATCTGGG GATTGAG	1847

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTTCCTCCAG CAAAATCCAC TGCTGAGAAG CTAAAGGGAG CGTGAGATAG CCCTCTTTCT	60
CTACTGGTTG GTCTGAAATC CGAGCCTCAG GAAACCAAGTC TTGTAGTTCT TTTTCCCTCA	120
TGTTCAGACC CTCCACTTTT TGGATGCACC ATGAAACCAA ACTCTCAAGA CGTTCCAGAT	180
TCTCAGTCAT ATGGAGATAG CCCATAACCG CTTCAAATCC CGTGGACATA CGATAAGTCA	240
CGACATCTGC ATTTTTAGCC TTTGTGTGGC TATTGGTATT GCGGCCACGT TTGTAGATTT	300
CTTCTTCTTT TTCCGTTAGG ACCTGCTCCT CCAACATGAG AGCAATCAGG CGAGCCTGAG	360
CCTTGGCTGA CACATACTTG GTTGCTTCTT GATGGAGTTT ATTGGGTTTG GTCATACCTT	420
TGAGGATGAG GTGACGGCGA ATATACATAG AATACACCGC ATCCCCCTCA AAGGCTAGCG	480
CAATCCCGTT AATGAGATTG ACATCAATCA CGTGTCCACC TCACTCCATC CTTGGTATCA	540
AGGAGCTTAA TTCTTGAGT AACCAATTGG TCACGGATTT GGTCTGCTGT CTCAAAGTCT	600
CGATTGGCAC GCGCCTCTTG GCGTTTTTGA ATCAAGTCTT CAATCTCTGC ATCCAAAAC	660
TCCTCAACAA AGACAATTCC AAAAATTTCT AACATATCTG CAAGAGCTTG CTTGACACTT	720
GCATCATAGT TCCCTGAGTT GATCCATTG GCCATTTCAA AGACAACTGT GATACCGTTG	780
GCAGATTAA AATCTTCATC CATAGCTGCT ACAAACCTAT CTTTAAAGTT TTGTAACCTC	840
TGGGCATCCA CGTTTCCTGT AAATGGTTGT TCGTAAGTAT TCTTCAGATA CTTGAGATTG	900
GTCTCGGCAT CGCGAACTGC CTTTTCCGTG AAGTTGATAG GCTTACGGTA GTGCTGGGTC	960
GCAAAGAAGA AACGAAGTAC TTGCCCATCA AGAGTTTTAA GGGCATCGTG TACCGTAATG	1020
AAGTTACCCA AGGACTTAGA CATTTTGACA TTGTCGATAT TGACAAAGCC ATTGTGCATC	1080
CCAGTTAGTT AGCAAAAGCC TTGCCTGTTT TAGCTTCAGA TTGGGCAATT TCATTGGTGT	1140
GGTGTGGAAT CTCTAGGTCA GCTCCACCAC CGTGGATATC AATGGTATCA CCTAAAATCT	1200

CTGTGACAT GACTGAACAC TCAATATGCC AACCCGGACG TCCAGGTCCC CAAGGACTAT	1260
CCCAAGAAAT CTCACCTGGT TTGGAAGATT TCCATAAAGC AAAGTCTACA GGATTTTCCT	1320
TACGAGCCGT TTCTTCATCG GTACGACCTG AAGCACCTAG	1360

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTATGAGGTG GCCCTGGTTT TACTGGATAT CCAGATGCCC AAGCTTAACG GCTTAGAAGT	60
CCTAGCTGAG ATTCGTAAAA CCAGTCAGGT TCCTGTCTTG ATGTTGACAG CTTTTCAGGA	120
TGAGGAATAC AAGATGAGTG CCTTTCCTC TTTGGCAGAT GGCTATCTGG AAAAACTTT	180
CTCCCTCTCC CTCTTAAAAG TGAGGGTGGA CGCGATTTTC AAGCGCTACT ACGATACAGG	240
ACGAATCTTT TCTTACAAGG ATACCAAGGT GGACTTTGAA AGCTACAGTG CAAGCCTCGC	300
AGGTCAAGAA GTGCCTATCA ATGCCAAAGA GTTGGAATTT CTGGACTATC TAGTGAAAAA	360
TGAAGGCCGG GCCTTGACTC GGTCTCAGAT TATCGATGCC GTCTGGAAAG CGACAGATGA	420
GGTTCCCTTT GACCGTGTTA TTGATGTTTA TATCAAGGAA TTGCGGAAAA AGCTAGACTT	480
GGATTGTATC CTCACTGTGC GCAATGTTGG TTATAAATTG GAGCGAAAAT GAAACGAACA	540
GGTTTATTTA CAAAGATATT TATCTATACC TTCTCGATAT TTAGTGTTCT GGTTATCTGC	600
CTTCATTTAG CTATTTATTT TCTTTTCTCT TCGACTTATC TGAGTCATCG TCAGGAAACC	660
ATTGGTCAAA AGGCAACAGC CATTGCCCAG TCCCTAGAAG GGAAAGATAG GCAGAGTATC	720
GAGCAAGTGT TAGACTTGTA TTCCCAGACT AGTGATATCA AGGGGACCGT CAAAGGTGAG	780
ATGACCGAGG ACAAGTTAGA AGTCAAGGAC AGTCTTCCTC TGGACACAGA CCGCCAGACA	840
ACCTCTCTCT TTATTGAGGA GCGCGAGGTG AAAACGCAAG ACGGTGGTAC TATGATTCTC	900
CAGTTTCTAG CTTCCATGGA TTTACAAAAG GAAGCGGAGC AAATCAGTCT CCAATTTCTT	960
CCCTATACCT TGCTGGCCTC CTTTCTGATT TCCCTCTTGG TGGCCTACAT CTACGCTCGG	1020
ACTATTGTTG CACCGATTTT GGAAATCAAG CGGGTGACCC GTCGGATGAT GGACCTGGAT	1080
TCCCAAGTGC GATTGCGCGT GGATTCTAAG GATGAGATAG GCAATCTCAA GGAACAAATC	1140
AATAGCCTCT ACCAGCATCT CTTGACTGTT ATTGCGGACT TGCATGAAAA GAATGAAGCC	1200
ATTCTCCAGC TGGAGAAGAT GAAGGTCGAA TTCCTACAAG GAGCTTCTCA TGAATTGAAA	1260
CACACCGCTG GCTAGTTTGA AAATCCCAAT CGAAAA	1297

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

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CTTGTTAGAG TCCTACTCGC GAGAGCAAGT CAACTTCTTT GTGGATCAAG GTGCTGTTAC      60
CATAGTCCAA AAGGAAGTTC GACGCTCGGC TGCTTATTTT GAAGGAATTG AAGCAAGTAG      120
ACCTTTGGAG TTAAATCCAG AACAAAGACA GGC GCGTGAT GCGGTTGTGA GTTCTATTGG      180
CAGTTCTCAA CCTCCCTTTC TACTTCAAGG GATTACAGGA AGTGGGAAGA CCGAGGTTTA      240
CTTGCAGATT ATCCAAGGTG CCCTGGATAA GGGCAAGACA GCTATTTTGC TGGTACCTGA      300
GATTTCTTG ACTCCTCAGA TGACCGAGCG TTTTATAGCA CGTTTGGGG ACAAGGTAGC      360
CATTTCTCAC TCAGGATTAT CCAATGGTGA AAAGTATGAT GAATGGCGCA AGGTGGAGCG      420
TGGCGATGCC CAAGTTGTTG TTGGTGCCAG ATCTGCTATC TTTGCTCCTC TGAAAAATCT      480
GGGTGTCATG ATTATTGATG AAGAGCATGA AGCGGCTTAT AAGCAGGACA GCAATCCCCG      540
TTACCATGCC AGAGAGGTAG CTATTTTACG GGCTCGGTAT AATCAAGCAA CTCTGGTACT      600
TGGATCTGCA ACGCCGAGCT TAGAGAGCCG GGCACGTGCT GGCAAAGCGC TCTATCAACA      660
CTTACGTCTA ACCCAACGTG CCAATCCTTT GGCTACAATC CCTGAGGTTT CAAGTGATTG      720
ACTTTCGAGA CTATATCGGA CAAAATGAGA CGTCAAACCT TACGCCTCCT TTGCTAGAGG      780
CTATCCAAGA CCGTCTGGTT AAAAAAGAGC AGGTGGTTCT CATGCTCAAT CGCCGTGGTT      840
ATTCTAGCTT TGTCTGTGT CGGGAGTGTG GGACGGTGGG TACTTGTCCT AACTGCGATA      900
TTTCTCTGAC CTTGCATATG GATACCAAGA CTATGAACTG CCATTATTGT GGTCTCTCGA      960
AGGATATTCC TCAGGTCTGT CCTAACTGTA AGAGCCGCGG TATTCGTTAC TATGGGACGG      1020
GAACTCAGAA GGCTTATGAT GAG                                          1043
  
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(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

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CTAGTGCCTC CTAGTTTACG GTAAGCCATG TATTCCTCCT TTATTTATCT TTTAATCCAA      60
GACCCAAATC AATGAGTTTG AGTTTCACTT CTCCAAACT CTGCGTCCA AGATTTCTGTA      120
CTTTCATCAT CTCTGCTTCA GATTTTCTG TCAAATCATG CACAGTATTG ATACCGGCAC      180
GTTTAAACA GTTGATGAA CGCACAGACA AGTCCAGTTC CTCAATCGTA CGATCTAAAA      240
  
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TACGGTCGTC AGATTCAGTA TCAGCTTCTT TCATCACTTC AGTTGACTTA GCAATCTCAG	300
TAAGATTTGT AAACAAATCA AGATGTTCTG TCAAAATACG TGCTGAAAGC CCTAAAGCAT	360
CTTCTGGAAT AATTGTTCCA TTTGTCAAGA TTTCAAGGGT TAATTTGTCTG AAACCATCAT	420
TGCTACCTAC ACGAGCAGGT TCCACTGAT AGTTGACTTT TGTAAGTGGT GTATAAATAG	480
AATCTACAGC AAGTGTTCCTA ACTGGTGCAT TATCCTTTTT ATTTTCATCA GCAGGTACAT	540
ATCCACGACC ACTGTTAACA GTCATAGTCG CTTTATAGAGA AGAACCTTCA CCAATTGTAA	600
AGAGATAATG ATCTGGATTT ACAATTTCAT TATCGCTATC TGTCAAAATG TCACCAGCTG	660
TTACTTCAGC AGGACCTTCA ACATCCAGTT CGATGATTTT TTCGTCTTCA ACGTACGATT	720
TCACTGCAAT TCCTTTAATG TTCAGAATGA TTTGCATCAC GTCTTCACGA ACACCTGGAA	780
CTGTGTCAAA CTCATGTAAC ACACCATCAA TGTTGATAGA TGTCACAGCT GCTCCTGGTA	840
GAGAAGCTAG AAGTACACGA CGAAGAGAGT TACCAAGAGT TGTACCGTAG CCACGTTCAA	900
GTGGTTCGAT TACAACTTG CCATAATCTT TATTTTCATC AATTTTGTGTT ATATTTGGTT	960
TTTCAAACTC GATCATTTAG TTACTCCCTC TTAAACGAAA AGCAGTGTA TCGCATGATT	1020
ATACACGGCG ACGTTTGGGA GGACGAGCAC CATTGTGTGG CACTGGAGTC ACATCACGAA	1080
TTGCTGTTAC TTCAAGACCA GCGGCAGCAA GCGCACGAAT AGCTGACTCA CGACCAGAAC	1140
CTGGACCTTT TACAGTAACT TCAACTGATT TAAGACCGTG TTCTTGTGCA GATTTAGCAG	1200
CAGCTTCAGA AGCCATTTGA GCAGCGAATG GTGTACATTT ACGAGAACCT TTGAAACCAA	1260
TGAGCACCAG CTGATGACCA AGCAATTGCA TTACCATGCA CATCAGTAAT CATAACAATA	1320
GTGTTATTAA ATGTAGCGTG AATATGAGCA ATACCAGATT CGATATTCTT TTTCACACGA	1380
CGTTTACGTG TTGGTTTAGC CAAGACTTTT ACCTCCTATA TTATTTTTTC TTACCAGCAA	1440
TCGCAACAG	1449

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTGTGTATG ATTTTCGATA TCCAAAATTT GTTGTTCAGA ACGGCCGTCA AATTTTACAG	60
TTGAAATTGA ATCTTTCAAA CCGATACGTT CAATCAAACC TTTGGCTAAC ACTTTTTCTT	120
CTGGCATTAA GTATAATTGC CATTTCAAAC TTGAACCTCC TGCATTGATT GCAATTGTTT	180
TTGTCATAAC ATGATACCCC TTTTAAAGCG TTTTCAACTA TTATAACAAA ATCTATTTTA	240
TATTTTCAGTA CCTTGAGTCC ATTTTGTAAA ATTTTCTTTA AATTTTCATTA AAACACTTGC	300
ATCTTGCAAG CTAGCAAGTG GATAAACAAA AGGCTCCACT GCTATTTTAC TTTTCTTCTG	360
TAGGATAAAA ATAGTCTTAG ATTGTTTAGC ATTAGCAAAG AGATTTTCAG GCAGACTAAT	420
CATAGCAACC AGACTCGCCT CTTCTTTCAG CCATTTCTTT AACAAATCAC TTTGAGGACT	480
GGTCAACAAA TCACTCGGAG CTAGAAAAAT AGGCGTATCC GTCTGACTTG AGGTACTTAA	540

GCCCTTGTTT	CATGAGCAAG	TGATGGGCGT	AAGTATGTTT	TTGGCTAGAA	GCAACTGGAT	600
GGCGCGACGC	AACGGCATCA	TCAGGATAAT	AGCCAACAGG	CAAGTCACTG	ATGACCACAT	660
CGCTTTCTTT	GAGCATTGTG	GGACGAACGG	CATCTCCTTG	GACAAAGCCA	GCCTGCAAAC	720
CAATTACATC	TGCCATGCTA	GCTGCCAGAT	CAATCAGCAA	ATCATCCACT	TCCATTCCCA	780
AATAATCCAC	CTTTTATAGTA	AGCGAGGTCA	AGAAAGTAGC	GCCCAAAATT	CCCATCCCAG	840
AACCCATTTC	GAGGATAGTA	ATTTCTCCTT	CTTTAAACAG	CTCTTCCACA	ATAAACACCA	900
AAAGTAAAGC	AATAGCATCC	GGTGTAAGT	GGTGATTGGC	CTGCAAGGGT	TCTGTTTGCC	960
CAGCCTTCAT	CAAGAGAAAC	TGGTAGGTCT	TGAGCCATTC	TTCTTTGCGT	AGTGCTAAAC	1020
GCTTAAGGGT	CTGATTGTTG	TCTTTGACCT	GTTCTAGCTC	AGTCTCACCA	TCCAGATAGA	1080
TGCTGTTTTG	CTCCACCAAG	GCGTCATAAA	AGTTGGNCGC	CAAATCACTT	TGGATGACTT	1140
GGACATNCNC	TAGTAAATAG	GTATAAG				1167

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TTTTTACCAC	TTCACCGGAG	TTTTTCTTCC	TTAACTTCCA	TCAGGATTAA	TCGCTGTAAA	60
GATACGTTTC	TTTAACCACT	TTTTCTTCTT	TGTTTCNACAC	GAGTTTCACC	TAGAAACAGT	120
GTTGAATCTT	TTTTCTCAAC	TGTCCTGAAG	GCCAAATCTT	TTTCAACAAA	ATTTCGAGTT	180
GTGGGGAAGA	TCTTTCTTGT	AACAGCAGCA	ACTGTCTTTC	TCCAGAAACT	GGTTTTTCCC	240
TTAGTCAACT	GGATACCGGT	ATTCCTTAAC	TTGTTTTCCA	CTTTCTGAAA	CGAGGCGAAC	300
AAGTACTGGA	AGGCAATCTT	CTCCACTATC	TACCACAGTT	GAAGCTACTT	GATTGTTTTT	360
TTCAACTGAG	ACTTTTGGCC	GTTGACCTTT	ATAGGTAATT	TGATAGTCTT	GACGATTTTC	420
AGCGAAATCA	GCAAGTTCTT	TTCCATCTAC	AAGAATCTTC	GATTGCGTGC	TTTCTTGAGG	480
CAATTCACCT	GGTGCAAGGA	AGGTCATCTC	AATCATCGCA	ACACCGCTCT	TATCTGCTTT	540
ACGCTCCATA	CGCCATCTCA	TAGCTTTGGC	TTTGACAGCT	TTAAATGTTA	CGTTGATTTT	600
ATCACCAGCT	GCGATGTCTT	TATCCGCACG	ATAAGGCACA	GCTTCCCAAT	TTTCTGGATT	660
GTTGAATGGA	TGGTCTGCGT	CGTAGGCTTG	GTAAGTTGAA	TAGTAGGTTG	GCACTTCAAA	720
CTCTGGACCG	ACATAGCGTT	CTAAAACGAG	TTTAGTTGGT	GCATCCGTAC	CACTATCTGC	780
AAAGAAGTGA	AGTTTGGCTT	GCGCAACAGT	CCGTTCTACA	ATCTTACCAT	TTTCACGGAA	840
GATCACACCC	GCTGATACTT	CTGGATTAGA	AGATGGTGTG	GGAGACCACT	TTGTCCAACG	900
ACGATTTTCT	GAATGATCTC	CGTCATTGAG	ATAGTCAACG	CGGTCATGAG	AGTTTTTGTG	960
AATATCATTG	GTTGCTGAAG	CAAAGGCCTG	GTTACTGTTT	TCATCATAGT	TAGGGTTATC	1020
TGAAAGAGCT	TCGCCTAGTT	TGTCTGTAC	TCGTACAGTG	ACCTCAGCAA	CAAGATCACT	1080
ACCAAGGACA	TGGCCTCGAA	CGGTAAATTG	ACCTGCTTTT	GTCAGATTTT	CTGCTGGAAC	1140

TTCTTCCCAT TCAACTGACA AATCTTTTGT TTCGTAGCCG TCTTTACCTG TGAAGTAAAC	1200
TGGAACCTTA GTCGGCAATT CAAGTGCTTG ACCTACTTGT AGCAAGCGAG CTTGTTTAAC	1260
CGCAGCAACT GGTATTATGAG AAAGTAAGTT CTTATCCTTA GTGAAGTGCA GACGGTATTC	1320
TCCTAAGATG TCGCCATTTT CAGCTTTCGC GATGACACGA ACTGGCTCAC CTTACGAAC	1380
GCTTGGAACG ACGGTAGCGA GACCATTGTT GCTAACACTT GGCTGTGACT GCCGGAACCT	1440
TCCCATCTAC AGACTCAAGG TAGTATCTGT CAGATCAGGT TGAAGTTTGC TAAGTCTTTA	1500
CCGTCAACTT GGATTCTTGT TGTCTTGCT TGGCTGCCGC AACTTGTTTC GCAAAGATTT	1560
GTACCTCTGT GATAACGTTT CTAATTTGTT GTCTGCTCTC ACCATGGCGA ATACGAACAG	1620
CATAGGTTTC AACTTTATCA AGAG	1644

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTCCCAGCAT GTACTCACCT GTTTGTAAT TCTTATAAAG CTGATGACGG CTCCTTCTTG	60
CACCAATTGC TCAATCCCCT TGTGGAAGGA TTTTGTCTTC ATAACATTCT TAGCAGAAAC	120
TTTCATGAAA ATTTCAGGAG TAAAGGTTGG CAGTGGTTCA AATTCAAAC TGTMTTTC	180
AACCGTCAAG GTATCCCCAA CCTGATAAGT ACCGGTATCG TAAACCCCGA TAATATCACC	240
TGCTACGGCA TTGGTCACAT TCTCACGACT CTCCGCCATA AACTGGGTAA CATTAGATAG	300
TTTGGCACCC TTACCAGTAC GAGGGAGATT GACACTCATG CCACGCTCAA ATTCGCCTGA	360
TACGATACGG ACAAAGGCAA TACGGTCACG GTGACGAGGA TCCATGTTGG CTTGGATTTT	420
AAAGACAAAG CCTGAGAAAT CCTGTGCATA AGGATCCACA ATTTACCGT CTGTTTCTT	480
GTGACCATGT GGTCTGGAG CAAACTTGAG GAAGATTTCAGGAAGGTCT GCACACCAA	540
GTTGTGTCAGG GCTGAACCGA AAAAGACAGG CGTCAATTCT CCAGCCAGAA TAGCTTCCTC	600
TGAAAACCTCA TTCCAGCTT CATTTAAAAG CTCAATGTCA TCCTTGACTT GCTCGTAGAA	660
AGGATTGCTA CCAAAAAGTT TGTCTCCATC TTCTAGGGCT AGCAAAACGC TCATCCCCTT	720
TGTAAAGCTC TAAACGTTGG TTATAGAGGT CATACAAGCC CTCAAAGGCT TTCCCCATCC	780
CGATAGGCCA GTTCATAGGG TAGCTAGCAA TGCCCAAGAT TTCTTCCAAT TCTTGCAAGA	840
GATCCAAAGG CTCACGACCG TCACGATCCA ACTTGTTTCAT AAAGGTAAAG ACTGGAATGC	900
CACGATGTTT CACAACCTCA AACAATTTCT TTGTTTGAGC CTCGATCCCC TTGGCAGAGT	960
CCACGACCAT GACCGCAGCA TCCACGCCA TCAAGGTACG ATAGGTATCT TCTGAGAAGT	1020
CCTCGTGCCC TGGCGTGTCT AAGATATTCA CGCGCTTGCC GTCGTAGTCA AATTGCATAA	1080
CAGATGAAGT AACAGAAATC CCACGTTGCT TCTCGATATC CATCCAGTCA GATTTAGCAA	1140
AAGTCCCTGT TTTCTTCCCT TTTACCGTAC CAGCCTCAG AATCTCACCC CCAAAGTAGA	1200
GTAAGTGTCT AGTGATGGTT GTTTTCCCCG CGTCCGGGTG GGAGATAATG GCAAAGGTAC	1260

GACGTTTCTT AATTTCTTCT TGAATATTCA TAAGTTCTCT TTCTTTGATT CTCTATTTTC	1320
CTTGTTTCAA TAGCTGAGAA TGATTTGTAC ATTGGATTTT ACCATCCTTT CGACACTCCA	1380
TTATATCGGA TGTTAGCATT TTTTCCAATT TCTATTTCTT TCCACTTCCC CCTCCCTTAT	1440
TTATAGGA	1448

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CTCCTAGAGC AACTTGAAGG ACACCTGATA TAAAGGAAAG GATAACAGCC GCTTTCATC	60
CGCCGCGTTT ATCAGCGTAG ACCGCAATGG CTGCATTGTC AAAGAACT GGTACAAATC	120
CTGTAATAAT AAGAATCGGA TTTTAAAGA CGATGAGCAA GACAATTGTA ATCAATTGAC	180
CAATCAAACC AAAGGTAAAT CCTGACAAGA CAGCATTGCG AGAACCAAAT CCATAAGAAG	240
CTGCAAAGTC AACCGCTGGG AATGAACCTG GCAACAATTT GTTTGAAATA CCTTGAAGG	300
CGTTTGTCAT CTCAGATACG AACATTCGGA CACCTTGCAT CAAAACGAAC AAGTAAACTG	360
AGAAGGTAAA GGCTGTTTGG ATAATGTACA TAAAGAAATC TTGTTTAGCA GGATTGAATA	420
GAGTTCCTGA AGTGATGACT TCTTTATTAG ACATAATGTC TGGACCCAAG ATTAAGAAAG	480
TGGCCCCGAA GAATACGAGC ATCAAAGGTA GCAGATGCAA CAACTGTATC GTGGAAGATT	540
GAGAGGAACT TAGGTAATTT AAGATTGTCT AAACCTTCTT CTTTCTTACC AAAGCGTCCT	600
GCTACTTTAT CTACAAACCA GATTGCAAAT TGCTGTTGGT GACCAATCGC AAATCCGCCA	660
CCACCAGTCA AGCGTTGAGT TGCCTCAACA GTCATATTTG AACTAACTGC CCAGTAAAGT	720
CCACAGATGA TACCAATCGC TGCTGTACCG TAAGCATTGC GCAATTGTGG TACTAAGAAT	780
AGAACCATAA GAGATACTGT TGCAGCTAGC CATGCTGATC AATTCCCTCA ACCAGTCCTA	840
TATCTCAGCC AAGAGAATCG AGGAGGTCTT TCGCGAATCT CCCGAAAACA TCCATTGAGA	900
ATTAGAACAA AAGCAAGTFA CCAGTGGTGC GGTTTTACAA GTCCAAGAAT TGACTTTTAC	960
CTATCCTGAT GCGGCCAGC CTTCTCTGAG AGACATTTCC TTTGATATGA CTCAAGGACA	1020
AATCCTTGGT ATCATTGGGG GGAAGGTTTC TGGTAAATCA AGCTTGGTGC AACTCTTACT	1080
TGGACTTTAT CCAGTAGACA AGGGGAACAT TGACCTTTAT CAAAATGGAC GTAGTCCTCT	1140
TAATTTGGAG CAGTGGCGGT CTTGGATTGC CTATGTACCT CAAAAGGTCA AACTCTTTAA	1200
GGGAACATT CGTTCCAAC TGAATTTAGG TTTAAATCAA GAAGTATCTG ACCAGAACT	1260
CTGGCAGGCC TTGGAGATTG CGCAAGCTAA GGATTTTGTG AGTGAAAAGG AAGGACTTTT	1320
GGATGCCCTA ATTGAAGCAG GGGGGCGAAA TTTCTCAGGT GGACAAAAC AAAGGTTGTC	1380
TATCGCCCGA GCAGTCTTGC GCCAAGCTCC GTTTATCATC CTAGATGATG CAACCTCGGC	1440
ACTGGATACC ATTACAGAGT CCAAGCTCTT GAAAGCTATT AGAGAAAATT TTCAAACAC	1500
GAGCTTAATT TTGATCTCTC AACGAACCTC AACTTTACAG ATGGCGGACC AGATTCTCCT	1560

CTTGGA AAAA GGTGAGTTGC TAGCTGTTGG CAAGCACGAT GACTTGATGA AATCCAGCCA	1620
AGTCTATCGT GAAATCAATG CATCCCAACA TGGAAAGGAG GACTAGAATG AAACGACAAA	1680
CTGTAAACCA GACGCTCAA CGTTTAGCCG TTAGATTTAG CAAACCATCC CTTCTCCTT	1740
TTCTAGCCT TTCTAGGAAC TATTGCCCAA GTTGGCTTAT CAATTTACCT ACCTATTCTG	1800
ATTGGGCAGG TCATTGACCA AGTCCTAGTG GCTGGTTCAT CACCAGTTTT TTGGCAGATT	1860
TTTCTCCAGA TGCTCTTGGT GGTAATAGGA AATACTCTGG TACAATGGGC CAATCCTCTC	1920
CTCTATAATC GTCTAATCTT CTCTTATACC AGAGATTTCG GAGAGCGGCT C	1971

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TNTTTTGCCC NTGCGCGTC CTTTTAGGAA AACGGTATCG AGGGCCNTGA TCTTATCTTT	60
TCAATNTATG TANAACCCAG TGAGTTGAAA AAAATTGCCA GTGAATTAGA CACGACGGAA	120
AACAACCTTG AAAAATTCAA CGAATGACTA TTGGTGGAAA AAATTGACCG TCTACTATAT	180
GATTGACGAT GCAGGGGTTG GTGTGAAAAT TTTGACATCA AGTAAAGATG CCAATGACTT	240
GTTAGAGAAA AAAATTGATG GGTTGATTGA GAAATTTAAA CATGCTTATG CAAATGTGAA	300
AATTGAAAA CTGGAAACCA TCAACTCTAA AGAAATTGAA CGCAAATGGT GAAACAGCGC	360
TTGGCTTAAA TGTGAAAAAT CTGATNCTNC GTTTAGTTGT TATTGGAGTG GTTTGTGTGA	420
TTTGGGTNGT GATGGGAAAT GTGTTAGTTT ATCTCTTTAA TCCACCAATC ANTAAANTAG	480
GTGATTTTCC CCNCCTACCN NNTNAATTTT GTTNCCAAAA NNTAANNCCA TTGCCNCCCT	540
NCCCAAATTT TTTGTNCTNC CCCNATTTCC NNACCGGAAT TTGTTCCCN NNTATTTAAC	600
CCCCCCCCC CCCCCCTTT	620

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGGTCCTNG	AGGTCAATCA	ATTCCCCCAG	ATAGGNCTCA	ACTCCCCAAA	CACCTCCTCC	60
CACTCGTGCC	AAAACACGAT	TGGTCAGGTA	GATTCGATCC	ATCTCCTCAA	ATGAANTTTC	120
AGAAATGACA	TGTGTTACAA	ATTNATCTAC	TAAGGTCACT	ATAGAGCCTC	CNTTNGACTA	180
GTCAAGGACG	CGAGTGCCAC	CTGAAACTTC	AGCGATATAG	AAGGCTNGGA	GGGTATCCAA	240
CTACTTCCTT	GTAGAGTTTG	CCTACAGCTT	CCTTAAAGGC	CTCAACAGTA	TCTTTTGTAA	300
CCAAGGCAAT	GGCACAGCCA	CCAAAACCAG	CCCCTGTCAT	ACGAGCACCG	AGAACTCCTT	360
CCTTGTGCCC	AAGCTGTGTG	AACAAGAGTA	TCCAATTCCA	AACCAGTTAC	TTCATAATCA	420
CGCTCCAGAG	AAACGTGTGA	CGCATTTCATC	AAACGACCAA	ATGTTTCCAA	ATCACCTGCT	480
TGAAGGGCTG	CTTGAGCTTT	AAGGGTACGT	TGGTTTTCAA	GCACAGCATG	GCGAGCACGT	540
CTCAAACGAT	TTTCATCTTT	AATCAGATAG	CTATATTGGT	CAACGGCCCA	CTCGTCCAAT	600
TCACCCAGGG	TCTGAATATC	CAAGGCAACT	TGCAATTCTT	CCACTGCTTT	TTCACACTCA	660
GCACGACGTT	CATTGTATTT	AGAGTCCGCC	AATTCACGGC	GTTTGTGGT	GTTTCATGATA	720
ACAACGACAT	TGTCCTTCAA	ATCAAGTGCC	ACCAAGTCGT	ATTCTAAAGT	ATTGGTATCT	780
AAGTAAATAG	CACGTTGGTC	AGCCCCCATA	CCAATAGCAA	ATTGGTCCAT	AATGCCAGAA	840
TTTACTCCGA	TAAAGTTATT	TTCTGTTTGT	TTTCCGATTT	TAACCAAATC	GAGACGCTCT	900
AGTTTTAAAT	CAAAGAGATG	CTCTGCCACA	ACTCCTGTCA	AGAGCTCCAA	GGATGCTGAA	960
GAAGACAAAC	CACCACCATT	TGGGATATTC	CCATAAACAT	AAAAATCAAA	ACCTTTGTCA	1020
ATCACGTGCC	CAGCTTCTTG	CAAGAAATGA	AGGACACCTT	TTGGATAATT	GGTCCAGTTG	1080
TGCTCTTTTT	CAAACCTGAG	GTCAGCGAGA	GGCACTTCGA	TAATGCCCTT	GTCCTCAAAG	1140
TTAGCTGAGT	AGAAACGCAA	GACTTGGTCG	TCACGCTTAC	GAGCTGCACC	GTAAGTTCCC	1200
AAGGAAATAG	CACCAGGTAA	AAACGTGCCC	ACCGTTGTAG	TCTGTATGTT	CACCAATCAA	1260
ATTAATGCGG	CCTGGTGAAA	AGAAGGTTTG	GTCTGCTTCT	TGACCAAAAA	CAGCAAGAAA	1320
GTCTTTGCGA	AGGGCTTCAG	TAGTAAGATG	TTGTGCCATA	TGAATTCTCC	TTTGACTGTC	1380
CGTTAAGCCA	TCTTAACGAG	TAATCGTTTT	CTTTCTATTG	TATCCAAGGA	ATTTTCCGAG	1440
GTCAATCCTT	TTTACTGAAA	TTTGTAGTAA	ATATCAGTAA	AAAGAAGAAA	AACATGATAT	1500
ACTAACCTAA	TCAAGGAGGA	TTTATGGCTA	CCTTAAAAGA	CATTGCACAG		1550

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTGGCGGCCG	CTTAAGAATT	AGTGGGATCC	CGGGGCTGCA	GGATTTGAAC	TCAATGCATC	60
CAAGGCGTCA	TCCATTGAAA	GAACCTCGTG	GAAGACACGT	TGTGTCAATT	CAGTTTTTTG	120
TTCTGGAGTG	AGGTATTTAG	TGTTTACACA	GTATCCAGAG	ATACGTACGA	TAACGTCTTC	180

GCCTGACATG	ATTTTTTCGT	AAACATCGTT	CAAGTCCATA	ACGTTCAAGT	TAACGTGTTG	240
TCCACCGTTT	TCGAAGTAAC	CATCAAGGAT	TGTTACCAAG	TTATCAACTT	GTTCATCACG	300
AGTCTTACCA	AGAGCGCGAG	GTGATACTTG	TGTAGTCAAT	GAGATACCGT	CAGCTGCATA	360
ACTAAAGTCA	AGGCTAGAAA	GTGAGTTCAA	GTTTTGCAAC	CAACCACCTT	TAGCTTTGTT	420
AGATGGGTTA	GCACCTGGTG	AGAAGAATTC	AAGTTTAGAC	AAGTTCACAG	AACCATCTTC	480
GTTGAGGTAT	ACACCTTTGT	GA A CTGGTGA	GTTACCAGTT	TGTTTAGAGT	AAGCAACGTT	540
AGATGTGATT	GTCAAAAGTG	ATACTGTAGC	TTCTGCGTCT	TTGTATAGTT	TGTGGCTACG	600
TAAACGAGTT	GTGTAAGCTT	CGATTAAACCA	TTCTGCCAAT	TCGTTTGAAC	GTGGGTCATC	660
TTCACCCAG	CGTGGGTAGT	CACCGATTGT	TTCGTAATCG	TAGATGTAGC	CATCTTCGTC	720
ACGGATTGGT	TTAACTGTAG	CGTATTTGAT	AGCTGACAAT	GTATCAACAG	TGTTAGCAAA	780
TCCACAGATA	CCGAATCCCA	TGTTGGCACG	TTGTTTAGTT	GGCAAGAAGG	CCATTTGAAC	840
AGCTTCGTAG	TTGTACCTAT	CAGTCATGTT	AGTGGATGAT	GTTCAAGGCA	TCTACGTAAG	900
TGTCAGTCAA	CCAGTCAAGA	GATTTTTCAA	AGTTCGCTTT	AACTGATTCA	AATTCAAGAA	960
CTTCGTCACG	GATTGGTTCG	ATATCAAATA	CTTTGTAGTC	TTTGTGAACA	TCGTCGTAAC	1020
CACCATTCAA	ACCAGTAAGA	AGGGCTTTAA	GAACGTTTAC	ACGAGCACCG	AAGTACTGGA	1080
TGTTGTGGCG	TTGTTCTTCA	TTTTCTGGAT	CAAGTGGAGA	CACACAGCAT	GAGATACAG	1139

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAAAACCAGT	CTTTCCTTGG	CTGAGAAAAA	CAGCTGTAA	GGCTCCAACC	AAGTCTCCTG	60
TCCCTGTTAT	CCAGTCTAAT	TCAGTACAGC	CATTCTCAAG	TACAGCAACT	TGATTCTCCG	120
AAACAATAAG	GTCCTTGGA	CCTGTGACTA	AGAATGACAT	ACCAGGATAG	GTCTGACACC	180
AGTCTTTCAA	GACTTGAAGC	AAATCCTCCG	TTTCTTGATC	TTTAGCACTC	GCATCGACCC	240
CAACGCCGTG	ATGCTTTAAT	CCAACAAGAC	TTCGAATTTC	TGACATGTTT	CCTTTAAGGA	300
CCGTAGGTCT	ATAGTCTAAA	AGGTCTTTAA	CTAAGCTCTT	ACGAATGGAT	GAAGTCGTTA	360
CGCCAACCGC	ATCTACTACC	ATCGGGAGAG	AAGATTGGTT	TGCATACAAA	GCTGCCATGC	420
GGATTGCTTT	TTCTTTTCA	GCTGACAAAT	GCCCCAAAT	GATGAAGAGA	GCCTGGCTTT	480
GCTTAGTAAA	ATCAACACT	TCACGGGGAT	CATCTTCAT	GACAGGTTTG	CATCCCAGAG	540
CCAAAATCCC	ATTTGCCAGC	ATCTCACAAG	AAATCTCATT	GGTCATACAG	TGAATGAGGG	600
AAC TAGAGCC	TATAGGAAAA	GGATTGTGCA	ATGCCTGCAT	CATTCTATCC	TTTCAGCAAA	660
GAAATATCCT	TGCACTTTTT	TAAAGAATTC	CTGCTTGATT	AAAAATCTAA	ATGCAATAAA	720
GGAAATCGCT	GTACCAATCA	AGGTTGCTCC	GAAAAATCGA	GGCGTGTAGA	TAAACCAACT	780
AAGCTTAGCA	GCCGATCCTG	TAAAGAGCAC	CATAACAGGA	TAGGAAACAA	TAGAACCAAT	840

AATACCTGTT CCCACAATTT CTCCCAAGGC AGAAAAGTAA AATTTTCGAC CGTACTTATA	900
AAAGAGACCT GCTAGAAGGG CTCCAAAAGT CGCTCCTGTG AGAGATAAAG GAGCTTATCG	960
GAATACCCCTT GAGTCGTCAT ACGGATAAAG GCTGTCACTG TAGCCATAGC CAAGGCATAA	1020
ACAGGTCCCA TCATGATTCC CGCTAGAATA TTGACTACAC TGGACATCGG TGCCATTCCC	1080
TCAATCCGAA AGATAGGTGT AAGGACTACA TCAAGGGCAA TCATCATAGA TAAAATGGTC	1140
AATTTGTGAA CTTGTAGTTG GTGCTTTCTC AAGTTTCTAT TCTTCTCCTT TTTCTAAAGA	1200
CTGTAAATCG CTCTTCCATG TCTGGTGTTG GTAAGCCATC TCCCAAACT TGGCTTCCAT	1260
ATGAACACTG ATGTGGAAGG CATCTAGCAT TTTTGTCTTA TCTGTCTCAT CACTTTCTCG	1320
ATAGAG	1326

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTAGTCCAGA GGGTGCAATG GCTAGTGATG GTACTTGCCA AGGAAAACAG TATCTGAAAG	60
AAGATGGCAG TCAAGCAGCG AATGAGTGGG TTTTGTATAC TCATTATCAA TCTTGGTTCT	120
ATATAAAAGC AGATGCTAAC TATGCTGAAA ATGAATGGCT AAAGCAAGGT GACGACTATT	180
TTTACCTCAA ATCTGGTGGC TATATGGCCA AATCAGAATG GGTAGAAGAC AAGGGAGCCT	240
TTTATTATCT TGACCAAGAT GGAAAGATGA AACGAAATGC TTGGGTAGGA ACTTCCTATG	300
TTGGTGCAAC AGGTGCCAAA GTAATAGAAG ACTGGGTCTA TGATTCTCAA TACGATGCTT	360
GGTTTTATAT CAAAGCAGAT GGACAGCAGC CAGAGAAAAGA ATGGCTCCAA ATTAAAGGGA	420
AGGACTATTA TTTCAAATCC GGTGGTTATC TACTGACAAG TCAGTGGATT AATCAAGCTT	480
ATGTGAATGC TAGTGGTGCC AAAGTACAGC AAGGTTGGCT TTTTGACAAA CAATACCAAT	540
CTTGGTTTTA CATCAAAGAA AATGGAAACT ATGCTGAAAA AGAATGGGTC TACGATTCTC	600
GAGAATAGTC AAGCCTAGTA CTACTTCTAA AATCCGGTGG CTACATGACA GCCAATGAAT	660
GGATTTGGGA TAAGGAATCT TGGTTTTACC TCAAATCTGA TGGCAAAATA GCTGAAAAAG	720
AATGGGTCTA CGATTCTCAT AGTCAAGCTT GGTACTACTT CAAATCTGGT GGCTACATGG	780
CGAAAAATGA GACAGTAGAT GGTATCAGC TTGAAAGCGA TGGTAAATGG CTTGGAGGAA	840
AAGCTACAAA TGAAAATGCT GCTTACTATC AAGTAGTGCC TGTTACAGCC AATGTTTATG	900
ATTGAGATGG TGGAAAAGCT TTCCCTATAT ATCGCAAGGT AGTGTCTTAT GGCTAGATAA	960
GGATACNAAA AAGTGATGAC NAGCGCTTGG CTATTACTAT TTCTGGTTTG TCAGGCTATA	1020
TGAAAACAGA AGATTTACAA GCGCTAGATG CTAGTA	1056

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

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CTGGACCACA CTATTTTCTG TGTGGCTAT CGTGTCTATG AAAAGGATCT AGAAGGGACG      60
CTGGATGCTG AAAAAGTCAA GGCTGCTGGT GTTCCGTTTC GCCCGCTTTT TGGTAAAATC      120
AAAAACGGCC AGGATCTTGT TTTGGAAGAC GGAAGTGAAG TCAAGGCAGC AGACTATATC      180
TCAGCGCCAC GTCCAGGTAA GATTATCACT ATTTTAGGAG AACTCGAAA AACGGATGCC      240
AGTGTGCGTC TGGCTGTCAA TGCAGATGTC CTAGTTCATG AGTCCACTTA TGGCAAGGGT      300
GATGAAAAAA TTGCTCGTAA CCATGGTCAC TCAACTAATA TGCAAGCTGC ACAAGTAGCG      360
GTAGAAGCAG GTGCCAAACG CCTCCTACTC AACCATATCA GTGCCCGTTT CCTCTCAAAA      420
GATATAAGCA AACTCAAGAA GGACGCTGCC ACAATTTTGT AAAATGTCCA TGTGGTCAAA      480
GACTTGGAAG AAGTGGAAT CTAGCAGTCA CAGAAAGGAT AAGTATGCCT ACTATTCTCA      540
TTACCGGAGC TAGCGGTGGT CTAGCTCAAG AAATGGTCAA ACTCTTGCCC AATGACCAAC      600
TCATCTTGCT TGGTAGAAAT AAGGAAAAAT TAGCCCAACT CTACGAAAT TATTTCCATG      660
CAGAATTGAT TGAAATTGAT ATTACCGACG ATTCAGCCCT AGAAGCTCTG GTAAGTATC      720
TTTATCTCCG CTATGGCAAG ATTGATGTCT TGATTAAACA CGCTGGTTAC GGGATTTTTG      780
AGGGATTTGA CCAGATTGCT GATAAAGATA TTCACCAGAT GTTTGAGGTC AATACCTTTG      840
CCCTGATGAA TCTGTCTCGT CACCTTGCGG CTCGTATGAA GGAAAGCAGC AAAGGGCATA      900
TCATCAACAT CGTCAGCATG GCAGGTCTAA TAGCTACTGG CAAGTCTAGT CTTTACTCAG      960
CGACCAAGTT TCGCGCTATT GGTTTTTTCAA ATGCTCTGCG ACTCGAACTT ATGCCCTATG     1020
GAGTCTATGT GACAACAGTC AATCCAGGTC CAATCCGAAC AGGATTTTTT GACCAAGCTG     1080
ACCCAGATGG AACTTATCTT AAATCGGTTG ACCGCTTCCT CTTAGAGGCA GATGCAGTGG     1140
CTAAAAGAT TGTCAAGATT ATAGGCAAAA ATAAACGAGA ACTCAATCTC CCGATTTTGT     1200
TGAACCTAGC CCATAAGTTT TATACTCTCT TTCCCAAGCT AGCTGATAAG TTGGCAGGGG     1260
AAACTTTTAA TTATAAGTAA AAAGAACCAA TGTGCAGGTT GTTGCTAGCC TACATATTGG     1320
TTCTTATCAT TTCTCAACTA TCAAACTGAA CTTCTTCTAG TAGATAGTCG ATAAAGCGTT     1380
CGCCCATCTT AGATAGGCTG GTTTTCTCAT GCTGGATATA GACCAG                      1426

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(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CCAAGCTTGC CCAATTGTCG GCAGGGTTTC GATGGACCAA ATCACTATTC GATTGCCTAA	60
GCTTTATCCG CTAGGAACCA AGGTAACCTT GATTGGCTCC AATGGGGATA AGGAAATCAC	120
TGCAACTCAG GTAGCGAACT ACCGCGTAAC CATTAACTAT GAGGTGGTTT GCCTCCTCAG	180
CGACCGTATT CCGAGAGAAT ATTATTAGAA AAGAAAGGAG TGGAGCATGA ATCTACATCA	240
ACCCCTGCAT GTCCTGCCTG GTGTGGGACC AAAGTCAGCA GAAAAATAAC GCCAAACTAG	300
GAATTGAAAA CTTGCAAGAT CTCTTGCTCT ACTTTCCTTT CCGTTATGAA GACTTCAAAA	360
CCAAGCAGGT GCTGGAAC TA GAAGACGGTG AGAAGGCAGT TCTTCTGGT CAGGTAGTGA	420
CTCCTGCTAG TGTCCAGTAT TATGGTTTCA AGCGCAATCG CCTGCGTTT AGTCTCAAGC	480
AGGGAGAGGT CGTTTTGCG GTGAATTCT TTAACCAGCC CTATCTGGCT GATAAAATAG	540
AGTTGGGAGC AACCCCTTGCT GTCCTTGGA AATGGGACCG CGCTAAGGGC TAGTCTGACT	600
GGGATGAAGG TTCTGGCTCA GGTAGAAGAT GACCTCCAGC CTGTCTATCG TCTGGCTCAG	660
GGAATCAGTC AGGCCAGTCT GGTCAAGGTC ATCAAGACGG CTTTGTATCA GGGACTGGAC	720
CTCTTGATAG AAGAAAATCT GCCCAGTCT TTAGTAGACA AATACAACT CATGTCCCGT	780
TGTCAGGCAG TCCGAGCTAT GCATTTTCCA AAGGATTGG CAGAAAACAA GCAGGCTCTT	840
CGCCGTATCA AGTTTGAGGA ACTCTTTTAT TTCCAAATGC AGCTGCAGAC GCTCAAGTCT	900
GAAAAATAGAG TTCAGGGAAG TGGTCTGGT CTGGATTGGT CTCAGGAAA AGTGACAGCA	960
GTTAAAGCAA GTCTTCCTTT TGCCCTGACC CAAGCTCAGG AAAAGAGTTT GCAGGAAATT	1020
TTAACTGATA TGAAGTCCGA CCACCACATG AATCGTCTCC TACAAGGAGA TGTGGGGAGC	1080
GGAAAAACGG TAGTCGCTGG CTTGGCCATG TTTGCGGCAG TGACAGCAGG TTATCAGGCT	1140
GCCCTAATGG TACCAACAGA AATCCTCGCA GAGCAACACT TTGAGAGTTT ACAGAACCTT	1200
TTTCCCAATT TGAACTGGC TCTCTTGACA GGTTCCTTGA AAGCTGCAGA AAAGAGAGAA	1260
GTCTTGAGGA CCATTGCCAA GGGTGAGGCT GATTTGATTA TAGGAATCA CGCTCTGATA	1320
CAAGATGGGG TGGAGTATGC TCGTCTGGT TTGATTATTA TCGATGAGCA GCACCGTTTT	1380
GGTGTAGGGC AAAGGCGTAT TTTACGGGAA AAAGGCGACA ATCCAGATGT CCTCATGATG	1440
ACGGCGACTC CCATTCCACG GACGCTTGCC ATCACAGCCT TTGGAGATAT GGATGTTTCC	1500
ATTATCGACC AGATGCCAGC AGGTCCGAAG CCTATTGTGA CGCGCTGGAT CAAACATGAG	1560
CAACTACCTC AGGTCTTGAC TTGGTTAGAG GGGGAAATTC AAAAAGGTTT CCAAGTCTAT	1620
GTCATCTCTC CTTTGATTGA AGAATCACAA GTCCTAGAT TTGAAAAAAT GCCATTGCCT	1680
TATCAGAGGA GTTGA TACTACT CC	1702

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CTATGAAGGA	CCTGGTTCAG	AAGTTGGCAA	GTAAAGAAGA	ATTGTCGACA	GCAGACAATG	60
AAATGATTGA	ATTATTGGCT	CGTTTTAATG	AACGCCAAGC	CTCCTTTTTT	GGTCAGTTTT	120
CGGTTAGAGG	CTATGTTAAC	TACGATAAGC	ATGTAGCTAA	GTATTTAAAA	ATCTTGCCAG	180
ACCAGTTTTT	TTATCAAGCA	ATAGAAGATG	TTGTCAAAGC	AGATGCTGAA	AAAAATACTT	240
CCAATAATGA	GATGGGAATG	GAAAATTATT	TCTATAATGA	GCAGATCAAG	AAGGATTTGA	300
AGAAATTAAA	GGATTCTCAG	AAAAGCTTTA	CCTATCTCAA	GTGCCCAGAG	TATAATGACT	360
TGCAGTTGGT	TTTAACACAG	TTTTCTAAAT	CTAAGGTAAA	CCCGATTTTT	ATCATTCCAC	420
CTGTTAATAA	AAAATGGATG	GA CTATGCTG	GTCTACGAGA	GGATATGTAC	CAACAAACGG	480
TGCAGAAGAT	TCGCTACCAG	TTAGAAAGTC	AAGGTTTTAC	CAATATAGCA	AATTTTTCTA	540
AGGACGGTGG	GGAGCCTTTC	TTTATGAAGG	ACACCATTCA	CCTTGGTTGG	TTGGGGTTGG	600
TTGGCTTTTG	ACAAGGCAGT	TGATCCTTTC	CTATCCATCC	CACACCAGAT	CGAAGTCCTG	660
CAG						663

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CTTGCTTTTT	GATTTTGGGA	GGTGTTGATG	AAAACATTTT	TTGTCAAACA	AAAGTTTCGT	60
CTTGGAGGCG	AACGCTTCGC	TATCAAGGAT	GACAGGGGAG	AAATTGCCTA	TCAGGTGGAG	120
GGATCATTTT	CTTAAGATTC	CCAAAACCTT	TACCATCTAT	GATGCGGCTG	GTGAACAAGT	180
CAGTCAGATC	AGTAAAGAAA	TCTTGACCTT	GCCTCCTCGT	TTTGGAGATT	CAGCTTCGGG	240
ATGGCTCGAG	TTTGTGCATT	CGTAAGAAGT	TGACCTTTTG	GCGAGATAAG	TATGAGTTTG	300
ATAATCTAGG	TCTTCGTATC	GAGGGCAATA	TCTGGGATTT	GAATTTCAAA	TTGCTGGATG	360
ATCGCGATCA	GTTGATTGCG	GAAATTAAGA	AGGAACTCTT	CCATCTGACC	TCTACCTATA	420
CCGTAACGGT	TCTTGAAGAC	GCTTATGCAG	ACCTAGTCAT	TTCCCTCTGT	GTCCGGATTG	480
ACTATGTGGA	AATACTGGAA	AGCCAATCAC	ATTAAACAAG	TGAATAAGGA	GACAATATGA	540
AACAACATATC	TAGTGCACAA	GTACGCCAAA	TGTGGCTTGA	TTTCTGGGCG	ACCAAAGGTC	600
ACTCAGTAGA	ACCATCAGTA	AGTTTGGTTC	CTGTAAATGA	CCCAACTCTT	TTGTGGATCA	660
ACTCTGGGGT	AGCAACCCTT	AAGAAATACT	TTGACGGGAC	CATTATCCCT	GAAAATCCAC	720
GTATTACCAA	TGCCCAAAAG	GCTATCCGTA	CCAACGACAT	CGAAAACGTT	AGGGAAAGAC	780
TGCGCGTCAC	CATACCATGT	TTGAAATGTT	GGGGAACCTC	TCTATCGGGG	ATTACTTCCG	840
TGACGAAGCT	ATCACTTGGG	CTTATGAGCT	TTTGACAAGC	CCTGAATGGT	TTGATTTCCC	900

TGCTGAAAAA	CTTTACATGA	CCTACTATCC	AGACGATAAA	GATTCTTACA	ACCGCTGGAT	960
TGAAGTGGGA	GTGGATCCAA	GTCAC TTGAT	TCCAATTGAG	GACAACTTCT	GGGAAATCGG	1020
TGCGGGACCT	TCTGGACCAG	ATACAGAAAT	CTTCTTTGAC	CGTGGGGAAG	CCTTTGACCC	1080
AGAAAAATATC	GGTCTTCGCC	TGCTTGCAGA	AGATATTGAA	AACGACCGTT	ATATTGAAAT	1140
CTGGAACATC	GTTTGTGCAC	AATTTAACGC	AGACCTTGCT	GTTCTTCGTA	GCGAATACAA	1200
GGAATTGCCA	CATAAGAACA	TTGATACGGG	CGCTGGTTTG	GAGCGTTTGG	TGGCCGTTAT	1260
CCAAGGGGCT	AAGACCAACT	TTGAAACGGA	CCTCTTCATG	CCGATTATCC	GTGAAGTCGA	1320
GAAATTGTCT	GGTAAGGTTT	ATGACCAAGA	TGGCGACAAC	ATGAG		1365

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTCCAGGTAA	TGTCAAGGCT	AACGTGGTTC	CAATTCAAAA	ACTGATTGAT	ATTTCAAAAG	60
ACCCACGTTT	TGGAGAAACA	CATGCCCTTA	TCTTGT TTGA	AACACCTCAA	GATGCCCTTC	120
GTGCCATCGA	AGGCGGCGTG	CCAATCAAGA	CTCTTAACGT	TGGTTCTATG	GCTCACTCAA	180
CAGGTAAAAC	ATTGGTCAAT	ACCGTTTTGT	CTATGGACAA	AGAAGATGTT	GCTACATTTG	240
AAAAATGCG	TGACTTGGGT	GTTGAATTTG	ATGTCCGTAA	AGTACCAAAT	GATTCTAAAA	300
AAGATTTGTT	TGACTTGATT	AACAAAGCCA	ATGTCAAATA	AGCCATTATT	TATGAAAGGA	360
TTTTAAACAT	GTCTATTATT	TCTATGGTTT	TAGTAGTCGT	TGTAGCCTTC	CTTTGCAGGT	420
CTTGAAGGCA	TCCTCGACCA	GTTCCAATTT	CACCAACCAC	TTGTAGCCTG	TACCCTTATT	480
GGGCTTGTTAC	AGGTCTTGG	AAGCAGGGAT	TATCCTCGGT	GGATCGCTTC	AAATGATTGC	540
CCTTGGTTGG	TCAAATATCG	GTGCTGCTAT	CGCTCCTGAT	GCTGCACTTG	CTTCTGTGCG	600
TGCTGCCATT	ATCATGGTTC	TTGGTGGTGA	CTTTACCAAG	ACTGGTATCG	GTGTTGCCCA	660
AGCGGTTGCT	ATCCTCTCTG	CCGTAGCTGG	ACTTTTCTTG	ACAATGATTG	TTCGTACAAT	720
TTCAGTTGGT	TTGGTTCATA	CTGCAGATGC	TGCCGCTAAA	AAAGGTGACT	TCGGCGCTGT	780
GGAGCGTGCG	CATTTCAATTG	CGCTACTTTT	CCAAGGACTT	CGTATCGCGC	TTCTGTCAGC	840
TCTTCTCCCT	TATGGTACCA	ACTGAACTG	TACAAAGTAT	CCTTAGTGCC	ATGCCAGACT	900
GGCTCAAAGA	TGGTATGGCT	ATCGGTGGTG	GTATGGTCGT	TGCCGTTGGT	TACGCCATGG	960
TTATCAACAT	GATGGCAACT	CGTGAAGTAT	GGCCATTCTT	CGCTCTTGGT	TTCGTTCTCG	1020
CTGCTGTGTC	AGATATTACT	CTAATCGGAT	TCGGTGCTAT	CGGTGTTGCT	ATCGCTCTTA	1080
TCTACCTTCA	CCTTTCTAAA	ACTGGTGGA	ATGGTGCCGG	AGGAGCCGCA	ACTTCTAACG	1140
ACCCAATCGG	CGATATCCTA	GAAGACTACT	AAGATAAGAA	AGGACTGAAA	ACATCATGAC	1200
TGAAAACTT	CAATTAAC TA	AATCAGATCG	TAAAAAGTT	TGGTGCGGTT	CAACCTTCTT	1260
ACAAGGGTCT	TGGAAC TTTG	AACGGATGCA	AAACTTGGGC	TGGGCTTATA	CACTCATTCC	1320

AG

1322

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

CTGGGATAAC CAAGCGAATC ACAGAACCGT CATTAGCCGG TGTGATACCA AGATCAGAAG      60
CGTTCAAGGC ACGTTCGATG TCTTTCAATG AAGACTTGTC AAATGGTGTT ACCAACAAAA      120
CACGCGCTTC TGAATCGTA ATTGAAGCGA TTTGGTTAAG AGGAGTTTCG ACTCCATAGT      180
ATTCTACATG TACACGGTCA AGCAAGCTTG CATTTGGCAGC ACCAGCACGG ATACCACCAA      240
ATTCACGAGC AAGTGATTGG TGAGACTGGG TCATTCTCTC TTTAGCTTTT TCAATAATTA      300
CGTTAGCCAT ATTCTTTCTT ATTCCTTTTC TTCGATATTA TTTGAAACTG TTGTTCCGAT      360
ATTTTCACCA AATACGACAC GTTTGATGTT GCCTGATTGG TTCATGTTGA AGACAACCAA      420
GTCAATGTCG TTGTCCATTG AGAGGGTTGA GGCTGTTGAG TCCATGATAC GAAGACCTTT      480
GTTGATAACA TCACGGTGGG TCAATTCTTC AAACCTTAACG GCTGTCTTGT CCTTCTTAGG      540
ATCGGCATG TACACACCAT CGACGCCATT TTTAGCCATG AGGATGGCAT CTGCTTCGAT      600
TTCAGCTGCA CGAAGGCCGC TGTGTATCT GTCGAGAAGT ATGGTGAACC AATTCCAGCA      660
CCAAAGATAA CGATACGGCC TTTTCAAGG TGACGAAGGG CACGTCCACG GACATAAGGC      720
CTGCCACTT GTTGCATAGC AATAG                                         745

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(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

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CTGATAAATC TATATCCAGA TTTAGATTTC ATTGTGACGA CGGTAGCTTT GCAGGAACCA      60
GCAAGTGTCG CGTTTGTCCT AGTTAGTGCT TTTCTAACCG AGGGTGATAA ACAACGCTCT      120
CAAGCAAAAA TTCAGGAGAT AAACATATGAA TAATCTTTTCG CTTGTCCTTA TGGATATATC      180

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TGTTCAAAT	CGTCAAGAAG	CCTACAAAGA	ATTAGCAAAT	CAAATCAGCC	TTCTTGTTTC	240
TGAAGATACA	GAAAAAATAG	AAGAGCTTCT	ATATTACCGT	GAGAGACAGG	GAAGTATAGA	300
GGTTGCTAAA	GGTGTCTTC	TACCACATTG	TGAAGGAAAC	TTTCAACATC	ATGTCTTAGT	360
GATTACTAGA	TTAAAACCAC	CTATCAGAGA	ATGGTCGAAG	GATATCCAGT	GTGTTGACCT	420
TATTATCGGT	TTGGCCATTG	CAGTATCACA	GGACAAGTCA	TGTATTAAAA	CATTGATGAG	480
AAGACTAGCA	GATGAATCAT	TCATAAATCA	ATTAAAACAG	TTAACAAAAG	AAGAATTACG	540
GGAGATAATA	TATGGAAATC	AAAGATATTC	TTAATGTGAG	TCTGATCCAG	ACGGATTTAC	600
AGATGCAGAG	CAAAGAAGAG	GTTTTTGAGG	CATTAG			636

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTGGTACAAT	CGGTGTGATG	GACGCTATCG	TGAAACAACC	AGGAGTTAAA	TCAATCATCG	60
GTGGTGGTGA	CTCAGCTGCC	GCAGCGATTA	ACCTTGCCCG	TGCAGACAAG	TTCTCATGGA	120
TTAGTACGGG	TGGTGGAGCA	TCAATGGAAC	TTCTTGAAGG	TAAGGTCTCT	CCAGGACTTG	180
CAGCCTTGAC	AGAAAAATAA	GATTTTATAA	ATAAATCAAA	GAAGAGAGGG	ATGAAAGTTC	240
CTCTTTTCTT	TTGCTTAAAA	TAAAAACGCT	TCCTCTCAAC	TATTACTCAT	AAAAATCACC	300
GATTTATGAT	AAAATGGAAA	TAGAAAGTTG	AGATTATGAG	TTATTTTAAA	AAATATAAAT	360
TCGATAAATC	CCAGTTCAAA	CTTGGTATGC	GAACCTTTAA	AACAGGTATT	GCTGTTTTTC	420
TAGTTCTCTT	GATTTTTGGC	TTTTTTGGCT	GGAAAGGTCT	TCAAATTGGT	GCTTTGACAG	480
CCGTTTTTAG	CCTGAGGGAG	AGTTTGTGATG	AGAGTGTTCA	TTTGGGACT	TCGCGTATTC	540
TAGGAAATAG	TATCGGTGGA	CTCTATGCCT	TGGTCTTCTT	CTTATTAAAT	ACCTTTTTTC	600
ACGAAGCCTT	TTGGGTGACC	TTGGTAGTTG	TTCCAATCTG	CACCATGTTA	ACCATTATGA	660
CAAATGTAGC	CATGAATAAC	AAAGCAGGGG	TTATTGGTGG	TGTAGCAGCT	ATGTTAATCA	720
TTACCCTATC	AATCCAAGT	GGTGAGACAA	TTTTGTACGT	GTTTGTGCGT	GTATTAGAAA	780
CGTTTATGGG	AGTTTTTGTC	GCAATTATCG	TAAATTACAA	TATTGATCGT	ATTCGTCTCT	840
TTTTAGAGAA	AAAAGAAAAA	TAATGTTACA	TTTTATAACA	TTATCAATTG	ACGTTTGTCT	900
TTTTTTAGAC	TATAACAGAC	AGAAAGAAGG	AAATTGTAAA	TGAAGGAAAA	AGAATTTTCG	960
CGAAATATGG	CTGTTTTTCC	TATCGGCAGT	GTTATGAAGT	TGACCGATCT	ATCGGCGCGT	1020
CAGATTCGTT	ATTATGAAGA	TCAAGAGTTG	ATCAAGCCCC	ATCGAAACGA	AGGGAAATCG	1080
TCGCATGTAT	TCCTTGAAAT	GACATGGATC	GTCTGCTTGA	AAATCATT		1128

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

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AGGCAGTTTC AGACTAATAT CCAAGTCGTA AGAAATGCCT GAAATAAGCT TTTCTAAATT      60
GTCCAAAGCT TCGGAAAAAC GCTCTTGGAA TAGTTTCTCT AAAGAACTTG CTGATATAAA      120
ACATCTTGTC TCCAACGCAA CTGTATTTCA TCTGTCACGA CGGGAACACG GGTATAGGTC      180
ATCTGACTGA GCAAGAGGGT CGCATGATCC GCATTGTGAG TATCAATCAA CACAAC TAGA      240
TTTTTAACAG GGGTCAAAAA AGTTTCCTCC TGCCCCAACA AGAAAGTCTC AAACCTCTTG      300
GCAATCATCG GCTAAACTCC TTGGACAAAC CTGGATACAC CTCGTGATCT CGTGTCAAAA      360
AGTCCACTTT GAAGTAACTA TCATCAATCT CCACACGAGC ATAGAGACAT TCTCTGATGG      420
TACCTCGTGG TTGACTGATA GAGCCTGGAT TTAGAAAGAG GATCTTGCCT TCCAACCAAG      480
CACTTGGCAC ATGCAAGTGA CCATAGAGGC AGATAGCGGC CTCTTCCTCC TGAGCCCAGT      540
AGTCCAAC TTGAAAGTTG AAATTGATGT CAAACAAGTG ACCATGAGTT TGGATAATCT      600
TGGTCGAACC AAGCTCAGTC ACCAGACGTT CTGGGTAGCC GGCCTAGAAG TCCATGTTCC      660
CTTTAACAAC GCGGATGCCC TCCCAAAGTG GAGAATCCGG ACGTAGTTCA GAATCGCCGT      720
TATGAAAAAC GGCATCGACT TTGCCCACAT AGCGATCAGC GACTTCTTCC ACAATCAAGC      780
TATCGCCATG GGAATCGCTC ATTACAATGA TGGTTTGCTT TGCCATGATG GAAATACCTC      840
CAAAAGTTTC TTAACGGCTA AGGCACGGTG AGATTGACTA TTTTTCCTT CCAGGGTTAA      900
TTCAGCTGAT GACTCACCTG TCTCTCCTAC AAGGAAGAGG GGATCATAGC CAAAGCCATT      960
TTCACCCTTA GGTTCAAAAGT TAATATAACC TGACCAGTCT GCTTCAACAA CTAAACTTTC     1020
CTTATTTGGG CTGGCTACGA CTAGGGTTGT GTGGAACTGA GCCGAGCGGT CCTTGAGTTC     1080
AAAGACCATG GCCAATTTCG GCAAGAGTTT GGCATTATTT TCACGGTCAG TAGCTCCCAC     1140
ACCTGCGAAA CGAGCTGACC AGACGCCTGG TAAGCCACCA AGGACNTCGA CTTNAGACNA     1200
GATTCAGTGC CAAAACCATC TTGNCCGTCA ATGAGAANTG GTTCTGTC      1249

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(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTAGACCATT	TAACAGTGAT	AGGGTTAAGA	CGAGTGACAT	CACCCCAGAT	GATTGGTGGT	60
TTTACCCAC	GGCATACCGT	ATGGATTGTA	AACCCAATCC	AATTTTAAAG	GAGGAAGGAG	120
GTATCCTGAA	CAAGTTTGG	ACCGGAAGTA	ACTTCAAACC	AATGTCATTA	ACGGCTCAAA	180
TTCAACCGTG	GAAACAAGGA	CATCAAAGTC	AATATCTTCT	TGCCAACTTG	AATCCATTCTG	240
TCAATCGTTT	CAGCAAGGGA	AAGCATCGTA	CTCTTTTGA	GACAATTAC	CTTTACGGTA	300
AGCCAAACGT	TTGGCACGAA	CTTCTTTTGT	TTGAGGGAAT	GAACCAATCC	TTGTTGTTGG	360
AAAAGCTGGA	AATTTGAAAC	CTTCTCCTTG	GATAGCTTCA	CGTTCTGCAA	AGGCTGGCAA	420
ACGAGTGTAG	TCTGCGTCTG	TCAAGCCAGC	GATACGCGCA	CGAAGTTCAG	CATTTTCACC	480
AACACGCTCA	GTCGCAAAGA	GTTCTTTGTT	GGCTGCAAGA	GCTTCTGAAC	CTTGACCATT	540
GCGGATAGCA	TCCAAGTCAC	GGATTTTCATC	CAATTTTTC	ACTGCAAAGG	CAAAGTGGTT	600
CAAGAGTGCT	GGTTCAAATT	CTTCATTAGC	AGTTGTAAAT	GGCACATGAA	GAAGTGAGCA	660
AGAGCTTGTC	AAAACGATGT	TTTCAGCTGG	GATTTGCTCA	AGAACAGCCA	AGCTCTTTTC	720
GTAGTTGTTG	CGCCAGATGT	TTTTACCATT	GACAATACCT	ACATAGAGAG	TCTTGTCAGC	780
TGGGAAGCCA	CCTTTAACGA	GTTCAAGAGT	TTTCTTACCT	TCAACAAAGT	CAAGACCGAT	840
AGCATCTACT	GGTAAGTTTA	CAAGGTCAGC	GTATACGTCA	CGAACATCAC	CGAAATAAGT	900
TTGAAGCAAG	ACTTCAAGAC	CTTTTTTGTC	AGCCAAGAGT	TTGTTGTAAA	GGTTCAAGAA	960
AAGAGCTTTT	TCTTCAGCTG	TCAAGCTTTT	TACAAGAGCC	GCTTCATCCA	ATTGGATGCG	1020
AGTCGCACCA	AGTTCAGCCA	ATTTAGCAAA	AACCTCTTGG	TAAGCAGCCA	CTAAGCTATC	1080
TACGAAGTCG	TCTGCTTTCA	CGCCTTCTTC	AAAGTCTGAC	AATTGAAGGA	AAGTGAAGGG	1140
ACCTACAAGA	ACAGGACGAG	TGTTCAATCC	AAGTCTTTTG	GCTTCTTGGA	ACTCATCGAA	1200
AATCTTGGA	CCAGCCAATT	TTACTTGAGT	GTCTTTTTC	AATTTAGGAA	CGATGTAGTG	1260
GTAGTTAGTG	TTGAACCATT	TCTTCATTGG	AAGGGCGCGA	ACGTCCCCTT	TTCTCCCTG	1320
GTAACCACGT	CCCAAAGCGA	AGTAGCGCTC	AAGGTCAGAC	AAGTCCAAGT	TTTGAACGTA	1380
GGCAGGCACT	ACGTTGAAAA	GGAAAGCCGC	ATCTAGGAAG	TTATCATAGT	GAGAAAAGTC	1440
ATTTGATGGG	ATTTCACTGA	TGCCCTTCCC	TTTGACAATG	TTCCAGTGTT	TACCACGCAA	1500
GTCTTTTGCT	GCTGCTAAAA	GTTCTTCTTC	TGAGATTTCT	TTTCTAAAGT	ATTTTTCAGT	1560
TGTAAATTTT	AATTCACGGA	ATTCGCCCAA	ACGAGGGAAA	CCGATGATTG	TAGTTGACAT	1620
GATGTGTCCT	CCAAAATTTG	TTGTTGAAAC	TATCTTAACA	GAAAAGAAAG	CGTCTGTATA	1680
ATTGTAAAAA	ATTAGGGTTT	GATATAGTTT	GAACTATAT	ATCTGTTTCG	GACAAAAGAA	1740
AAAGACTTGA	AGCAAACGTC	TCAAATCCTT	TGTAATTCCT	ACTTTACAGC	TATATTCCAA	1800
TTAGAATACT	AAAACATGTT	ATTAGTAATT	CTTATAAGTG	ACTATGACCT	GTTATTAGAA	1860
AAGACTATAA	CTGATCTAG	TCAACTTTTT	CCCTGTTCAA	GTGGGACGAT	TGCTAGTGTC	1920
TTTCCTAAAC	TGGCTAGGAC	TTTAAAGACT	GTATCCAAC	GAGGACTAGT	CTTTCCTGTC	1980
TCCATCCTAG						1990

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTTTATAATN NACAANNACT TGGATTTGAA CACTGATTAC CCATATAATG AGATTAAAGG	60
ACAGGTTAAA GTATGGCCAA GGATGGAAGT ATTCTTCTTC TTCGGAAAGA TTTTGTTAAG	120
ATTAATTAAA GGAACCTGGC TTAAAAGGGA GCCAAAAGTT CTTTATCCCA TCCCGAAAAA	180
CAAATTTTGT AAGCGGTAA GGATTTATCG TTTGAGGTTT CAAAGGGACA AATTTTAGGT	240
TTTATTGGTG CTAATGGGGC AGGTAAGTCA ACAACGATTA AAATGTTGAC AGGGATTTTA	300
AAACCGACAT CTGGTTTTTG TCGCATTAAAT GGGAAGATTC CTCAAGAAAA TCGTCAGGAT	360
TATGTTAAGG ATATTGGTGT TGTTTTTGGG CAACGCACCC AGCTTTGGTG GGATTTGGCT	420
TTACAAGAGA CATACTCAGT TTTAAAAGAA ATTTATGATG TCCCTGATGC AGTATTTCAA	480
AAACGCATGG ATTTTPTAAA TGATGTTTGA GACTTGAAAG AGTTTATTAA GGATCCTGTG	540
CGGACACTAT CATTAGGTCA ACGTATGAGA GCGGATATTG CGGCCTCCTT GCTCCACAAT	600
CCCAAAGTTC TTTTPTTAGA TGAGCCGACC ATTGGTTTGG ACGTTTCGGT TAAGGATAAT	660
ATTCGTCGGG CAATTACTCA GATCAATCAA GAGGAAGAAA CTACCATTCT TTTGACCACT	720
CACGATTTGA GTGATATTGA GCAATTTGTG ATCGGATTTT CATGATTGAC AAGGGGCAAG	780
AGATTTTGA TGGAACAGTG AGCCAACCTCA AGGAGACCTT TGTAAGATG AAGACTCTCT	840
CTTTTGAAC TGTACCAGGT CAAAGTCATC TCGTCTCTCA CTATGAAGGT CTGTCTGATA	900
TGACCATTGA TAGACAAGGA AACAGCCTCA ACATTGAATT TGATAGTTCT CGCTACCAGT	960
CAGCTGACAT TATCAAGCAA ACCCTGTCTG ATTTTGAAAT CCGCGATTG AAGATGGTGG	1020
ATACGGATAT TGAGGATATT ATCCGTCGCT TCTACCGAAA GGAG	1064

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTCTAGTGCC TGGTTTGGTA GTGATTTTGG TTGGGGATAA TCCAGCCAGC CAAGTCTAAC	60
GTTGCAACA AGGAGAGGTC AGCTCTTGCG GCTGGTTCCC GTACCGAAGT AGTCCGAGTT	120
CCAGAGACCA TTACTCAAGA GGAATTGTGA GACCTGATTG CTAAATATAA TCAGGATCCA	180
GCTTGGCATG GGATTTTGGT CCAGTTGCCA TTACCAAAAC ATATCGATGA AGAGGCGGTT	240
TTATTAGCCA TTGACCCAGA AAAGGATGTG GATGGTTTCC ATCCCCTAAA CATGGGACGT	300
CTTTGGTCTG GACATCCAGT CATGATTTCC TCGACACCTG CAGGAATTAT GGAAATGTTT	360
CATGAATATG GGATTGACTT GGAAGGTAAA AATCGGTCG TAATCGGTCG TTCAAATATC	420

GTGGAAC	CTATGGCTCA	GCTTCTTTTG	GCTAAAAATG	CGACAGTAAC	CTTGCCCCAC	480
TCACGAATC	ATAATCTTGC	CAAGGTGGCT	GCTAAAGCAG	ATATTCTTGT	AGTCGCAATC	540
GGCCGCGCCA	AGTTTGTGAC	TGCTGACTTT	GTCAAACCAG	GTGCGGTTGT	CATTGACGTT	600
GGGATGAACC	GAGATGAAAA	TGGGAAGCTC	TGTGGAGATG	TTGATTATGA	GGCAGTTGCA	660
CCACTTGCTA	GCCATATCAC	GCCAGTCCCT	GGAGGTGTCG	GTCCTATGAC	CATTACCATG	720
CTGATGGAGC	AACTTATCA	AGCAGCACTT	CGACATTGG	ATAGAAAATA	AGAGAAACAT	780
TCGATTAATA	GAGTGTATTT	TCTATAGCTA	TATCTAAAAT	GGCAGAAATG	AATATTAAAT	840
TTTAGATATA	AGATTACAAA	AGGAGGTCTG	CGTCTCCTTT	TTGTTGTATA	ATAAAAGTGA	900
GAGGGAAAAA	GGATGAAAGT	GATTAATCAA	ACCTTACTAG	AAAAAGTTAT	TATTGAACGT	960
TCTCGTTCAA	GTCATAAAGG	AGATTATGGT	CGTCTGCTGC	TGCTTGGTGG	TACTTATCCT	1020
TATGGAGGTG	CCATCATCAT	GGCTGCTTTA	GCAGCTGTAA	AAAGCGGTGC	AGGATTGGTG	1080
ACCGTTGGAA	CGGACAGGGA	AAAATATCCC	GGCTCTGCAC	AGCCATTTAC	CTGAGCCTAT	1140
GGCCTTTTCT	CTTCAAGACC	AGCAATTGTT	AAAAGAGCAA	TTGGAGAAGG	CAGAAGTTAT	1200
CTTGCTGGGG	CCTGGTTTAC	GAGACGATGC	TTCTGGAGAA	AATCTAGTAA	AACAGGTCTT	1260
TGTTAATTTA	AGCCAAAATC	AGATTTTGAT	TGTAGACGGA	GGTGCCTTGA	CCATTCTTGC	1320
TAGGACAAGT	TTGTCATTTT	CCTCAAGCCA	GTCAATCCNG	CCNCCCGGGG	T	1371

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TTTTGGGGGT	NTGGCTCCTT	NGGTNCTTTA	NAAAAGGCCC	TANGGCCNTG	ATCTGNAATT	60
CCCATTNNTG	GCTCNTNANC	TACCATCCGA	TTTNNCANGG	NCCCCTNNCT	TTCCAATTTN	120
NTTGTTNANA	ATNTGGTCAT	CCTTGGANGT	NCACTCGATG	ANAGTGATTA	ATCAATCCTT	180
ATTANANNAA	GTTATTATTG	ATCGTCCTCG	TTCAAGTCTT	AAAGGAGATT	ATGGTCGTCT	240
GCCGCGCTT	GGTGGTANTT	ATGGGGGCGG	AGGTGNCACC	TCCATNGCTG	CTTGNTCNGG	300
TGNNNNAANC	NGTGCTTGAT	TGGTGACCGT	NGGNNCTNAC	CNGNNTTATT	TCCCGGCTCT	360
GCACNTCATT	NNCCTGACCC	TNCGGCCATT	TCTCTTCAAN	ACCAGCNATN	GTTNAANGAC	420
CNTNTGGNNA	ATGNNGAATT	TTNTCTTGCT	GGGGCCTGGA	TTTACTANNA	CGATGCTTCC	480
NGNANGAAAA	TNTNGTTAAA	ACATGGTCTT	TGNTNAAATTN	TAATCCCNAA	TTCCAAATTN	540
TGAATGTATA	ACNGAGGTGC	CNTNGNCCAT	CCTTGCNAAG	AANAATTTGT	TNTTTTCCCC	600
TCAANNCAAA	ATTGAAATNC	TGGCNCNCNG	GGGGG			635

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

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CTCCTGTGGT AATAGAGAAA AAACCTCCTG AAACAGGAAC TCACGATTCT GCAGGACTAG      60
TAGTCGCAGG ACTCATGGCC ACACTAGCAG CCTATGGACT CACTAAAAGA AAAGAAGACT      120
AAGTCTTTTC GATAAAAAAT AAACAGCGAG ATTGAAGCTC GCTGTTTATT TTTTAATTAA      180
TCACCTAGTC CAAGACGTTT AAAGATATCA TCCACTCGTT TGGTGTAATA AACTGGGTTG      240
AAGATTTTCAT CGATTTCTTC TTGTGTGAGA CGTGATGTTA CTTCTGAATC TGCCTCAAGA      300
AGTGGTTTAA AGTCTACTTG GTTGTCCCAA GAGTAGGCTG TTTTGGTTG CACCAAGTCA      360
TAGGCTTGCT CACGGGTCAT GCCTTTTTC AATCAATGTCA ACATAGCCCG TTGGCTAAAG      420
ATAAGACCAA AAGTCGAGTT CATGTTTCGG ATCATATTTT CTGGGAAGAC TGTCAAGTTC      480
TTGACGATAT TTCCAAAACG GTTGAGCATG TAGTCAATCA AAATGGTCGT ATCTGGTGTG      540
ATGATACGCT CAGCTGATGA GTGAGAAATA TCGCGTTCGT GCCAGAGAGC GACGTTTTCA      600
TAAGCCGTAA TCATGTGACC ACGAATGACA CGCGCCAGAC CAGTCATATT TTCAGAACCG      660
ATTGGGTTGC GTTTGTGAGG CATTGCTGAA GACCCTTTT GCCCTTTAGC AAAGAAGTCT      720
TCTACTTCGC GTTGCTCAGA TTTTGTAGA CCACGAATCT CAGTCGCCAT ACGTTCGATT      780
GAAGTCGCAA TGCTGGCAAG AACCACAAAG TACTCAGCGT GAAGGTCACG AGGAAGGACT      840
TGTGTTAAAG ATTCTTGGG CACGGATGCC AAGTTTATCG CAGACATACT CCTCTACAAA      900
TGGTGGGATA TTGGCAAAGT TCCCAACCGC ACCAGAAATC TTACCAGCTT CTACACCAGC      960
AGCCGCATGC TCGAAGCGCT CCGATATTGC GTTTCATTTT GCTGTACCAA GTTGCTAATT     1020
TAAGACCAAA GGTTGTCGGC TCAGCGTGCA CACCATGAGT ACGCCCCATC ATGATGGTGA     1080
ACTTGTGCTC CTTGGCCTTG TCAGCGATGA TATTAGTGAA GTTTTCAAGG TCACGACGGA     1140
TGATGTCGTT GGCTGCTTG TAGAGGTAAC CATAAGCAGT ATCCACCACG TCGGTAGAAG     1200
TTAACCATA GTGAACCCAC TTGCGCTCTT CACCAAGAGT CTCAGAAACC GCACGCGTGA     1260
AAGCCACCAC ATCGTGGCGC GTCTCCTGCT CAATTTCCAA AATACGGTCG ATGTCAAAGT     1320
CCGCCTTCTT GCGAATCAAA GCCACATCTT CCTTAGGGAT TTCCCCAAC TCAGCCCATG     1380
CCTCGTCAGA GAGGATTTCC ACCTCAAGCC AAGCACGGTA TTTATTTTCT TCACTCCAAA     1440
TATTCGCCAT CTCAGGGCGA GAGTAACGGT TGATCATGTG TTAATTTTTC CTTTCTTCTT     1500
AAGAT

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1505

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CGGTGGTGGT	GGACTGGCTG	CTCCCCAGTT	AGATATCTCA	AAACGCATTA	TCGCTGTTTT	60
GGTACCTAAT	ATTGTTGAAG	AAGGCGAAAC	TCCACAGGAA	GCCTACGATT	TGGAAGCCAT	120
TATGTACAAT	CCAAAAATCG	TCTCTCACTC	TGTTCAAGAT	GCTGCTCTTG	GCGAAGGAGA	180
AGGTTCGCTG	TCTGTTGACC	GTAACGTGCC	TGGCTATGTT	GTTGCGCCATG	CCCGCGTTAC	240
TGTTGACTAC	TTTGACAAAG	ATGGAGAAAA	ACACCGTATC	AAACTCAAAG	GCTACAACCTC	300
CATTGTTGTT	CAGCATGAAA	TTGACCACAT	TAACGGTATC	ATGTTTTACG	ATCGCATCAA	360
TGAAAAAGAC	CCATTTGCAG	TTAAAGATGG	TTTACTGATT	CTTGAATAAA	GAAAATCCCG	420
TTGCAAGACG	GGGTTTTGTG	TTATAATAGA	GGCATGAAAA	CAAATGATAT	TGTCTATGGT	480
GTCCACGCCG	TTACCGAAGC	CCTCCTTGCA	AATACAGGAA	ACAAACTCTA	CCTCCAAGAA	540
GATCTCCGAG	GTAAGAATGT	TGAGAAAGTT	AAGGAACTAG	CGGTGACATT	TTGAACAAAT	600
ACCAATTTTG	AAATTGTTAT	TC				622

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CTCCACCTCG	AAACTTAATC	TTAGCCAGCA	ATCCCTTAGA	AACCTCGTGC	TTTTTTAAAA	60
AGGTCTTAAC	CTTGACATGT	TCATCTGCGA	TAAATTCAAA	CCTCATTCAT	CCACCTCACC	120
GATAAAGGCA	TCCTTAACAC	GGTTCCAGAA	ACTGGTATGG	CTAGGAGTCG	CGACAAAGTG	180
AATCTTATGA	TGGTCGATTT	GATACTCAAT	ACGCTCAATA	TTACGGAAAG	AATAAACGCT	240
ATTGTCAACC	GAAATAGTAT	GATAATCGTT	TCTTGTTGGA	ATAAGTTCAA	TCTTATCCTT	300
CTTAGGCACA	ATAATGGAAG	AGCCCACTGT	TCGATAAACA	CGATTATTAA	GGCTGGCAAT	360
TTCCGTTAAT	TGCAAAGCTT	CAATGGTAGG	GTGTAACAACA	GCACCGCCAA	GAGACTTGTT	420
ATAGGCAGTA	CTACCAGTCG	GTGTCGAAAC	TGTTAGCCCG	TCTCCACGAA	AACGTTCAAA	480
GGGAACACCA	TTTATTACAA	TATCTGCCAC	CATGGTTCGA	TCAGACCTGC	GGATGCTGGC	540
TTCGTGAGT	GCTCTGAAAA	TCTTAACTTC	ACCATTTTCA	AGAAAGACCT	TCACATTCAG	600
AACAGGGTAA	GAAACCCCTG	CCCCAGTATC	TAGCTGCAAA	TTAGTCACTA	GCTTGTCCAA	660
CTCAAAATCA	CGATAATCTG	TATAGAAGCC	CAAATGTCCA	GTATGAAGAC	CGATAAAGCG	720
GACCTTGTC	AGCTGATTTT	CGTACTTATG	AAAGGCCGAC	AAGAGCATAC	CATCCCCGCC	780

AATGGAAATG	ACAATATCCG	GATTGGTATC	ATTGAGTTAT	AAACTGATTT	CTCTTCAAAC	840
GATCTCGCAA	TTCATACAAA	ACCCTTTGAC	TCTGCGGTTT	TCTATTGGCT	ATCAGATCAA	900
TTCGTTTACC	TGTATTCTTC	ATCTGTATCG	TCACTGNNTC	CAACACCGTC	ATTTAATTTT	960
CTACTCAAAG	GATCAAAAAG	TGCCTGGGCT	TCTTGGATAT	CATCACGAAT	TTCACCCATT	1020
TCTTCATCCA	ACTGATGGGC	GATTCTAGCT	GTAATTTCCA	GTCGCTTCTT	AATCTCATCT	1080
GGGAAATCCC	CTTGGTACTT	GTAGTTGAGA	GAATGTTCTA	TCGTTGCCCC	GAAATTCATG	1140
GCCAAAGTAC	GAATTTGAAT	TTCTGCCAAA	ATAGTCTTAG	CTCCATTGAT	GGTATCAACC	1200
GTATATTCTA	CTACCACATG	ATAGGAACGA	TAGCCTGATG	CTTTTCTATG	AGTAATGTAA	1260
TCTCGTCTCT	GTATGATTCT	CATATCCTGA	CGTTTGTGCA	AAATATCCAC	TACTTCCTTG	1320
ACGTCATCTA	CAAACCTGAAC	CATCACACGT	AAGCCAGCAA	TATCCTGCAA	ATCGTGTTC	1380
AAGGTCGCAT	AAGTAATGCC	ACGACGAGCC	ATTTTCTCTT	TGATGCTCTC	AATTGGCTTG	1440
ACTCGACCGG	TCACAAACTC	AATTGGAGAA	TGCTTATTTT	GCTTACGATA	TTGCTTACGA	1500
ATACCACGAA	GTTTAATCTT	TAACACCA	ACAG			1534

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTCGTAAAAA	CACTAAAGGA	GGTAAATAAC	CAATGTTAGT	ACCTAAACGT	GTTAAACACC	60
GTCTGTAATT	CCGTGGAAAA	ATGCGCGGTG	AAGCAAAAGG	TGGAAAAGAA	GTAGCATTCG	120
GTGAATACGG	TCTTCAAGCT	ACAAC TAGCC	ACTGGATCAC	TAACCGCCAA	ATCGAAGCTG	180
CTCGTATCGC	CATGACTCGT	TACATGAAAC	GTGGTGGTAA	AGTTTGGATT	AAAATCTTCC	240
CACACAAATC	ATACACTGCT	AAAGCTATCG	GTGTGCGTAT	GGGATCTGGT	AAAGGGGCAC	300
CTGAAGGTTG	GGTAGCACCA	GTTAAACGTG	GTAAAGTGAT	GTTGAAATC	GCTGGTGAT	360
CTGAAGAGAT	TGACAGTGAA	GCGCTTCGAC	TTGCTAGCCA	CAAATTGCCA	GTTAAATGTA	420
AATTCGTAAA	ACGTGAAGCA	GAATAAGGAG	AAGGCATGAA	ACTTAATGAA	GTAAAAGAAT	480
TTGTTAAAGA	ACTTCGTGGT	CTTCTCAAG	AAGAACTCGC	GAAGCGCGAA	AACGAATTGA	540
AAAAAGAATT	GTTTGAACCT	CGTTTCCAAC	CTGCTACTGG	TCAATTGGAA	CAAACAG	597

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

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CTGCTTATGA TTTTCAAGTT TGGACTCGAA ATCAATGGCT TCCCCGTGCT TTAAATGATT      60
GGCGATTTCGT TCTCCTAGTT TCTGATTGGA AGTTTGGGAA TTTTCCCTGA TTAGGAAAT      120
GCGACTATTT TAGTCTTGGT TTCCTTGATT ATGTATACAG TTAGTGGAAT CGCTTATCGC      180
TGGTTTTTCAA CCATTCTGGC ACTCGTATCT GCCACTTCTG TCTTTGTCTT GACCACTATC      240
AGCCTAATCG GTGTTGAGAC CTTTTCAAAA ATTCCAGTAT TTGGCTATGT AGCCAAGCGC      300
TTTAGTGCCT TTTTAAATCC TTTTGCCGAT CGTGCTGATG CAGGTCACCA GTTAGCTAAT      360
TCTTATTTTG CCATGGTCAA TGGCGGTTGG TTTGGTCTAG GTCTTGGAAA CTCGATTGAA      420
AAACGAGGTT ATTTGCCAGA AGCTCATACA GACTTTGTCT TTTCTATCGT GATTGAAGAA      480
TTTGGCTTTG TTGGTGCCAG TCTTATTTTA GCTCTCTTGT TTTTCATGAT TTTGCGGATT      540
ATCTTGGTGCG GTATCCGAGC GGAGAATCCT TTCAATGCCA TGGTTGCACT CGGTGTCCGA      600
GGGATGATGT TGGTTCAGGT ATTTGTCAAT ATCGGAGGGA TTTCCGGGCTT GATTCCATCT      660
ACAGGAGTGA CTTTCCCTT CTTATCCCAG GGTGGAATA GTCTTCTAGT CTTATCAGTG      720
GCAGTAGCCT TTGTCTTAAA TATTGATGCC AGTGAAAAAC GCGCTAAGTT GTACCGAGAA      780
TTGGAATAATC AACCAATGAA CCTTCTGTTG AAGTAGGATA AAGAAAGGAT AGTTTATGTC      840
TCTTCAAAAA TTAGAAAATT ATAGTAATAA AAGTGTTGTG AAAGAAGAAG TCTTGATTCT      900
AACAGAATTA CTGGAAGATA TACTAAAAA TATGCTTGCC CCAGAGACCT TTGAAAAAAT      960
AATACAGTTG AAAGAATTAT CAACGCAGGA AGATTATCAA GGTCTAAACC GTCTAGTGAC     1020
TAG                                                                    1023

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(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

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CTGGATTGAG AAAAGATAAC AAGCTATTCT CCACTCTCCA ATTCATCCAT ATCTTGTTCA      60
AATTTTTTCT GAGCCCATTC GCCATAGCTC TTAAGACCAA GATTGCCAAT AAAGACCCAC      120
GGAAGGTAAA TGACATAAGT AATGACCCAA GCAGACAGGT ATTTAAAATT CAAAGGATTG      180
TGCTGATAAA TTTCTATGTT GAATTGATAA TTCTGCAACA TCAAAAGAGC CGTAATAGCC      240
AAGGTTAGGA AAAAACAACC CAAAATCGTA AAATGAAAAC GACTATAGTA GGTCACTCCC      300
AGATAACGGG CACGATTGAA AAAGTAAAT GTCCCTATGA TGATAACGAT TAGCAGCATA      360

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TTAGAATTAA AAAGGCTTGG TGCTAATACT GAAATGATAT AAGATAGGAG CGACAAAGCA	420
ATGCAGATAT AGAAACTTTC AGAGCCCGCT TTATTGAACA GTTGTTCCTC TCTTTCGTCT	480
AGTAATTGAT AATAATAAAA TCTATTTTTC ATCTTCTTCC TCCCAAATA GTTGGTCTAG	540
GGTTTTCCCT AAACATCTGC AAATAGACTG GCAGAGCGAG AGACTGGGAT TGTATTTTCC	600
CGCCTCTATC AAACCAATAG TCTGGCGTGT CACCCCGACA GCCTCTGCCA GTTGACCTTG	660
TGTTAAATCA CGCTCTACCC GAGCTAATTT TAATTTTAAA TTTTGTAGCCA CCTTCGTCCT	720
CCTTATAGTT TTAATACTCA TCTACGCTTA AAAAATCCAA AACCAACACA AGCTATCAG	779

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCATAAGGAA GCTGTCGCTC GTTCCGCTAA GGTATGGACA CCACGGTGAA CATTTGGCATT	60
GTCTTGCTCA TAGTAACTGT TAATAGCTTT CAGAACTACT AGTGGTTTTT GTGTCGTCGC	120
AGCATTGTCC AGATAGACCA GAGGTTTCATC ATTGACAATC TGATCTAAAA TTGGAAAATC	180
CTTGCGAATC GCTTCTACAT CTAACATAGG CTTCCCCTTA GCGTTTTGAC AATTTCTCTT	240
CGATAGTTGC AATCATTTCA TCACGAACCT CTTGACTGG AATCTCCACG ATAACAGATC	300
CAAGGAAACC ACGAACAACC AAACGCTCTG CAGTTGCCTT ATCCAATCCA CGACTCATGA	360
GGTAATACAT GTCTTCTGGA TCAACTTGTC CGATAGACGC TGCGTGTCCT GCAGTGACAT	420
CATTTTCATC AATCAAAAGA ATTGGGTTAG CATCTGAACG CGCTTGGTCT GAAAGCATGA	480
GAACACGGCT CTCTTGTTGC GCATCTGCTC CCTTAGCACC CTTGATGATG TGGCCGATAC	540
CATTGAAAGT CAAAGTTGCT TTTTCAAGGA TAACCCCATG TTGTAGGATA TTTCCGATAG	600
AGTTGCAGCC ATAGTTAGTT ACACGAGTAT CAATCCCTTG TACCTGACGA CCACTTGAAA	660
GAG	663

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CTCAAGTTTA	AAACCAAGCA	AGTCAAGGAC	AGTCTCTACA	AGATTGCTGG	AATTGCAGAT	60
GTAGAAGTTG	CTGAAACGCT	TGGTATGGAA	CATCCAGTCA	AGTATCGCAA	TAAGGCGCAG	120
GTGCCCCGTT	GTCGAGTGAA	TGGTGTCTTG	GAAACAGGAT	TTTTCCGTAA	GAATTCGCAC	180
AACCTCATGC	CCCTTGAAGA	TTTCTTTATC	CAGGATCCTG	TCATTGACCA	AGTCGTAGTA	240
GCTCTTCGAG	ACCTGCTCCG	TCGTTTTGAT	TTAAAACCTT	ATGACGAAAA	GGAACAGTCT	300
GGATTGATTC	GGAATCTTGT	GGTGCCTCGT	GGTCACTATT	CAGGACAAAT	CATGGTCGTT	360
TTGGTGACAA	CTCGTCCAAA	AGTTTTTCGT	GTTGACCAAT	TGATTGAACA	AGTTATCAAG	420
CAGTTCCAG	AGATTGTGTC	TGTCATGCAA	AATATCAACG	ACCAGAATAC	CAATGCGATT	480
TTTGGTAAGG	AGTGGCGCAC	TCTTTATGGT	CAAGACTATA	TTACGGACCA	GATGTTGGGA	540
AATGACTTCC	AAATCGCTGG	CCCAGCCTTT	TACCAAGTCA	ATACTGAAAT	GGCGGAGAAA	600
CTCTATCAAA	CAGCCATTGA	CTTTGCAGAG	TTAAAAAAG	ATGATGTGGT	TATTGATGCT	660
TATTCTGGTA	TTGGAACCAT	TGGTTTATCA	GTCGCCAAGC	ATGTCAAAGA	AGTCTACGGT	720
GTTGAACTGA	TTCCAGAAGC	GGTTGAGAAT	AGTAAAAAAA	ATGCTCAGCT	GAACAATATT	780
TCAAACGCCC	ACTATGTCTG	TGACACAGCT	GAAAATGCTA	TGAAGAATTG	GCTTAAAGAT	840
GGGATTCAAC	CAACCGTTAT	CTTGGTTGAT	CCTCCACGCC	AAGGGCTTGA	CAGAAAGCTT	900
TATCAAAGCA	AGCGCCCAAA	CAGGAGCCGA	TCGCATCACC	TATATCTCCT	GCAATGTTCCG	960
CAACCATGGC	GCCGTTGATA	TTAAACTATA	CCAAGAGTTG	GGATATGAAT	TGAAGAAAGT	1020
CCAGCCGGTG	GATCTATTTN	TTCAAACGCA	TCACGTCGAG	ACGGTAGCAC	TTTTGTCCAA	1080
ACTCGATGTC	GATAAGCACA	TAAGTGTTGA	AATTGAGCTG	GATGAGATGG	ATTTGACAAG	1140
TGCGGAGAGC	AAAGCAACAT	ATGCTCAAAT	CAAAGAATAT	GTTTGGAATA	AATTTGAATT	1200
AAAAGTTTCG	ACATTATATA	TTGCACAGAT	AAAAAAGAAA	TGTGGAATAG	AATTACGAGA	1260
ACATTACAAC	AAGTNTAAAA	AGGATAAACA	AATTATTCCA	CAGTGTACAC	CTGAAAAAGA	1320
AGAAGCCATC	ATGGATGCTT	TGAGACANTT	CAAAATGATT	TAATAGAAAA	GAATGACAGT	1380
ATATGACTTT	CTGCATTTAT	TACATTCTTA	CTTGGTATAG	GAACAG		1426

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTCTGACGGA	GGCTGGTTAT	GTGGGTGAGG	ATGTGGAAAA	TATACTCCTC	AAACTCTTGC	60
AGGTTGCTGA	CTTTAACATC	GAACGTGCAG	AGCGTGGCAT	TATCTATGTG	GATGAAATTG	120
ACAAGATTGC	CAAGAAGAGT	GAGAATGTGT	CTATCACACG	TGATGTTTCT	GGTGAAGGGG	180
TGCAACAAGC	CCTTCTCAAG	ATTATTGAGG	GAAGTGTGTC	TAGCGTACCG	CCTCAAGGTG	240

GACGCAAACA TCCACAACAA GTAGATGATT CAAGTGGATA CAAAAAATAT CCTCTTCATC	300
GTGGGTGGTG CTTTGTATGG TATTGAAGAA ATTGTCAAAC AACGTCTGGG TGAAAAAGTC	360
ATCGGATTTG GTCAAAACAA TAAGGCGATT GACAGAGAAA CAGCTCATAC ATGCAAGAAA	420
TCATCGCTGA AGACATTCAA AAATTTGGTA TTATCCCTGA GTTGATTGGA CGCTTGCCCTG	480
TTTTTGCGGC TCTTGAGCAA TTGACCGTTG ATGACTTGGT TCGCATCTTG AAAGAGCCAA	540
GAAATGCCTT GGTGAAACAA TACCAAACCT TGCTTTCTTA TGATGATGTT GAGTTGGAAT	600
TTGACGACGA AGCCCTTCAA GAGATTGCTA ATAAAGCAAT CGAACGGAAG ACAGGGGCGC	660
GTGGACTTCG CTCCATCATC GAAGAAACCA TGCTAGATGT TATGTTTGAG GTGCCGAGTC	720
AGGAAAATGT GAAATTGGTT CGCATCACTA AAGAACTGT CGATGGAACG GATAAACCGA	780
TCCTAGAAAC AGCCTAGAGG TGACTATGGA ACTTAATACA CACAATGCTG AAATCTTGCT	840
CAGTGCAGCT AATAAGTCCC ACTATCCGCA GGATGAACTG CCAGAGATTG CCCTAGCAGG	900
GCCTTCAAAT GTTGGTAAAT CCAGCTTTAT CAACACTATG TTGAACCGTA AGAATCTCGC	960
TCGTACATCA GGAAAACCTG GTAAAACCCA G	991

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTGGCTTGGC TCTGATTGTC AATAAAGGAG GTTGATGTTG ATAACCTAAC GACAGAGCAA	60
CTTCGTCAA TCTTCATAGG TGAGGTAACC AATTGGAAAG AGGTTGGTGG TAAGGACTTA	120
CCCATCTCTG TTATCAATCG GGCAGCCGGC TCTGGCTCTC GTGCTACCTT TGATACTGTC	180
ATTATGGAAG GTCAGTCTGC CATGCAAAGT CAGGAGCAGG ATTCAAATGG AGCGGTAAAA	240
TCAATCGTAT CAAAAAGTCC AGGAGCTATC TCTTATTAT CTCTTACCTA TATAGATGAT	300
TCGGTCAAAA GCATGAAGTT GAATGGCTAT GACTTAAGTC CAGAAAATAT AAGTAGCAAT	360
AATTGGCCCT TGTGGTCTTA TGAGCATATG TATACATTGG GGCAGCCCAA TGAGTTGGCT	420
GCAGAATTTT TCAATTTTGT TCTCTCGGAT GAGACCCAAG AAGGGATTGT CAAAGGATTG	480
AAGTATATTC CGATTAAAGGA AATGAAGGTT GAAAAAGATG CTGCCGGAAC TGTGACAGTG	540
TTGGAAGGGA GACAATAATG AATCAAGAAG AATTAGCTAA GAAAATGTTG CTTCATCAA	600
AGAATTCTCG TCTGGAGAAA TTAGGAAAAG GTTTGACCTT TGCCTGTCTT TCTTTGATAG	660
TCATCCTTGT GGCCATGATT TTGGTTTTCG TAGCGCAAAA AGGCTTGTCTG ACCTTCTTTG	720
TCAATGGTGT GAATATCTTT GACTTTCTTT TGGGAGGAAC TTGGAATCCT TCTAGTAAAG	780
AATTTGGTGC CCTTCCTATG ATTTTGGGTT CCTTTATCGT TACCATTCTC TCAGCCCTTA	840
TCGCAACACC CTTTGCTATT GGTGCAGCAG TTTTATGAC CGAAGTATCA CAAAAGGGG	900
CGAAGATTTT GCAACCAGCT ATTGAACTCC TGTTGGGAT TCCTTCAGTA GTGTACGGAT	960
TTATTGGCTT GCAAGTCGTC GTTCCCTTTG TTCGAGTGT CTTTGGTGGG ACTGGTTTTG	1020

GGATTTTGTC AGGGATTTC GTCCTCTTTG TCATGATTTT GCCGACCGTA ACCTTTATGA 1080
 CAACGGATAG CTTGCGTGCG GTTCCTCCNT TATTATCGTG AAGCCAGTTT CGCTATGGGA 1140

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CTGGGACTCT CTTCGTAGAA GTCATGCAAG AATATTTTGA TCAAAAGAGG AAATCATGAA	60
AAAAAGAGCA ATAGTGGCAG TCATTGTACT GCTTTTAATT GGGCTGGATC AGTTGGTCAA	120
ATCCTATATC GTCCAGCAGA TTCCACTGGG TGAAGTGCGC TCCTGGATTG CCAATTTCTG	180
TAGCTTGACC TACCTGCAAA ATCGAGGTGC AGCCTTTTCT ATCTTACAAG ATCAGCAGCT	240
GTTATTCGCT GTCATTACTC TGGTTGTCGT GATAGGTGCC ATTTGGTATT TACATAAACA	300
CATGGAGGAC TCATTCTGGA TGGTCTTGGG TTTGACTCTA ATAATCGCGG GTGGTCTTGG	360
AAACTTTATT GACAGGGTCA GTCAGGGCTT TGTTGTGGAT ATGTTCCATC TTGACTTTAT	420
CAACTTTGCA ATTTTCAATG TGGCAGATAG CTATCTGACG GTTGGAGTGA TTATTTTATT	480
GATTGCAATG CTAAGAGAGG AAATAAATGG AAATTAATTA TGAAACTGGT GGTCTGCGTT	540
TGGATAAGGC TTTGTCAGAT TTGTCAGAA TATCACGTAG TCTCGCGAAT GAACAAATTA	600
AATCAGGCCA GGTCTTGGTC AATGGTCAAG TCAAGAAAGC TAAATACACA GTCCAAGAGG	660
GTGATGTCGT CACTTACCAT GTGCCAGAAC CAGAGGTATT AGAGTATGTG GCTGAGGATC	720
TTCCGCTAGA AATAGTCTAC CAAGATGAGG ATGTGGCTGT CGTTAACAAA CCTCAGGGAA	780
TGGTTGTGCA CCCGAGTGCT GGTGATACCA GTGGAACCCCT AGTAAATGCC CTCATGTATC	840
ATATTAAGGA CTTGTCGGGT ATCAATGGGG TTCTGCGTCC AGGGATTGTT CACCGTATTG	900
ATAAGGATAC GTCAGGTCTT CTCATGATTG CTAATAACGA TGATGCGCAT CTAGCACTTG	960
CCCAAGAACT CAAGGATAAA AAGTCTCTCC CGCAAATATT GGGCGATTGT TCCATGGAAA	1020
TCTGCCTAAT GATCGTGGTG TTAATTGAAA CGCCCGAATT GCGCAATGAA AAAGAACCCTT	1080
AAGAAACCAG GTGGTAACTG GCTAAAGGGA ACCCGGCATG ACCCCTTTTC CCCTTCTTGG	1140
AACGCCTTGG CGAAT	1155

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CTAATCCAAT TGTGGCTGGT GCTCTTGCCA TGACAGCAGG TTATTGTGGG ACCTTATTGA	60
CCCCAATGGC TGCTAATTTT AACGCTCTAC CAGCAGCATT GATGGATATG AAAGATCAGA	120
ATGGCGTTAT AAAGGCTCAA GCAGGTGTTG CTCTAGTAAT GATTGTTATT CACATATTCT	180
TAATGTACTT TCTCGCATTT TAGTAAAGGA AAATAAAATG AAAATATTGG TTACAGGTTT	240
TAATCCTTTT GGAGGTGAAA AGATTAATCC AGCTTTGGAG GCTGTAAAAT TATTACCATC	300
TGAGATTAAT GGGGCTGAAG TTCGCTGGGT AGAAATTCCA ACGGTTTTTT ATAAGTCGTC	360
AGAAGTTTTA GAGGCAGAAA TATTACGATA TCAACCAGAT GCTGTACTTT GTATTGGACA	420
AGCAGGCGGC AGGACCGGCT TAACACCTGA ACGAGTGGCT ATTAATCAAG ATGATGCTCG	480
CATACCTGAT AACGAAGGCA ATCAACCAAT TGATACACCG ATTCGTATTG ATGGAGCATC	540
GGCCTATTTT AGTAGTTTAC CTATCAAAGC GATGGTACAA GCTATCAAAA AACAAGGACT	600
TCCGGCAGTT GTATCCAATA GTGCAGGAAC CTTTGTTTGC AATCATTTGA TGTACCAAGC	660
TCTCTATTTA GTAGATAAAG AAATTCCCTA ATATGTTAAG AGCAGGTTTT CATGCATATT	720
CCATATATGA TGGAACAAGT AGTGAACAGA AGCCGAATAC TCCAGACTAT GAGTTCTATG	780
TGGATATTCG GCGTAAAGGC ATAGAAGCAG CAATCGGCGC TATGATAGAA CATGGAGATC	840
AGGAACTCAA GTTGGTAGGC GGAGAAATTC ATTGATAGAA AAAAGCTTGA GGGGAAAACC	900
TTCAAGCTTT TGGACGTTTT CGAGCCAATA CTGCTCGGTA AAACATAATT TTAGTGCATT	960
GGATATAAGG TAGGAGTGAA AAAGTAGCAA TGCCAAAGGT AATCCAATTG AGGAAGTACC	1020
AAGGAAGAAG	1030

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTGTAAAAGA AGTTAATCAA GTTGATAAAG CACTTTTAAA ACAAATTGGT GCAGTTGATG	60
TCTTAGAAGT GAAGGGTGGC ATTCAAGCAA TCTATGGAGC AAAAGCAATC TTATATAAAA	120
ATAGTATTAA TGAAATTTTA GGTGTAGATG ATTAAGTACT TACTGACTTA ATAAAAACA	180
GAGGAGAGTG ATGGATGAGT AGGATGAAAT GAAATCGCAT ACAAGAAATA AAGAATCAT	240
TATCCAAGTT GGATACGCTT ATTACATAGG AGAATACAAA TGAAATTTAG AAAATTAGCT	300
TGTACAGTAC TTGCGGGTGC TGCGGTCTT GGTCTTGCTG CTTGTGGCAA TTCTGGCGGA	360
AGTAAAGATG CTGCCAAATC AGGTGGTGAC GGTGCCAAAA CAGAAATCAC TTGGTGGGCA	420

TTCCCAAGTAT TTACCCAAGA AAAAAGTGGT GACGGTGTG GAACTTATGA AAAATCAATC	480
ATCGAAGCGT TTTGAAAAAG CAACCCAGAT ATAAAAGTGA AATTGGAAAC CATCGACTTC	540
CAGTCAGTCC TGAAAAATCA CAACAGCCAT CGAAGCAGGA ACAG	584

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGAATTAA AACGCACGAG TATTGCACGA ATAACCAACC AAACAACCAC TCAGACCATG	60
TGGATCCATA CCCTTACTTG GCAAAATGGG GCATTAGCCG TGAGCAGTTT AAGCATGATA	120
TTGAGAACGG CTTGACGATT GAAACAGGCT GGCAGAAGAA TGACACTGGC TACTGGTACG	180
TACACTCAGA CGGCTCTTAT CAAAAGACA AGTTTGAGAA AATCAATGGC ACTTGGTACT	240
ACTTTGACAG TTCAGGCTAT ATGCTTGCAG ACCGCTGGAG GAAGCACACA GACGGCAACT	300
GGTACTGGTT CGACAATCC AGGCGAAATG GCTACAGGCT GGAAGTCTCC AACTCTTCTC	360
TTTTTTAATA CAAGCTATTT TGATTTAACC GGCTGGTCTT GAGCTGTCTG CAAAGCTGTG	420
GCAATCGTAT CTGCATACAA TTTTGCTCCT GCTTCGATAG TGCTACTCTC ACTCCCGAAA	480
TGAACCTGGT CTGTTCCAGC CCAAATTCTT GGATGCTCTT TCGCAACTTG ATTCCAATCT	540
GCTATCGTAA TGTAAGGTGT CTTCTCTGCC AATTCTCTCA TATAGGCAGC AGCCTTCTCA	600
ACGATGGCAT AGGTCTCTTT TGTCTTATCT CCCTCATAAG GAGTCACCAA AATCATATGG	660
TGTCCTTAG GAAGATTTT CACGATACTG TCCAGTCAT CTTGTAATT CTCAGGATTA	720
TTTACCCAG TCGCAATGAC CACCGCTTA GGTAAAAATT TATTCTGGCT ATTATTTAGC	780
ATGATTTTAT TTGCGGTCTT GGTGTTACG CTGACCTGCG CGTTAATCTG TGCTCCAGGA	840
AGAGCTGTCT GTAGTGCTGT ATTTGCCCTT AAAGCCACTG AGTCACCAAT TAACATAGTG	900
CCATCAGCAA TTCCCAAAT GTTGCATCT GCCCGTTCTG CCATCACCTT GGTCTGG	957

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CTCGTGCGAC GACAGATGTT ATTCGTCATG GTGCACCAAA GGCAGAGATT GAGGGGCTTT	60
TCTCAGTTGA GAATAGTCGT CTTTACAGG AAATTTTGA TGAGCAAGGT TTAGAATTAG	120
GTGATGAAAT TATCATCCGT CGGGAAATCT TGCAAAATGG TCGTAGTATC AGCCGTGTAA	180
ATGGTCAGAT GGTTAATCTG TCTGTTTGC GAGCTATTGG GCAACATCTT GTAGATATTC	240
ATGGTCAGCA TGACCATGAG GAGTTAATGC GTCCCCAACT GCATATCCAG ATGTTGGATG	300
AATTTGGTGA TGCCGCTTTT TGGGACTTGA AAGAAACCTA TCAAACGAGT TTTGATGCCT	360
ATCGGAAAAT GCGCAAGCAG GTTCTGGAAG TCAAGAAAAA CCAACAGGAA CACAAGGCAC	420
GTATCGAAAT GTTGAATTT CAAATGGCAG AGATTGAGGC AGCAAACCTG CAGGCTGGAG	480
AAGACTTGGC TCTCAATCAA GAGCGAGATA AACTCCTCAA CCACAAAAAT ATTGCGGATA	540
CACTGACCAA TGCCTACAGT ATGTTGGACA ATGAAGATTT TTCAAGTCTG GCCAATGTTC	600
GTTCAGCTAT GAATGACATG GAAAGTGTG AAGAGTATGA TCCTGAATAC CGTGAAATTT	660
CAAGCTCTCT GTCTGAGACC TACTATGTTT TAGAAGACAT TAACAAACGT TTGGAAGCTA	720
TCATTGAGGA CTTGATTTT GATGGCAATC GCCTGATGCA GGTGAGAAT CGTTTGACC	780
TCCTTCATAC TATTACTCGT AAGTATGGTG GGACTGTTGA TGATGTTTTG CTTTATTTTG	840
CCAAGATTAC GGAAGAATAC AATCTCTTGA CAGGCAATAA TCTTCCGTC TGAGGACATG	900
GAAGCAGAGC TTAAGAAGTT GGAAGTCAAT CTTGTCAATT TGGCAGGTCA ACTTGCTTCT	960
GCTCGTCATA ATTTGGCTCA GCAACTCGAA GCTGAGATTA AACAAGAACT GCAAGATCTT	1020
TATATGGAAG AAGCCCAGTT TCAGGTTTCGT TTTAGTAAGG GAAAATTCAG TCGTGAGGGA	1080
AATAAAATGG TTGAGTTTGA TATTTCAACC AACCTGGAG AAGACTTTAA ACCCTTGGTT	1140
AAGGTTGCTT CTGGAGGGGA ATTATCTCGT CTCATGTTAG CCATTAAGTC TGCCTTTTCA	1200
CGTAAAGAAG GCAAGACTAG CATTGTCTTT GATGAGGTGG AAACGGGAGT TTCAGGTCGT	1260
GTGCTCAAG CTATTGCTCA GAAAATTCAT AAAATTGGTC AGCATGGTCA GGTTTTGCT	1320
ATCTCCCAT TGCCACAAGT AATTGCGATT GCAGATTATC AATTCTTTAT TGAGAAGATT	1380
AGTAATGACC ATTCAACGGT TTCGACTGTT CGTCTCTTGA CGGTCGAAGA GCGAGTGGAG	1440
GAAGTTGCCA AGATGTTGGC AGGTGATGAT GTGACAGAAG CAGCCCTGAC GCAAGCCAGA	1500
GAATTGTTGA GAAACAGGGA GAAATAAGAT GACAGATTAT TATGTAATTG GAGATGTTCT	1560
CGGAAAAG	1568

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CCAAAGGGTC AGGAGACCAG CCAGAAATTG TGGAAGTGTG ACCAGATGCC CTTATTCCTT	60
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ACGCTGCAGT GGTACCGCAT CAGGCAGAGG TCATTTTTCG CCAGCGCTTT GAGATGACAG	120
ACAAGGGAAT TGAAAGAACG AATTGAGTCT TATTATGATG GGGGAAAATC TTTTCCGCTC	180
TATCAAGATT CGGGGGGAAT TTTTACATAT GCATGTGCGT ATGATTCCTA AGTCAACACC	240
CGATACCAAG TTTGCTGATG TCGCAACCCA TCAACCGGAA TATAGTCGTG ACAATGTTGC	300
GGGGACTATT GTTGGTTTCT GGACGCCTGA GATTTTCCAT GGGGTCACTG TGGCAGGCTA	360
CCATCTGCAC TTCATATCAG ATGATTTGAC CTTCCGTGGA CATGTCATGG ATTTTGTCAT	420
CAAGGAAGGC ATTATCGAGG TGGGAGCAGT TGACCAGTTG GACCAACGTT TCCCAGTCCA	480
AGACCGTCAA TACTTGTTTG CTAAGTTCAA TGTGACGAG ATGAAAAAAG ATATTGAAAA	540
GGCAGAATAG GAGAAGAAAA TGACCATTCA TATCATTATT ACCATGTTGC TGTGCTAGC	600
TTTCTGATA GGAAGCATTG GGTTCGCCAA AAAGAAATAT CAGATTAATC TAG	653

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTATTATTGC AAGGTNNTGA AGTCGAACGA AAAAATTACT CTAGTCCTTT TGATTGGA	60
TGTCATCATT TCCTTGATTT ATGGAATTGA CATATTCAAG GCAAGAAAAA GAGCTTGCGG	120
CATCCCAGAG AAAATCTTAC TCATATTACC CCTTACTTGT GGTGGTTTGG GGGCCTGGTT	180
TAGCTGGAAT CACTTTTCAC CACAAGACTC GAAATGGTA CTTTAAAACA GTTTGGTTTC	240
TTGGGATGGT GACCACACTA GTAGCCTTAT ATTATATTG GAGGTAATGG ATGGCAGGGT	300
CTTCGAGGGA CCACGCTGCT TGGGCTCTAG CGGACTATGG TTTTAAGGTC GTGATTGCAG	360
GATCTTTTCG TGACATTCAT TACAATAATG AACTCAATAA TGGCATGTTG CCAATCGTTC	420
AGCCTAGAGA GGTTAGAGAG AAAGTAGCCC AGTTAAAACC AACCGACCAG GTAAGTGTGG	480
ACTTGGAACA ACAAAAAATC ATCTCACCAG TTGAAGAATT CACCTTCGAG ATAGATAGCA	540
AGTGGAACA TAAACTCCTA AATAGTTTGG ATGATATCGG TATTACCTTG CAGTATGAAG	600
AGTTGATTGC TGCTTATGAA AAACAACGAC CAGCCTACTG GCAGGATTAG AAAAAATAGA	660
AAAGGAAATA TAGTAACTG AAATAAGATG TAAACAAATG AATTGGAG	708

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

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CTCGTGTGTG GGACGAGTTA GACATACCCG TCATGGCTTT TGGCTTGAAA AATGACTTTC      60
GCAATGAATT GTTCGAAGGT TCCAAATATC TCTTGCTTTT AGCGGACAAG ATTGACGAAA      120
TCAAGACCAT CTGTCAGTAT TGCAAGAAAA AGGCGACCAT GGTGTTGCGA ACACAGGATG      180
GACTGCCCGT TTACGATGGA GAACAGATCC AGATTGGTGG TAATGAAACC TATATCTCGG      240
TTTGCCGTAA ACATTATTTT GCCCCTGAAA TCAATAAGGA GAATGAAGAA AAATGAACAT      300
CTATGATCAA CTACAAGCTG TAGAAGACCG TTATGAAGAA CTAGGAGAAT TGCTGAGTGA      360
CCCTGATGTC GTTTCAGACA CCAAGCGTTT TATGGAGCTT TCAAAAGAAG AAGCTTCAAA      420
TCGTGACACC GTAATAGCCT ACCGTGAGTA TAAACAAGTC CTTCAAAATA TCGTCGATGC      480
CGAAGAGATG ATTAAGGAAT CAGGCGGAGA TGCGGACTTG GAAGAATTGG CCAAGCAAGA      540
ACTCAAAGAT GCCAAGGCTG AAAAAGAAGA ATATGAAGAA AAATGAAAA TTTTGCTCCT      600
TCCAAAGGAT CCAAACGATG ACAAGAATAT CATCCTTGAA ATCCGTGGAG CAGCTGGTGG      660
AGACGAAGCG GCACTTTTCG CTGGAGATTT GCTAACTATG TACCAAAAGT ATGCGGAAGC      720
CCAAGGTTGG CGCTTTGAAG TCATGGAAGC CTCTATGAAT GGTGTCGGTG GTTTTAAAGA      780
AGTGGTTGCT ATGGTTTCAG GTCAGTCTGT ATACTCTAAG CTTAAGTATG AATCAGGTGC      840
CCACCGTGTG CAACGTGTTC CTGTGACAGA AAGCCAAGGC CGTGTCATA CTTGACAGC      900
GACAGTTCTT GTTATGCCAG AAGTTGAAGA GGTGAATAC GACATTGATC CAAAAGACCT      960
TCGTGTCGAC ATCTATCACG CCTCTGGTGC TGGTGGACAG AACGTCAATA AGGTTGCGAC     1020
TGCCGTTTCG ATCGTTCACT TGCCAACCAA TATCAAGGTG GAGATGCAGG AAGAACGTAC     1080
CCAGCAGAAG AACC GCGAGA AGGCTATGAA GATTATCCGT GCACGCGTCG CTGACCACTT     1140
TGCTCAGATT GCTCAGGATG AACAAGACGC TGAGCGTAAG TCGACAATCG GTACTGGTGA     1200
CCGTTTCAGAA CGGATCCGAA CTTATAACTT CCCACAAAAC CGTGTACAG ACCACCGTAT     1260
CGGCTTGACC CTCCAAAAC TAGATACGAT TTTGTCTGGT AAATTGGACG AAGTTGTGGA     1320
TGCCTTGGTG CTTTATGACC AAACACAAA ACTAGAAGAA TTAAACAAAT AATGAAATTA     1380
G

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(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

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CTCCCATTTG CGATACTGGG ATACCTGTCA TTCGTTCCAC AGATTCAGCC ACATCGTTGA      60

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CACTTGCAGT	CACTTTCATA	TCTTCTGTGT	GGTTTTCGAT	TTTCCTTTCC	AATTCTGCAA	120
TGCGTGTTTT	ATAGTTTAGA	GCTGCTTCAA	AATCTTCTGC	TTCAACTGCT	TTTTCTTGCT	180
TGTCTTTTTT	CGTTTCGATT	TCTCGTTCAA	CAGCATGCAC	ATCTGTTACT	GGATGTTGAG	240
CCGCCAAGTG	AGCAGCCGTT	ACATCGACAA	GGTCAATAGC	CTTATCTGGC	AAGCTACGTT	300
GAGGAATGTA	TTGAACAGAA	TAATCCACCG	CTGCTTTCAA	GACTTCGTCT	GGCAAGATGA	360
CATTGTGGTG	TTGTTGATAG	AGGTCACGAA	TGCCTTGAAG	AATTTTAAAA	GTATTCTCTG	420
CTGAAGGAGC	ATTGACCTTC	ACTTCGTGTA	AACGACGAGC	AAGAGCAGCA	TTCTTCAAGA	480
AGGTGTTACG	GTATTCGTCT	TGAGTTGTTG	CCCCAATCAC	TGTCAATTCT	CCACGAGAGA	540
GACTGGCTGA	GAATATCCGC	AAGCCCTTTA	GAACCACTGT	CTCCACAAGT	GCTACCAGCA	600
CCAAGAATTG	TGAATTTTAT	CAAAGAAGAG	GATAATATTC	CCTGCTTCTT	TCACTTCATT	660
GACTAAGTTT	TGGACATTTT	CTTCAAAGCT	ACCACGGTAT	TGAGTACCAG	CCTCAAGACC	720
TGAGATATCA	ATAGAAATAA	TTTCCTTGTT	CTTGATAGCA	GCAGGAACAT	CTCCGTTTAC	780
AATGGCTTGC	GCTAGACCTT	CGACAACTGC	TGTCTTACCA	ACACCTGCAT	CTCCGACCAA	840
AACAGGATTG	TTCTTGGTGC	GGCGTGAGAG	GATTTTCAGAT	GTTTCTTGAA	TTTCCTTGTT	900
TCGTCCGATA	ACAGGATCCA	ACTTGCCCTC	ACGCGCTTCT	GCTGTCAAGT	TTGACCTTAG	960
TTTTCGAAGG	ACACCGTCTT	GTTTCATACC	TGATGCCTGT	TGTGGCATT	GCACATCAGT	1020
TTCTGCATTT	CCTGGTAATT	GACCAGTCGT	ACGATAGTGA	GCAAATTCCT	CAGGTGTGAC	1080
TTCCGCTCCA	TTAATTAAGT	AACGGCGATT	TTCAGAACTG	TATCCTCGCA	TACCACCCAT	1140
CAATTGGTTA	AATAAATCAT	CCATGTTATT	AAAATTATTA	AAGTTGTTAT	TCATATTCTT	1200
TACCTCTTTT	TGTTTACTTA	GTTATGATTA	CTGATATTGA	CTATCTTTGA	CCTTTGTTTT	1260
AAAAAATTTA	GACTAG					1276

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTTGGCAGAA	TTTGCCGGTC	TATCAGACGC	ACTTAAAGGG	CAAGGACTCT	AAGTATGCAG	60
GGACAAATCA	TTAAAGCCTT	GGCAGGTTTC	TACTATGTGG	AGAGTGATGG	CCAGGTTTAT	120
CAAACACGCG	CGCGTGGGAA	TTCCCGTAAA	AAAGGCCATA	CCCCTTATGT	TGGGGACTGG	180
GTACATTTCT	CTGCCGAGGA	AAATTCAGAA	GGCTATATCC	TAAAAATTCA	CGAACGGAAA	240
AACAGTCTAG	TTGCTCCGCC	TATTGTCAAT	ATCGATCAAC	CTGTAGTAAT	CATGTCCGTC	300
AAGGAACCTG	ATTTTAACAG	CAATTTGCTG	GATCGTTTCT	TGGTTCTTTT	GGAGCACAAG	360
GGCATCCATC	CCATTGTCTA	TATTTCCAAA	ATGGATTGTG	TGGAAGATAG	GGGAGAACTG	420
GATTTTACC	GGCAGACCTA	TGGTGACATC	GGCTATGACT	TTGTGACCAG	TAAAGAGGAA	480
CTCTGTCTT	TGTTAACAGG	CAAGGTTACG	GTCTTTATGG	GGCAGACAGG	TGTTGGGAAG	540

TCAACTCTTC	TCAATAAACT	CGTACCAGAC	CTCAATCTTG	AAACGGGAGA	AATTTTCAGAC	600
AGTCTAGGTC	GCGGTCGCCA	TACCACTCGA	GCTGTTAGTT	TTTACAATCT	CAACGGGGGT	660
AAAATCGCAG	ATACACCAGG	CTTTTCATCT	CTGGACTATG	AAGTATCAAG	GGCTGAAGAC	720
CTCAATCAGG	CTTTCCCAGA	GATTGCTACT	GTTAGCCGAG	ATTGTAAGTT	CCGTACTTGT	780
ACCCATACCC	ATGAGCCGTC	TTGTGCCGTC	AAACCAGCTG	TTGAAGAGGG	TGTTATTGCA	840
ACCTTCCGTT	TTGATAATTA	CCTGCAATTC	CTTAGTGAAA	TTGAAAATCG	TAGAGAAACC	900
TATAAAAAAG	TCAGCAAAAA	AATTCCAAAA	TAAGGAGAAA	CCTATGTCTC	AATACAAGAT	960
TGCTCCGTC	ATTCTGGCAG	CAGATTATGC	CAACTTTGAA	CGTGAAATCA	AACGTCTAGA	1020
AGCAACTGGG	GCAGAATATG	CCCATATCGA	TATCATGGAC	AGTCATTTTG	TACCGCAAAT	1080
CAGTTTTGGT	GCAGGTGTGG	TCGAGAGCCT	TCGTCTCAT	AGTAAGATGG	TTTTCGATTG	1140
CCACTTGATG	GTGTCAAACC	CTGAACATCA	TCTGGAAAAA	TTTTGCGCCC	GTTGCAGGGT	1200
TGCAAAAAAT	TCATCCAGTT	ATCCCATGTT	TAAA			1234

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTCTTAAGAC	CAATTCCGAG	TTACTTCTTC	ATCAGCCTTT	AACCGATCCA	CTAATTGGTC	60
AAGTGAATCA	AATTTGGTCA	TATCTCGAAT	GCGATCAAGC	CAATAAACCA	TGACGGTTTC	120
CCCATAAATA	TCTTGATTAA	AATCAAAAAT	ATTGACTTCA	AAACGTGCTT	CTTCTCCATC	180
AAAGGTCACA	TTTTTCCCGA	CACTAGCCAT	AGCACGATAC	TTCTGTCTTT	GAATCTCAAC	240
ATCAACGACA	TAAACGCCAT	CTGCTGGCAT	ATAAGTACGG	TCTAAAAGCA	CTAAATTCGC	300
TGTCGGATAA	CCAATTGTAC	GACCACGAGC	ATTACCATGA	ACTACCATAC	CTCTTGATGG	360
AAGCGGTGCC	CCCAAAGTT	TTCTGTCTTC	TTTCACATTT	CCATCTAAAA	TAGCTTGACG	420
GATACGAGTT	GAACTAATCT	TTCTTTCTTC	ATCTTCTACA	GGTGAACAA	TGATAACTTC	480
TCCATCAAAG	TAATCCTTTA	AATCTTCTGC	TGTTTTTTTG	TCAGAACCAA	ATGTATAATC	540
AAAACCTGCA	ACAATAATTT	TGGCATTTCAT	AGCCTTGATA	TAAGTTGCAA	AGAATTCTTG	600
TGCAGTGAGA	CTAGCGAATT	GACTACTAAA	ATCAAGGAGA	TATAATTCTT	CTACACCTTC	660
GCGCTTTAAT	TTTCTTTCAC	GTTTCAGCAGG	GTTCAAAAATA	TGCAAAAACA	AATCTGGATG	720
ATAAGGCTCT	AAAGCGATCT	TTGGAGATTC	ATTAAAGGTC	ATAACGACGA	TAGGCAATAA	780
ATCCTTTCTC	GCAGCCTTGT	TGGCAACACG	AAATAATTCT	TGATGCCCCCT	TATGTATGCC	840
ATCAAAATAG	CCGAGAACAA	CAGCTGAATC	AGATGGTGTG	CCAATATCTT	TTTGGTTTTT	900
TATAGGAATA	GTAATAATCA	TAAAATAATT	ATATCATAGC	GATAG		945

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

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CTATTTTAAA AGGAGAATTG GCAGATGGCG ACTACTGAGT TGATTGAACT GGCAATTGAA      60
ACCAGCAAAC ATGCCTATGT CCCCTATTCT CACTTTCCTA TCGGAGCAGT TTTAGTAGCC      120
AAAGACGGAA ATGTTTACAC GGGAGTGAAT ATCGAAAATG CTAGCTATCC TTTGACCAAT      180
TGCGGTGAGA GAACAGCTAT TTTTAAGGCT ATATCTGAAG GCCAAAGAGA ATTTTCAGAA      240
TTGATTGTCT ATGGTCAAAC TGAAAAACCG ATTTACCCAT GTGGTGCTTG TCGCCAAGTA      300
ATGGTCGAAT TTTTGAACA AGATTTAAAA GTGACCTTAG TCGCAAAGA TAAATCGACG      360
GTCGAGATGA CGGTCGGGGA GTTACTTCCA TATTCTTTTA CAGACTTAA TTAGTCTGAG      420
TCGCTCTTTG AGTGGCAAGG GTCTTTGTGA CCAATCAATC CATACTTGCA ACATCGTTGC      480
ACATCTTATT TAGGAGGTTT AGTAATGAAC AAGAAACAAT GGCTAGGTCT TGGCCTAGTT      540
GCAGTGGCAG CAGTTGGACT TGCTGCATGT GGTAACCGCT CTTCTCGTAA CGCAGCTTCA      600
TCTTCTGATG TGAAGACAAA AGCAGCAATC GTCAGTATA CTGGTGGTGT TGATGACAAA      660
TCATTCAACC AATCAGCTTG GGAAGGTTTG CAGGCTTGGG GTAAAGAACA CAATCTTTCA      720
AAAGATAACG GTTTCACCTA CTTCCAATCA ACAAGTGAAG CTGACTACGC TAACAACCTG      780
CAACAAGCGG CTGGAAGTTA CAACCTAATC TTTGGTGTG GTTTTGCCCT TCACAATGCA      840
GTTGAAGAAG CAG

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(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

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CTCAGCTACT TCGCCTTCT TTTTATTCTA CTGGTTTTTC TTGATTCCA GTAGTTGTAG      60
AAGATTCTGT TGTTTTATTT TCTGAAGTTG ATTCAGCAGG TTTAGAATCT CTTGTATTGC      120
TTGGTTTGTT TTCGTCGCTA GCAGTTTCAA TGTTAGATTC TGCAGTTGCG TTTGGTTGGT      180
TCTCAGCACT GGTGTTATCA CCATTGCTT CAGCATTTCT TGCTGGACTT GTTCTTCAC      240

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TTGCGCTAGC	TTTTGACTGG	ATTTGATGAT	TCAAACTAG	AATAGCTTTT	GTGATTCAA	300
GTAAAGCTGT	TTTGTCTTTA	CTATTAGCAG	AAAGTTGATC	TAATAATGCA	TCCACCTTAT	360
CAAAAGTCCG	CATCAGATCC	ATTATTACTT	TCTAAATAAA	AGTGAAGCGA	CATGAGAATA	420
TCGTAGAGTT	TTTGATAGAG	TACAAGTGTC	TGAGGATCTT	GCTCAGCATT	TTCCTTTTCT	480
TGTTGAAGGG	CGCTAGCGAT	ACGAGTCAAG	ACATCTTTTA	CCTGACTGTT	TACTTCATCC	540
AAGTCTGCAT	CAGCCTTGTT	TGTGGCAGCT	TTTAGATTTT	CTACTTCTTC	TGCCAAAGAT	600
TGCTGATTC	CTTCTTCATG	GATTCGTTCC	AAGAGTTGAT	TTGCCTTGCT	CAAAAGACTT	660
TCTACTTCTT	CCTTGCTATC	TGTCGCAGAT	TATTGGTTGC	TATCTACCAT	GTACTCCTAA	720
AACAGGAGAG	TTATAATCCA	AGATTACAAG	GCCTTACAGA	AATAAGAAAT	CCAGATAAGA	780
CAATGTTTCT	CCAAGACGCT	ATTCGCTTCG	CACAGCAGCA	CGGATTCAAT	ATGCTTTAAT	840
TTTAAAGTTT	AGGTGTCAAG	ACCTCTTTTT	AGTGTGCCCA	AAATTTAGAG	AAGTAATCAA	900
TCAACTAACT	TTTATTTTTT	TCAAACTTTC	AGTAACTGA	CCTAAAGCTA	ACTCAATCTG	960
TCTTTGTTCT	ATAGGCTTGT	CTTTGTAGAT	GCTTCTGCTA	TCAGATC		1007

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTCATTGAGA	GCTTGAAAAT	GCAGCCTGTG	TCGTGATTGG	GACAGGGATT	GGCGGAGCCA	60
TGATTATCAA	TGGTAGACTT	CATCGAGGTC	GCCACGGCTT	GGGTGGAGAA	TTTGGCTACA	120
TGACAACCTT	TGCCCCTGCT	GAAAACTTA	ATAACTGGTC	GCAACTAGCG	TCAAACTGGG	180
AATATGGTAC	GATACGTGAT	TGAAAAATCT	GGTCATACTG	ATTGGGACGG	TCGCAAGATT	240
TACCAAGAGG	CCGCAGCTGG	TAATGCTCTT	TGTCAAGAAG	CCATTGAGCG	CATGAACCGC	300
AATCTGGCGC	AAGGCTTGCT	CAATATCCAG	TATCTCATCG	ATCCAGATGT	CATCAGTCTG	360
GGTGGCTCTA	TCAGTCAAAA	TCCAGATTTT	ATCCAAGATG	TCAAGAAGGC	TGTTGATAAC	420
TTTGTGATA	CCTACGAAGA	ATACACGGTC	GCACCAGTTA	TCCAGGCCTG	CACCTATCAC	480
GCAGATGCCA	ATCTCTACGG	TGCTCTTGTC	AAC TGCTAC	AGGAGGAAAA	GCAATGGTAA	540
GATTTACAGG	ACTTAGTCCC	AAACAAACGC	AAGCTATTGA	GGTTTTAAAA	GGTCACATTT	600
CTCTACCAGA	TGTGGAAGTG	GCTGTCACTC	AGTCTGACCA	AGCCTCTATC	TCTATCGAGG	660
GTGAGGAAGG	TCACTATCAA	TTGACCTACC	GCAAACCTCA	CCAACTCTAT	CGTGCCTTGT	720
CCTTGTTGGT	AACAGTTCTA	GCAGAAGCTG	ATAAAATAGA	GATCGAAGAA	CAAGGCAGCT	780
TACGAAAATT	GGCTTACATG	GTTGACTGTT	CTCCAAATGC	GGTGCTGAAT	GTGGCTTTCC	840
TGCCNAAGCA	GATGACTGAA	GGTCTTGGCT	CTCNTGGGCT	ACTCCACCCT	TTGAAG	896

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTAGCAACAA GNGGNGCTAA AATCAAGGTT ACCTTATCGC CGACACCACC AGTAGAATGC	60
TTGTCAACTT TCACCCATC AATGGCTGAC AGGTCAAACCT CTTGCCCAGT CTTAACCATA	120
TTCATCGTTA AATCAGAGAT TTCTCGAGTC GTCATTCCCTT TAAAATAAAC AGCCATAGCA	180
AAGGCAGACA TCTGATAATC AGGAACAGTT CCTGATACAT AGCCTTCTAT CAGCCATTCA	240
ATTTCACTTG AAGTCAGTTC TTGACCGTCT CGTTTTTTTT GGATTAAATC AACTGCTCTC	300
ATTCTTTTCACT ACTTCTAAGG ATATAGTATC CTTTGTCTTT TTTAAGGATT TCACAATTAC	360
CAAACACATC CTCCATCTTG GACTTAGCAC TTGGAGCCCC TTGTTTTTTC TGGATGACGA	420
TTGTCAAATC CCCACCAGTT TCCAAGAAAT CTTTACTTTT CTCAATGATT TCATGAACGA	480
CTTGCTTGCC CGCACGGATA GGAGGATTGG AAATGACATG ATCAAATGT CCTTCAACTT	540
GTTCATAGAT GTTGGACTGG AAATCTCCTT GCATTATTTT TCACATTCTC CAAG	594

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CTAGTGTTTT ATAGCCTGTT TCTTTCACAA ATTGAGCAAA TTCTTGATTG GTAAGTGGAG	60
TATCCGCAAT GGAAAAATCC TTTACACTAA CAGCGACTTG AGGACCTTCA AAATCATCTA	120
AAAAGCCCTC TTCAGAATTT GTTCCCATCA TAAATGTCCC ACCCTTGATT TTTTTCATTT	180
TCATGATTGA CTATCCCCCG TTTTCGTTAG AGTTGGCGTT ATTTTAGAAA GTTCAACAGG	240
AACTAACTCT TCATCCACAA CAAAACCTTC TTCTCTATAT CTAAGAAAGT CTAATAATTT	300
TTTCTTCATC TGACGAACAA TAGGTTGATA TTTTTCACCT GGATACAAAT CATTCAATTC	360
ATGCGGATCT TTTTTCATAT CAAATAACTG ATAATGATTT AAAACAGGAA ACCAGATAAA	420
TTTCCACTGG TCTGTCAAAA TATATTGACT AGAATCTTTT CCTAAAGCAT GTTCACCATG	480
AAATTCTGTT CGCCACCCCT CGTACTGTCC AAATAATAAA TTCCTTAACA CTCCGTCCAT	540

CTAGTTCATC TGTAGTAGTT CCTCCCTGCC AAATCCACGA AGTGAAGGAA AAATATCTTG 600
 AATTTTCACT AATTGCTTGA TTGTTCCCTA TTACCAGATC GAN 643

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTGTTCTCAA TCATATTGTC AGTCGCTTTG ATATCATTTGG TATCCTTGGT AACGGGGCCG 60
 ATTTTGCCAT TCTTGAGCAA GCCAGCGTCC CAAGATTGTG ATATCTTTAT CGCCCTGACT 120
 GAGCACGATG AAGTCAACAT GATTGCAGCA GTTCTAGCCA AGAAAATGGG AGCTAAAGAA 180
 ACTATCGTTC GGGTGCGGAA CCCTGAATAT TCTAACTCTT ATTTCAAGGA AAAGAATATT 240
 CTCGGTTTTT CTCTTATCGT TAATCCTGAG CTCTTGGCTG CCCGCGCTAT CGCGAATATC 300
 ATTGACTTCC CCAACGCCCT GTCTGTGCGAA CGCTTTGCTG GTGGACGCGT TAGCCTCATG 360
 GAATTTGTCTG TCAAGTCCAC CAGCGGTCTT TGCCAAATGC CCATTTCTGA TTTTCGTAAA 420
 AAATTTGGTA ATGTCATTGT CTGTGCGATA GAGAGGGATC ATCAAATTAT CATTCCAAGC 480
 GGTGACATGA CTGTACAGGA TAAAGATAGA ATCTTTGTCA CTGGAACCG TGTCGATATG 540
 ATACTCTTCC ATAATTATTT TAAATCACGC GCCGTGAAGA GCCTTCTCAT CGTTGGAGCA 600
 GGTAGAATTA CCTATTATCT ACTTGGTATT CTCAAAGATA GTCGTATCGA TACAAAAGTC 660
 ATTGAAATCA ATCCTGAAAT CGCCAGCTTC TTAGCGAGA AATTCCCAA TCTCTACATC 720
 GTTCAAGGAG ATGGAACCGC AAAAGATATC CTGCTGGAAG AAAGTGCTCA ACACTATGAT 780
 GCCGTTGCGA CTCTAACAGG AGTCGATGAG GAAAATCTGA TTACATCTAT GTTCCTTGAC 840
 AGGGTAGGTG TACAGAAAAA TATTACTAAG GTCAATCGTA CCAGTCTCCT CGAGATTATC 900
 AATGCGCCTG ATTTTTCAAG TATCATCACA CCTAAAAGCA TCGCTGTAGA TACGATTATG 960
 CACTTTATTC GTGGTCGAGT TAATGCCCAG TATTCAAGAC CTTCAAGCCA TGCACCATCT 1020
 AGCCAATGGC CAAATCGAAA CCCTGCAATT CCATATCAAG GGAAGCCAAT AAAATGA 1077

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTTGAATGGC	AGAGCATTCA	CGGTAGTCTC	GCCCCCAACT	ATAAGGAGAG	AAGTCAGGGT	60
GAAAGTTTCC	TTGATTGTCT	CGTGCTCGCA	TGTAACCTGT	CTCAGCGTCA	AATAGCTGGC	120
GGTAATTTTG	TGAAGCAGCC	TTGTAGGTTT	CAGCGATTTT	TATGTTCTCT	AGTTTTTTTG	180
CACAGCTGGC	GATACAAAAG	TCACTATAGG	CATAGTCTAG	AGTATGGCTA	ACACTTTCGT	240
GGTGGTCGGT	AGAGAGGTAA	CCTAGTTCTT	GGTATTGGGC	TAGTCCGTGG	CGGCCATTGA	300
TTCCGAGAGG	GTCGGCTTTG	CTGGCTGTTT	CGGAGCATGG	CTTGGAAGAG	TTCTCCTTCT	360
AGGTCAGGGG	CCATGTCCTT	GCAGGCGCTA	TCTGCGATAA	TACCGTCTAA	AAGTGTACCT	420
GGCATCATAC	CCCGTTCATC	TGGAGCCAGC	CATTTTGGAA	GGAAACCACT	ATCGCGGTAG	480
CTATTGAGGA	AACCTTCTAA	AAAGCGTTGA	TAGTGCTCCG	GTATGATAAG	GGCAAAGAGG	540
GGGAAGGTGG	TGCGGAAGGT	ATCCCAGAAA	CCATTGTTGC	TAAAGAGGAC	ACCAGGCTTG	600
ACAGTACCAG	TAGCCAGATC	CATGTGGATG	GCTTGCCCTG	ATTCATTAAT	CTCATAAAAA	660
GTCTGTGGGA	AGAGGAAGAG	TCTGTAGAGG	CAGTGGTCAA	AGAAGGTTTC	GTCAGCCTCT	720
CCTATCTCTA	TAATGTCAAA	ACGATGGAGG	AGATTTTCCC	AATCCGCTTG	GGCACTTGAT	780
TTACAGCTAT	CAAAATCTTC	TTGAGGTAGA	TTAAGCAGTG	CTTGAGAAGG	AGAGATGAAA	840
GAAGTGGCTA	GTTGCATCTC	GGTTTGACTA	CTTGCTAAGT	CAATTCGCCA	GTCTCCAACCT	900
TCTTGGCTGA	TAGCAAGAAT	ATCCGTGTTT	ATTTGCAGGG	CAGTGAAGAG	CATCAGTGGA	960
TTTTTATTGG	TCTCTGTTTT	GCCTTCTTGT	CTGAGAGCCA	GAGTCCGCTT	ATCTACCTGC	1020
TCAACTGTTA	GTTTCATCTG	TGCGTGAAGA	TAGAGGGAGA	AGGGCTTTGC	CTTGCTTTTG	1080
CTTCAAACGA	ATAGAAGCAC	CATAGCAAGT	CGGTGTGAGC	TGGGTTTCAA	TTTGATAGCG	1140
CAGGGAAAAG	AGCTTCAAAT	AGTGAGGCTG	GAAGCAAGCT	TTATCTATAT	CATAAGAAGA	1200
CTGGCGGTGA	AAGAGGCTGT	CTCCACCCAG	TTGACTGGTG	ACAGGTGTCA	GAAGGAGCCA	1260
AGAGTAGTCC	CCAATCCAAG	GACTGGGCTG	GTGAGTTAAT	CGAATCCCCT	GAAAGATAGG	1320
CAGATGCGGA	TCAAAAACC	AAGATCCATC	CTGGTCACTG	GTCTGGGGCA	CAAAATAATT	1380
CATCCCAAAA	GGCACGCCTG	TGTATGGCAG	GGTATTTCCC	CGAGAGAAGG	CATGCTTGCT	1440
AGCAGTACCA	AAGCGGTAT	CGATGGTTTC	AAGTAGTGGT	TTCATAGTCT	TTCTTTTAG	1499

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A). LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CTCCATCTGC	AATCGGCATC	AGACAAGATC	TCCAAGTGTT	GTTTCACGTA	ATCAATACGA	60
CCATCATCGT	AAACAGTGTT	ATTAACGAAC	TCATCTTTAT	AGCCGAGACC	ATTTTCAGTG	120

ATATAAATTT TCTTGTAAGT AGGATAATCT TTCTTCACAC GCATGATTTG GTCATACAAA	180
CCTTGAGGGT AGATAATCCA ATCCCAATCC GTGCGTGGAT ACATAGTCAG GGAGCTACAA	240
GACGACCAAT ACCTTTGATT TGATACTTAG AGCTTCCTTT TTCACCTTTA CCATTATGGA	300
TAATTTCACT TTCTCCATCA AAGGCTTCCA TCCAGTCACT CATATAGTAG TTGATTCCTA	360
GGAAATCATT CAAGTCTTTT GCAGCTTCTA ATGCTGTAAA ATCTTCTTCA CGAAGATCCA	420
AACTACCACC ATTGACTGAT AAGATATGGT TGACACCTTC CATGGTTTCA GCTGAATAGC	480
GACCTAGATA AGTTGCGTCT AAGATGAATT TATTGTGGAT GATATCTTCC AACTCTGCTG	540
CACGAACATC TGCTGGATTT TCAGGATCTA GAGGATATTT AGTAGGCAGG GCGTGAACAA	600
CACCAATTTT CCCTTTATAG CCTTTCTCTT TGTACAATTT TACCGCGCAT GCATGAGACA	660
CCATCATATT GTGGTGTGAT TGAAAACTT TGGCAAGGTC GTACTGGATA CCTGGAGGGA	720
ATTTCCCAAC CAAATATTGA CCATCACCGA TTGGTCCAAT TTCATTAAAG GTTGTCCAAT	780
AGTTTACTTC TGGAAATTCT TCCAAAACAG AAGGCAGCGT TAGTCTACAA AATGTTTCGAT	840
ATTTTCACCG TTTAAGAAGT CTCC	864

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACGAGCAATN TTTTCGGATC CATTTCTTCT CCTTTGTAAT AAGATAAAGT CCGTTTATCA	60
AATTTTATTT AGTGTTAATT TGGTTAAAAC AAGCAAACCTA AGCTGCTTTC TTGGTTAGTT	120
GTGACAAGAT TGCCAAACGA TTTTGACGGA CAGCCTGATC TTCAGCCATT ACCATAGTAT	180
TTTCAAAGAA AGCATCAATG ACTGGGCTAA GCGCAAAGAG TTGTTTCAAT TGCTGACTTG	240
CAGGTCCTGA TAAAACGAGT GTTTCTACTG CTTCTGCCAA AGCTTTTTCT TGGTCATTCT	300
CAAATAGTGC TGAATCAACT GTAGCAACCC CTTCTGCCCT CTCAGCCAGG TTAAAGGCAC	360
GAGAAAGTGA TTCAACAGAT GGTTTAAAAT CTTCTTCCTT GCTTACTTCT ACGAGAGCAC	420
TTGCTGCTTC CAACATATCT GCCACAACAA AGTTTGAACC TGCAAGAACT GCTTCCTTGA	480
TATCTTTTGG AGTAGAGCCC ATCATCTTAT CAACACGAGC CTTGATAAAG TCCATAACCT	540
CTGCTTTTATT TTCATAAGTC AAACGTCAA ATTTCAATGC ATAAAGGCTA TCAATCAGCT	600
CCAACTGTAT AACAGAGTCC GCCAGTACC ATGAGAATCC AGAAAACGGG TGTNGTTTGA	660
CTGATAATGG CAGGAATGAT AGCCATACC AACCAGCCCA TAATCAGGTA AAGAGCAAGG	720
CTAAATTTCT CATTGACCTT TTTAGCAAG ATTTTATAGA GAATACCAA GATGGTCGTT	780
CCCCATTGGA TGACAATAAT CAGATAGCCA AACCAGTTAT TCATCAAGGT CAAGACAACG	840
GGCGTGATG AGCCGGCAAT GGCAACGTAA ATCATAGAAT GGTCAATGAT TCGCAAAACA	900
TATTTGTGGG TCGAACCATA GGCCATAGAG TGATAAATGG TGGATGATAG GAACATGAGA	960
AAGAGACTGA TGACGAAAAT GGAAACGCCG ATAGAGGATA AAAATCCGTG TGCTTCATAA	1020

CTATAGATGG	ATGAAATAGG	CAGCAAGATA	AGCATGATGA	CTGCACCCAC	AGCATGGGTC	1080
ACGCTATTAG	CAATCTCCTC	TCCAAAACCTG	AGTTGTTTGC	TGAGTTTAAG	ACTAGTGTTT	1140
ATTGGATTAC	CTCCTCTTGA	GTATGATCGA	TTAAGTCTAG	AGTTTGATGA	TAGAGTTTAA	1200
CGGTTTGGCA	GCTGGTTTGG	ATAATAGGGT	TAG			1233

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TACTATTAAC	CTTCCTGTGA	CTAAAGATCT	CCACCTAAAC	CGTTCGCGCT	CAGCTCAATC	60
TTCGTATCAA	ATCCAGTACA	AACAAGGGGC	TCTTATCTGC	CCAAC TGCTA	GAATTTGGGC	120
AAAAGAAATA	CCTACAACCT	TATCCAGCTA	TTTTAAGTGC	TAGAACCATT	GATAACGGTC	180
GCTATCACAT	GTTGGAAAAT	CTCTGTGAAT	TGCCATTTAG	ACCAGAGGCA	CAACGAGTCG	240
TGACAAAAGG	TTACCTTAAT	TTACAAAATA	GAAATGATTT	ACTGTTAGTA	GAGGATATTA	300
CTGCAGATGA	ATGGATGGAC	GTTCAATTTG	AACTGCAGCC	AACTATTTAC	AAGCTAAAAG	360
AAGGAGACAC	TCTCCGTTTA	GTCCTCTATA	CTACTGACTT	TGAAATCACC	ATCCGTGACA	420
ATACAGACTA	CCACTTGACT	GTCGACCTCG	CTCAGTCCAT	GCTTACCTTA	CCTTGCTAAA	480
AGGAGTTACA	TTATTATGAA	TAAATCAGAA	CACCGCCACC	AACTTATACG	CGCTCTTATC	540
ACAAAAACA	AGATTCATAC	ACAGGCTGAG	TTGCAAGCCC	TTCTTGCTGA	GAACGACATT	600
CAAGTAACCC	AGGCAACCCT	CTCACGCGAC	ATCAAAAATA	TGAACCTATC	AAAAGTCCGC	660
GAAGAAGATA	GCGCTTATTA	TGTTCTTAAC	AATGGTTCCA	TCTCAAAATG	GGAAAAACGT	720
CTCGAACTCT	ACATGGAAGA	CGCCCTTGTC	TGGATGCGCC	CAGTTCAACA	CCAAGTCCTA	780
CTAAAAACCC	TTCTGGACT	GGCTCAATCC	TTTGGTTCTA	TCATTGATGA	CTTTGAGCTT	840
CCCTGACGCT	ATCGCTACCC	TTTGTGGTAA	TGATGTCTGT	CTTATCAT		888

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGTGATTGT CTTTTTGGTC TATCTGATCA TTA	CTGTGATCA AAAGCTTGGT CGTGT	60
ATGAAACAGA AAAGACGATT AAAACCTTGA CTT	CAGATGT GGATGTGACC TTGCATCACA	120
CCAATGAGTT GTTGGCTAAG GTCAATGTCT TGG	CAGATGA TATCAATGTC AAGGTGGCTA	180
CGATTGATCC ACTCTTCAGT GCTGTTGCAG ATTT	TATCTCTCT ATCTGTTTCA GACCTCAATG	240
ACCATGCGCG TGTCTTGAGC AAGAAAGCTT CAT	CAGCTGG TTCAAAAACA CTCAAGACTG	300
GTGCAAGTCT GTCAGCTCTT CGTCTTGCAA GTAA	ATTTTTT CAAAAAATAA AAAAGGAGAA	360
TCCTTATGGG TAAATTATCC TCAATCCTTT TAG	GAAACCGT TTCAGGTGCA GCTCTTGCC	420
TGTTTTTAAC AAGTGATAAG GGCAAACAAG TTT	GCAAGTCA GGCTCAAGAT TTTT	480
ATTGAGAGA AGATCCGGAG TATGCCAAGG AGCA	AGTCTG TGAAAAACAG ACAGAAGTTA	540
AGGAGCAGGC TACAGATTTT GTTCTGAATA ACAA	AAGAAC AGGTGAGTC AGGTGAAATC	600
ACTGTGGACA GTATACTTGC TCAAGGCTAA ATC	CTATGCT TTTCAAGCGA CAGAAGCATC	660
AAAAAATCAA TTAAATAATC TCAAGGAACA ATG	GCAAGAA AAAGGTGCAG GAATTCGATC	720
TCTTGATGAC TCAGAAGAGA TTGTGATTGA TATA	ACAGAA GAATAAACCA TCACCATCTC	780
CGGACGGACT AAGTATCTGG GGATGGTGAT TTT	TATCACG AATCTAGTCT TTGTGGCATA	840
ATAATTACTA TGCAGAAAAA ACCAACGTCA GCCT	TATGTGC ACATCCCAT TAGTACCCAG	900
ATCTGATAAC ATTGTGATTT TTCAAAGGTC TTC	ATCAAAA ATCAGCCAGT CGACAGCTAT	960
TTAGAGCATC TGCTGGAAGA GTTTCGTTCT TAT	GATATTG AAAAGTTGTC AACCTTTTAT	1020
ATCGGTGGTG GAACACCGAC AGCCCTGTCG GCT	CCGCAAC TGGAGGTGTT ACTGAATGGC	1080
TTGACTAAAA ACTTGATTT GTCTGTCTTG GAAG	AGTTGA CCATTGAAGC CAATCCAGGC	1140
GATTTGGATG CGGATAAGAT AGCTGTTTTG AAAA	ATTCCGG CTGTCAATCG TGTTCGCTA	1200
GGTGTCCAGA CCTTTGATGA TAAGATGTTG AAAA	AGATTG GGCAGTCA TTTGGAGAAG	1260
GATATTTATG AAAATATCGA TCGCCTGAAA CTG	GCTGGTT TTGACAACAT CTCCATTGAT	1320
TTGATTTATG CTCTGCCTGG TCAGACCATG GAG	CAAGTAA AGGAAAATGT GGCTAAAGCC	1380
ATTGGATTGG ATATTCCCA CATGAGTTTG TATA	GTTTGA TTTTAGAAAA CCATACGGTC	1440
TTTATGAACC GGATGCGACG TGGGAAATTG CCT	CTGCCTA AGGAGGAACT AGAAGCGGAG	1500
ATGTTTGAGT ACATCATTCG AGAG		1524

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTAAGTGACG ACCAAGCGTA GCCTCGCTAA TCACCAATTC	TTGAGCCAGC TGATGGGCTA	60
AAAAGTGTG GTGGTAGAGA AGATAAACCA AAATCTGGTA	TTTAACAGCA CTATCCAAAA	120

AACAAGCTCC	GAATATCTCT	CCCCTTAGTA	GCTGCACCTA	TAGACAGACG	CAGATTTTCA	180
TCTTCTGAGT	GAATAGTCAG	TTCTAAGCCA	CTATCCAAAG	CCTTGTCATT	GAGCAGGGTG	240
ACATATTTGG	TTAGGGTTGC	TTTGTAAAAT	CCTGTTTCTT	CCATTACAGC	CTTGACGGTC	300
GTCTGAGACT	CTTGTAATAG	AAAGGAAAGG	ATTGAAAATT	GACCACACTC	GGCTTTCTCC	360
ATCAAATCTC	CTAAATACAT	TTGTTATCCC	TTTCATTTTC	TACCTTAAGC	ATAGCATAAA	420
TCTGACAAAT	GCTAAAATAA	TCTGTTTCTC	TTTTTATTTT	CATGCTGATT	TCCTGGTCCA	480
TTATCCTGAA	AATCAGTAAA	CACACGGCTC	CCCCTTTGGG	CATTTTTATG	CTAAAATAGT	540
AGCTATGGAT	AAAATTATTA	AAACTATATC	AGAAAGCGGA	GCCTTTCGTG	CTTTTGTCTT	600
TGATAGCACG	GAAACCGTCC	GCACTGCTCA	AGAAAAACAT	CAAACCCAAG	CTAG	654

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTTGAACATA	TTCATCAAAA	GAACATGAA	CAAAGATTAC	ATCCGGGAAG	AGTTCATTTG	60
CAACACGGAA	TGGCTTCGCT	CAGATTTTTC	TTGGGACAGG	CTGGTGGTCA	CAGCCGTTTC	120
ATCATCAACC	ATTGGTTGGT	CGAAGCGTAG	GCAACGCACA	TCTGACAATT	TTTGTTTCCA	180
GAAGGTCAAG	GCCTCATCTT	TGTCAACTGG	AATTTTCATC	CCGTTACTGT	ACCAGTTGGC	240
AAAGAGAATA	CCTAAAACAC	GACTACCATC	CACACCCTGC	CAGTACATTT	CTGAAAACCTG	300
AGACGTAAAC	TGCTCATCTT	CAAGGACTTG	GTTGTCAAAT	CCAATCGGCT	TCACACCACG	360
ACCAAAGGCC	GCCACGTGAA	TGCCTGATTT	TTGAAGAATT	TGAGGCGCTT	GTCCCATATT	420
TCCAAAGGTA	TCTGGAAAGT	AGCCAATCTG	GGTTGATTTA	CCCCATTTGG	CAGCTTCTTG	480
TTGACCAATC	AAGGTATTGC	GGACATTGGC	TTCACTGGAG	ATCAAATAAT	CATCCTGCAA	540
GATGTAAAAG	GGACCAATTT	TAAGCTTGCC	CTCGTCAATG	TAGCGTTGGA	CCTTGTCGCG	600
ATTTTCAGGG	CGAATTTGTA	AGTAGTCGTC	AAGGACAATA	GTTTGTCCAT	CCAAGTGGAA	660
ACTCTTGAAC	TCAGGGTCAT	TTTCAAAGAG	ATCAAAGAGA	TTGTCAAACA	ATTCCACCAA	720
TTGCATACGA	TGGCTTTCAA	AAGGCAAGTA	CCACTCACGA	TCCCAGTGGC	TATGTGAGAT	780
AATATGTACA	ACAACATTTT	CCATGAAGTA	AAACCTCATT	CTAAATTTAA	ATTTTAACGT	840
TTTAAATGTA	AACTTGTGAT	TCTGATAAGA	ATCGGTTGAG	CTAAAGCGAG	CCCCTTAGCG	900
AATATCCAAG	TAATCCAAGA	CCAACTCACA	GAACATCATG	TTAGCCCAGG	AGAACCATTTC	960
ACGAGAGTAG	AGGGTCGGAT	CATCTACATG	GAAGCTTTTCG	TGCATGACAC	CTGTACCACC	1020
ATCGCAGGCA	ACCAGCTGAT	CCAGCAAGAA	TTTTTTCTCT	GCCTTATCTC	TTGTTGTCAA	1080
TCCCTGGATA	AAAAGGCGAA	TGGGCCAGAT	ATAGCGATAG	AAGTATGAGA	ACTTCCGAGA	1140
CCGCTAGCGT	ATCTCCTTGG	TAGAAGTATG	GATTTTCAGA	A		1181

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

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CTCTGACGGC GTCGCCACTT AAGAAGAGTA TCAAAAAGAA AAATAGAAAA TTAAC TAACA      60
AGGNAGAAAA ACACATGTCT AAAATTATCG GTATTGACTT AGGTACAACA AACTCAGCAG      120
TTGCAGTTCT TGAAGGAACT GAAAGCAAAA TCATCGCAAA CCCAGAAGGA AACCGCACAA      180
CTCCATCTGT AGTCTCATTC AAAAACGGAG AAATTATCGT TGGTGATGCT GCAAAACGTC      240
AAGCAGTCAC AAACCCAGAT ACAGTTATCT CTATCAAATC TAAGATGGGA ACTTCTGAAA      300
AAGTTTCTGC AAATGGAAAA GAATACACTC CCACAAGAAA TCTCAGCTAT GATCCTTCAA      360
TACTTGAAAG GCTACGCTGA AGACTACCTT GGTGAGAAAG TAACCAAAGC TGTATCACA      420
GTTCCGGCTT ACTTCAACGA CGCTCAACGT CAAGCAACAA AAGACGCTGG TAAAATTGCT      480
GGTCTTGAAG TANAACGTAT TGTTAACGAA CCAACTGCAG CAGCTCTTGC TTATGGTTTG      540
GACAAGACTG ACAAAGAAGA AAAAATCTTG GTATTTGACC TTGGTGTTGG TACATTCGAC      600
GTCTCTATCC TTGAATTGGG TGACGGTGTC TTCGACGTAT TGTCAACTGC AGGGGACAAC      660
AAACTTGGTG GTGACGACTT TGACCAAAAA ATCATTGACC ACTTGGTAGC AGAATTCAAG      720
AAAGAAAACG GTATCGACTT GTCTACTGAC AAGATGGCAA TGCAACGTTT GAAAGATGCG      780
GCTGAAAAAG CGAAGAAAGA CCTTCTGGT GTAAC TTCAA CACAAATCAG      830

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(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

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CTGGGAAAGG AGATATGTGA CAATAATAAA CTGTATTCGT TGATAGAATT TAGAAATAAA      60
ATATATGAGA ATTAGAACTT TCCAGAAGTG ATTTAGCGAT TTTACTATGT GCCANGCTTA      120
TCGCCTCTAT CGGATTAAAT ATGGATTCTA CTCCCGTGAT TATNGGAGCC ATGTTAATCT      180
CTCCTTTGAT GACACCTATT CTGGGAGTGG GGCTCTCTCT AGCTATATTT GATTTTAAAT      240

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TGTTAAGAAA ATCTTTTAAA ATATTAGCTA TTCAAATTCT TGCCAGTTTA ATAGCTTCAA	300
CACTTTATTT TTATCTTTCT CCCATTTTCGT ATGCTAGTTC GGAAATTGTT GCTAGAACCT	360
CTCCGACTAT TTGGGATGTT CTCATTGCTT TTGTAGGAGG GATAGCAGGT ATTATTGGTG	420
CTAGGAAAAA AGAGACCAAT AATATTGTTC CTGGTGTTGC TATTGCAACC GCCTTGATGC	480
CTCCTCTTTG TACAGTAGGT TATGCTATTG CTTCTGCTAA TCTAAAATTT ATCATAGGCT	540
CCTCTTACCT ATTCTCATC AATTGTAGCT TTATTGTCAT TGCGACTTAT ATAGGTGTTA	600
GGTTGATGAT GGTTAAGAAA CATTATTTTA AAGATAATGA AGAAGACTCT AAAATGCGTA	660
GGATTTTGCT TCTAGTTGCT GTTTTGCTGA TGATTCCGAG TTTCATCTCT GCAACGACTT	720
TAGTGAGAGA AACGTTGAAA AAAGAGTCCC TTAAGAAATT TATATCAGAG CAGTTTCAGG	780
GGCATAATAT TTTGAAAAA ACCTATTCTA AAAAGACTCA TACCCTAAAG CTAACCATTT	840
CAGGAAATTA TTTGACAGAA GAAGAACTCG ATATGATTTT AAGTAAGAGA GGTGACTATG	900
GTTTAAGTGA TGTTTCTGTT CAAGTTTCAC AATTGTCTGA TTCAGAACAA CTTAGTAAGG	960
AAGAACTGGT GGAGTATTTT TTCCAGTATA TCAAGGATAA GGAAGCAAAA GAAAAGGAAA	1020
AAGCTAATAA GTTTTATACA GAGTCTGAGG AGCAATAATT TCTTGAGAAT AGCTGGTTTT	1080
TCTCGTGAGT CTTCTATGTA TATCAAAGGA AGACTGAGGT TTTAAGTATG AAACCTTTCT	1140
TCTATTATAG TAG	1153

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CTGCAATGGT TAGCGAGGAT GGTGAAATAG AGGAGCCTTA ACTATTTTGA GGAATCCAAG	60
CTGACAGGAC TGGTATGTCT GCTCTTTGGC TCTGAAGGCA GACTATACCA GCTGGAAGTT	120
TGACAGATGT GGCACGTGAG AATTATTGGA GGCNTTGACN TANTCAGAGG ATTCTCTCTT	180
GATATTGGGT TTGGCAGAGT TGGATAGTGA GTTGGAATAT TACCAAGCGG TTATTCAAGC	240
CTATGCCAG TTAGATAATC GCTCGATTTA TGAGCAAACG GGCATTTCCT CCTATCAACG	300
AATTGGCTTT GCCTATGCTC AGTTAGGGAA ATTTGAAACG GCTACTGAGT TTTTAGAAAA	360
AGCCCTGGAG TTAGAATACG ATGACTTAAC AGCTTTTGAG TTGGCCAGTC TTGATTTTGA	420
TCAAGAAGAA TATCAAAAAG CCACCCTCTA CTTTAAGCAG CTTGATACCA TTTCTCCTGA	480
CTTTGAAGGC TATGAGTATG GGTACAGTCA GGCTTTACAT AAGGAACATC AAGTTCAAGA	540
AGCCCTGCGT ATCGCTAAGC AAGGATTAGA GAAAAATCCC TTTGAAACTC GCCTCTTGCT	600
AGCTGCTTCA CAATTTTCTT ATGAATTGCA TGATGCTAGT GGTGCAGAAA ATTATCTCCT	660
TACTGCAAAA GAAGACGCTG AGGATACAGA AGAAATCTTG CTTGTTTATG CCACTATTTA	720
TCTGGAGCAG GAGCGTTATG AGGATATTCT AGACTTGACG AGTGAGGAGC CAGAAAATCT	780
TTTGACCAAG TGGATGATTG CTCGTTCTTA TCAAGAAATG GACGATTTGG ATACTGCTTA	840

TGAGCATTAT CAAGAGTTGA CAGGAGATTT GAAGGACAAT CCAGAATTC TGGAACACTA	900
TATCTATCTC TTGCGTGAAT TGGGACATTT TGAAGAAGCA AAAGTCCATG CTCACACTTA	960
CTTAAACTG GTTCCAGATG ATGTGCAAAT GCAAGAACTG TTTGAGAGAT TGTAAGAATG	1020
TTTAAACATA TAGAACTGTA GTTTATCTCT TTTGATAG	1058

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTTGTTGCTT GTCCAATTGG TGTAATTG GAACCGATTG ACCCATCTGC AAAGAATGCT	60
AGAGGAAACA CAGGAAATTG TTGCAGGTCC TGTGCTAGT GTTGAAACAT TGAAGCGAAT	120
AGAGGAGTTA GGTTTTGACT TTGTCTGTTT GACTGGAAT CCTGGAACAG GAGTTAGCAA	180
TCGAGAAATC ATTAAGGCTG TTCAAATGCT TAAGGAAAAC TTTTCTGGTT TGATTATTGC	240
AGGTAAGATG CACGGGGCAG GAGTGAATGA GCCTGTGGCA GAGCTTCTG TCGCAGAGCA	300
ATTGTTGGAA GCAGGTGCGG ATGTGATACT TGTTCAGCA GTTGGAACCG TTCCAGCCTT	360
TCATGACCAA GAGTTGCGTG AAGTCGTTGA TCTCGTTCAT AGTAAGGGTG GTCTTGTATT	420
GAGTGCTATT GGTACTAGCC AAGAAACATC TGATACAGAT ACTATTAAGG AAATTGCACT	480
TAGAAATAAA ATTTGTGGAG TTGATATTCA ACATATAGGT GACGCAGGAT ATGGGGGACT	540
GGCAACAGTC GATAATATTT ATGCATTGAG CAAGGCAATT AGAGGAGTGA GACATACAGT	600
ATCTCGCTTG GCTAGGTCAG TAAATAGGTG ATAAAGGAGT AAGCTATGGC TAAAGTAACA	660
ATTATGTTAG CATGTGCAGC AGGTATGAGT ACAAGTCTGC TAGTGACAAA GATGCAAAAAG	720
GCAGCAGAAG ATAAGGGGTT GGATGCAGAA ATTTTTCAG TTCCAGCTCC TGAAGCAGAA	780
GAAATTGTAG CAACAAAAGA AGTAAATGTG TTGCTTTTAG GTCCTCAAGT TCGCTATTTA	840
CTAGGGGACT TTCAAGAAAA ACTAAAAGAT AGACAGATTC CTGTGGCGGT TATTCCGATG	900
ACAGATTATG GAATGATGAA TGGTTCTAAA GTCTTAGATT TAGCTGAAAG TTTATTAGAC	960
TAAGATTGAG GAGAATGTTA TGGATGAAAG TAATTTAGAA TCTGTAATGG GGCTAATTAT	1020
GTATGGTGGG GAAGCCAAAA GTAATGCTAT GGAGGCTATT CAGGCAGCAA AAAAAGGGGA	1080
TTTCTCTAAA GCCAATCGAA GATTAGCTGA TGCGAATGCT GCCTTATTAC AGGCGCATAA	1140
GGCTCAAACA GAAATGTTGA CAAGAGAGGC ACAGGGGGAA GAAACATCAA TTAGCCTCTT	1200
GATGGTACAC G	1211

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CTTCAGCCAT CTTTAGTAAA GACTTCCTGT GTTGACAATT GGTGGGCAT CATGATTGCC	60
ACAAAGAACG ACAAGGAGAT TTGAAACCAT GGCAGCTTTT CGTTCTTCGT CAAGTTCTAC	120
CAATCCCCCT TCATTGAGCC GTTCTAGTGC CATTTC AACC ATTCTACAG CACCATCTAC	180
AATCATCTTC CGTGCATCAA TAATGGCAGA TGCTTGTTGG CGTTGAAGCA TAACGGCAGC	240
AATTTCTGGA GCATAAGCTT AGGTAAGTGA TACGTGCTTC AAGGATTTC AAGCCAGCAT	300
CTTCTACGCG ACTTTGAATT TCCTCACGAA TACGGTTAGC AACAATTTTC CTAGAGCCAC	360
GGAGACTACC TTCATCTGCT TGCCCGTCAC CCGTAGTATC CACATTAGGA GACACATCGT	420
AAGGATAGAT GCGGACAATA TTACGGAGGG CGCTATCACA TTGCAATGAA AGATATTCTT	480
TGTAGTTATC AACGTTGAAG ACTGCCTTAG CGGTATCGAC AACTCTCCAA GTTACCGCGA	540
TACCGATTTC TACAGGGTTT CCTAAGCAAT CATTGATTTT TTGACGAGAA TTGCTCAAGG	600
TCATGACTTT GAGGGAAATG TGTTTCTTGC CAATTTCAAG ATTTACATCA TTGTCATTG	660
ATGATTTAGC TCCTAAAAA GGAGATTTTG TGCTAACATC ACCACTTTGT CCAAGTCGAA	720
TGTGGTTTGC AGGGTTGACT GCTACGCTGA AGGGATTGAC AAAGTAAAA CCAGGTTCTT	780
TCATGGTACC TGTATAATTA CCAAAGAGTG TCAGAACCAG AGCTTCCTGA GGTTTGACAA	840
CTTTTAAACC AGCATGAG	858

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TTACTTCGCT AAACAATCAA AGGAACAGTC AAAAATTCAG TTGGAGCTGG TGATTCTATG	60
GTTGCTGGAT TCACAGGTGA ATTTGTCAAA TCAAAAGACG CAGTAGAAGC CTTCAAATGG	120
GGAGTGCTT GCGGAACGGC AACTACCTTC TCAGATGACT TGGCAACGGC GGAATTTATT	180
AAAGAAACAT ATGGAAAAGT TGAGGTAGAA AAACGATGAA AATTCAAGAT TTATTGAGAA	240
AAGATGTCAT GTTCTGGAT TTGCAGGCAA CTGAAAAGAC TGCTGTCATT GAAGAGATGA	300
TTAAAAGCCT AACAGGCCAC GGTATGTGA CAGATTTTGA AACCTTTAAA GAAGGCATTT	360
TGGCGCGTGA AGCTTTAACT TCTACTGGTT TGGGTGATGG AATCGCTATG CCTCACAGCA	420

AAAACGCTGC TGTCAAAGAA GCGACAGTTC TCTTTGCTAA GTCAAACAAG GGTGTTGACT	480
ATGACAGTTT GGATGGGCAG GCAACTGACC TCTTCTTCAT GATTGCAGCT CCAGAAGGTG	540
CCAATGATAC TCACTTGGCA GCATTGACAG AATTGTCTCA ATACTTGATG AAAGACGGTT	600
TTGCAGACAA ACTTCGTCAA GCAACATCTG CAGACCAAGT TATCGAACTT TTTGACCAAG	660
CTTCAGAAAA AACTGAGGAA CTTGTTCAAG CACCTGCTAA TGACTCTGGT GACTTTATCG	720
TAG	723

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AATCTCGTTG ATTTAGACTT TAACCGTGTG ATCTATTTTA GGCGCTGGTC CTTTTCTTTG	60
GACTTGCTCA TGAAGCTCAG CTCAAGATTT TGGAAATTAAC TGCTGGTCAA GTTGCGACCA	120
TGTATGAAAG CCCAGTTGGC TTCCGTCACG GTCCAAAATC TCTTATCAAC GACAATACAG	180
TTGTTTTGGT CTTTGGTACA ACGACGGA CTACGCTGTA GTACGACTTG GACTTGGTTC	240
GTGAAGTTGC TGGTGACCAG ATTGCTCGTC GTGTTGTGCT TTTGAGTGAT CAAGCTTTTG	300
GTCTTGAAAA TGTCAAAGAA GTGGCCCTTG GTTGTTGGCGG TGTCTGAAT GATATTTACC	360
GTGTCTTCCC TTACATCGTT TATGCCCAAC TCTTTGCCCT ATTGACTTCA CTCAAGGTAG	420
AAAATAAACC AGATACACCG TCTCCTACAG GTACAGTAAA CCGTGTAAGTA CAAGGTGTCA	480
TAATTCACGA ATATCAAAAG TAAGACAGTG TTTATGAATT CTTGACAAGA GGATTTGTAA	540
ATTATCAGAT AAACCATAGA TTGTCAGTAC GCTTTCTATG GTTTGTTTGC TTGAGAGAAA	600
TAGTAAAAGG AGAACAGAAT GAAAGCATA ACAGAGCGTG TATTTGGAAA TGTTGAGGGT	660
GAGGATGTCT TGGCCTATCG ATTTGAGACA GACGGTGGCT ACCAACTTGA GGTATGACT	720
TATGGTGCGA CTATCTTGGC CTATGTCGCA CCTGACAAGG CTGGAAATTT TGCCAATGTT	780
ATCTTGGGAT TTGATGACTT TGATAGTTAT GTAGGCAATA GTCCCAAGCA TGGAGCAAGT	840
GTAGGTCCTG TAGCGGTCG TATTGCAGGT GCGACCTTTG AG	882

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CTCAAGGGCT	TGAAATCATC	CAGATAAATG	AAGAACAAGG	CCAATTTGGT	TTTGACCGCG	60
TTAAGGAATT	GGTTGATACT	TACAAGGTGG	AACGATTTGT	AGTGGGCTTG	CCTAAAAACA	120
TGAACAATAC	AAGTGGACCG	CGCGTAGAAG	CTAGTCAAGC	CTACGGAGCA	AAGCTAGAAG	180
AGTTTTTTGG	TTTACCAGTA	GACTATCAGG	ATGAACGCTT	GACAACAGTG	GCTGCTGAGC	240
GCATGTTGAT	TGAACAAGCA	GATATCAGTC	GCAATAAGCG	CAAGAAAGTC	ATTGATAAGT	300
TAGCAGCTTC	AGCTGATTTT	ACAAAATTAT	TTAGATAGAA	AATTTTAATA	TAAAGGAGAG	360
GCTATGTCAC	ACGATCATAA	CCACGACCAC	GAAGAACGTG	AACTAATCAC	ACTAGTAGAT	420
GAGCAAGGAA	ATGAAACCTT	GTTTGAAATC	CTTTTGACAA	TTGATGGAAA	AGAAGAATTT	480
GGTAAAAACT	ATGTTCTTCT	AGTACCAGTT	AACGCAGAAG	AAGACGAAGA	CGGACAAGTT	540
GAAATCCAAG	CTTACTCATT	CATCGAAAAC	GAAGATGGAA	CAGAAGGCGA	ATTGCAACCA	600
ATCCCAGAAG	ACTCAGAAGA	CGAATGGAAC	ATGATTGAAG	AAGTCTTCAA	CAGCTTTATG	660
GAGGAGTAAA	AACGTCCGGG	GGACGTTTTT	AGCCCTGCGC	TAGAAATTAG	AAACGCAGGT	720
AGTCTGAGAG	ACTGTATCAG	CCCAACTCCC	AGAAATGGGG	AAGAGTTGGA	ACGTCCAGTG	780
AACATTTTTA	CCCCAACTCC	TAGAAATTGA	GAAGAGTTGG	AACATCTAGT	GGATATTTTT	840
AGCCCACGTT	CACATTCATA	G TAG				864

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GTATCGTTCA	ATTCCAAAGA	TACGGAGGAA	GCTGCGTTTC	GCGAGAAAAC	TCTTGTTAGA	60
CCAGATAGGG	ATTAGCCAAA	ATCCTTCTAT	GNGCTTATAT	CCAAATGGAG	ATGCAAACTT	120
CTGCCCAACT	CTTGACCAAT	AAGATCTTTC	TTAAAAATCC	ACTCAAGGCT	CTGGTAGAGG	180
AAAAATATGG	GATTGAGTAT	GAAGAATTTA	CCAATCCTTG	GCACGCTGCC	ATTTCTAGCT	240
TCGTTGCCTT	TTTCCTTAGA	AGTTTGCCTC	CAATGCTGTC	AGTGACCATA	TTCCCAAGTG	300
AATATCGCAT	CCCTGCTACT	GTCCTTATTG	TCGGTGTGGC	CCTTCTTCTC	ACTGGTTACA	360
CTAGTGCCAG	ACTTGGAAG	GATCCGACTA	GAACAGTATG	ATTCCGGAACC	TTGCTATTGG	420
TCTCTTGACC	ATGGGAGTTA	CCTTCCTGCT	CGAACAACCT	TTCAGCATTT	AGAATACAAG	480
AAATACCTCG	ATTTTGAAGT	CGAGGTATCT	TTTTTACATT	TGCACAATCT	TGCGATAACT	540
TCTTGAAGTA	ATCATGAAAA	TCAGCACATA	GGCGATGAGG	AAGATAGCGC	AGATAGACAA	600
GGTCACAATC	AACATCATAG	TCGTATCCAG	TACACCAATC	ACTTTTAAAA	TCAGGCTAAG	660

CATATGGTAG GCAAAGGCGA GATGTATGAA GGCAAAGAGC AAAGGAAGGA AGAAAACAGT	720
TAAAACTGT TTGTTGATGG TTTGCTTGAT TTGCTTTTGG TCCAAACCGA CTTTCTGCAA	780
GATAATAAAG CGTTCACGGT CTTTCGTAGCC TTCAGAAATT TGTTTGTAGT AGATGACCAG	840
AACAGTTCCG ACCATAAAGA TAATGGATAG GAAATACCG ATAAAGAAGA CACCGCCAAA	900
GAGGACACTC ATTTGAGCAC TAGCATCTGC TAGATTGCTA CCATAAACAT AG	952

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

ACAGAATTAC TCACTATTCT GCGTCTTCTG CTAAAAGTTT AAATCGTGT TTCTTCATCC	60
AAAAGTGGGT AACCTAGGCG TTTGCGTTCT GCAACAAAGG TTTTGGCTAC AACACGGGCC	120
AAGTTACGGA TACGGAGCGA TATAGCCTGC ACGGCTCTGT TACAGATACG GCACCACGCG	180
CGTCAAGCAG ATTAAAGGTA TGTGAACATT TGAGAACATA GTCATAGGCA GGGTGTACCA	240
AGCCTTCTTC TAATGCACGA CCAGCTTCTT TTTCAAACTT ATCAAAGTTT TCAAGCAACA	300
TTTCTTGGTT CGAAATTTCA AATGAATATT TTGAGTGCTC ATACTCAGGC TGGATAAAGA	360
TTTCTCCGTA TTTTACACCA TCAGCCCACT CGATATCATA GACAGAGTCT ACTTCTTGAA	420
TGTAAGAAGC CAAGCGCTCC AAACCATAGG TAACTTCCGC AGTCACAGGG CCAGTTGCCA	480
ATCCACCGAC TTGTTGAAA TAAGTGAAT GAGTGATTTT CATTCGTCA AGCCAACTT	540
CCCAACCAAG ACCAGCTGAA CCAGTTGATG GGTTTTCCCA GTTGTCTCA ACAAACGAA	600
TATCGTGCTC CAAAGGATTG ATTCCCAATT TTTCAAAGA CTCAAGGTAA AGTTCTTGA	660
TATTTGATGG AGAAGGCTTC ATGACCACCT GGAATTGGTG GTGTTGGTAG AGACGGTTAG	720
GGTTTTCCTC ATAACGACCG TCAGCAGGAC GACGTGATGG CTCTACATA GCTGCATTCC	780
ATGGCATCAG GTCCGATAGG CACGAAGGAA AGTGTAAAGG CTCATTGTTC CCGCACCTTT	840
TTCATTATCA TAAGCCTGCA TAAGCATACA ACCTTGGTCA TTCCAAAATT GTTGCAAAGT	900
CAAAATAATT TCTTGAAATG TTAATTCCTT AGACATTGAA TACTCCTTAA TAAAAAATA	960
TTTCTTGCGA CACGAGTTCT GCCTCGTCGA TTATACCNAG GCACANAAAT TANTNCTNGC	1020
TTCCAAATTC GAATCCCGCN NCCCCGGGGG ATTCNNTTTT CNTAAACCGG CCCCCCCCCN	1080
GNGGGAACCC CCCCNTTTTT NCCNTTATTT AAGGGTTANT CNCCCNCTTG NCN	1133

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCTAATTTT TTCATTAGAT CCTCCAATTT ATTAGGGCTT TGCCCCCTTAT TTAAACAAAT	60
GTTTATTTTT CAGTTTCAA TATCGTTGTT TGGGAGCGAT AAAGAAGCTA ATGAGAAAGA	120
AACTAGCAGC TGTAAGCACG ATACTAGAAC CTGCCGCAAC ATTAAACTA TAGCCAATAA	180
AGAGTCCCAA AACTGAAGCA GTAGCTCCGA AGGTTGAGGA AAGGAAATC ATGCTTTTCA	240
GACTATTAGC ATACAGATAA GCAGTTGCAG CTGGGGTAAT CAGCATGGCT ACAATCAGGA	300
TAGTTCCGAC ACTTTGCATG GCTGTCACAG ACACGAGAGT CAGGAGTACC ATGAGAAGGT	360
AGTGATAGAA ATTGACAGGC ATTCCCATGG CTTTAGCCAA GAGTTCATCA AAGGAAGTTA	420
TCAAGAGTTG CTTGAAGAAA ATCCAGATTA ACAAGAGGAT GGCTGCCCCC ACACCCATAG	480
TAATAAACAT ATCCGTATCT TGGACGGCCA GGATATTACC AAAAAGGATA TGGAAAAGGT	540
CAGTTGAACT TTTAGCGACA CCAATCAAGA TGATACCGAG GGCTAAGAAA GAAGAAAAGG	600
TAATGCCGAT GGCGGTATCG CTTTGTGATA TCGAGTTTCC TTTGATGTAG GTAATGATGA	660
TGGCAGCTAG CAATCCAAAG ACAATGGCTC CGATAAGAA TCAAGGCCCA AGATGAAGGA	720
GAGGGCTACA CCTGGTAAGA CAGCATGTTG AAATGGCATC TCCCATGAAT TGACATCCCG	780
CGTAGAATAA TGAAACATCC CACAGA	806

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1096 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTAACATTTT CTTTGCTACT TCTAATAATG TCATAGTGGT CATTAAATGA TCTTGAGCAT	60
GTACCATGAT AATTTCATT TTAATTTCCA CTCCACTTGC GTATTCTTGC AAGAGTTTGG	120
TTTGTGCATG ATGCGCTTCA AGAATTATCT CATTTGATTG ATTAAATTTA CTTTCTGCAT	180
CATCAAAACT ACCTTCTCTC ATTTTGTGCA AATGCTTCAT GTATTCTGA CCTTGCATTT	240
CCCGAATGCA GGATAATTTT AAATGCTGCA ACCTGCAGTT CCTCTTGATT CATATGAACC	300
TCCTATTTTA TCTTCTCAA TATGTTAATA AAATCTTCAA AGTTATTGCA AGATATTAGC	360
TGATTTTGCA ATTCATCATT CTCTGTCAA GAGACTATCT TTTAGTCAC AGTTGCCAA	420
CCTTCCGTTT CCATATATTG ATGGAGATAG AAGAAATAGC TAGTCTGGAC ATGTGAACTT	480
TGATTATCCC AGAGTAACGA ATCTTTACAA ATTGCAACCG AAACCTTTT CTCTGTACCA	540

AAGGGCTGAA	TAGGATGCGG	AACTGCAATT	TTTTCAGAAA	AAACAACTGA	ACTTAATTCT	600
TCGCGCTGTT	TAATTCCATA	AAGTAAAGAT	TGTTCAAAC	CATTTGATTC	ACCAACAGAT	660
AAACTCTCAA	CCATCTTTTC	AAGTAAATTT	ACCTTGCTG	ATTCAGTACA	TATTA AAAAG	720
TTTTCTTTAC	TAAAATACTG	TCTAAAGCCG	TTGTTTTC	ATTTGTAAAT	CTTTGATGAT	780
TGTACATAAC	TAGAACTTG	CATCTGAACC	ATAGCTTTTC	TAATCATTTT	CATCTCATCA	840
CTCTTAAGAA	ACACACTAAC	TTTAAAAACT	GGGATTTGAA	AATATAGATT	TGATAAATCA	900
ACAGCTGACA	CTATAAAATC	TATTCCTTTA	AGTTTTTCTT	GATTCAATTC	ATAATAGCCT	960
ATTACATCAA	CAACTTCTAC	TCGCTTCCCA	AACTCCGTTT	CCAAACGATT	TCCTAACATT	1020
TGGGCTGCAC	CAAATCCTGT	TGCACAAATA	GCAAGAATAT	TAAACTTAGT	ACTCTCTTTG	1080
CTACGTTCCA	TAGCAG					1096

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GGGGATTTTG	GTTGCTGGGG	TAACACGTGG	AGATGTTCAA	ATGTGAAAAT	ATCACAGATA	60
CTTCAAGCGT	GTTAAGGACA	TCCCTTTGAC	TTTGCCAGAA	GAAGTAGATA	TCACAGTTCG	120
TGGGGAATGT	TACATGCCAC	GCGCTTCCTT	TGACCAAGTT	AACCAAGTGC	GCCAAGAAAA	180
TGGAGAGCCT	GAATTTGCTA	ATCCTCGTAA	TGCGGCAGCA	GGAAGTATTG	TGTCAGTTGG	240
ATACAGCAGT	AGTTTCCAAG	CGTAATCTTG	CAACGTTTCT	TTATCAAGAA	GCCAGCCCTT	300
CAACTCGTGA	TAGCCAAGAA	AAGGGTTTGA	AGTACCTAGA	ACAAGTAGGT	ATTGTGGTCA	360
ATCATAAGCG	AATCTTTGGC	TGGAAAATAG	ATAAAATATG	GAATTTTATC	CAAGAAGTAG	420
GACAGGAACG	GGAAAATTTG	CCTTAAGATA	TTGATGGAGT	GGTAATCAAG	GTCAACGACC	480
TAGCAAGTCA	AGAAGAACTT	GGTTTTACCG	TTAAGGCTCC	AAAGTGGGCA	GTAGCCTACA	540
AGTTCCTGTC	TGAAGAAAAA	GAAGCTCAAC	TCTTATCAGT	TGACTGGACA	GTTGGCCGTA	600
CCGGTGTTGT	AACTCCAAC	GCTAATCTAA	CACCAGTACA	ACTTGCCGGT	ACGACTGTTA	660
GCCGTGCGAC	CCTGCACAAT	GTAGATTATA	TTGCTGAAAA	AGATATCCGA	AAAGACGATA	720
CGGTCAATTGT	ATATAAGGCT	GGTGACATCA	TCCCTGCCGT	TTACGTGTG	GTAGAGTCCA	780
AACGGGTTTC	TGAAGAAAAA	CTAGATATCC	CTACAACTG	TCCAAGTTGT	AACTCTGACT	840
TGTTGCACTT	TGAAGATGAA	GTGGCCCTAC	GTTGTATCAA	TCCGCGTTGC	CCTGCTCAAA	900
TCATGGAAGG	CTTGATTCAC	TTTGCTTCTC	GTGATGCTAT	GAATATTACA	GGCCTTGGTC	960
CATCTATTGT	TGAGAAGCTT	TTTGCTGCTA	ATTTAGTCAA	GGATGTGGCG	GATATTTATC	1020
CGTTTGCAAG	AAGAAGATTT	CCTCCTTTTA	GAGGGGGTTA	AGGAAAATCC	GCTGCTAAAC	1080
TGTATCAGGC	TATCCAAGCA	TCAAAGAAAT	TCCTGCCGAG	AAGA		1124

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTTGGTAGAA	CTTGCTAATC	AAGCTGGCAA	GCCTGTAGTC	TTGGACTGCT	CAGGTGCAGC	60
ACTTTCAGGC	TGTTCTTGAA	TCACCCATA	AACCAACAGT	CATCAAACCA	AATAATGAAG	120
AATTGTCTCA	GCCTTCTTGG	AAGAGAAGTT	TCTGAGGATT	TGGATGAATT	AAAAGAAGTA	180
CTTCAAGAAA	CCTTTGTTTG	CAGGGATTGA	ATGGATTATC	GTTTCACTTG	GTGCCAACGG	240
TACTTTTGCC	AAACATGGTG	ACACTTCTA	CAAGGTAGAT	ATTCCTAGAA	TTCAGGTGGT	300
AAATCCTGTT	GGATCTGGAG	ACTCTACTGT	GGCAGGAATT	TCTTCAGGAC	TTCTTCACAA	360
AGAATCGGAT	GCAGAATTAC	TCATCAAGGC	AAATGTCCTT	GGTATGCTCA	ATGCTCAAGA	420
AAAAATGACT	GGTCATGTCA	ACATGGCCAA	CTATCAAGTT	CTATATGATC	AATTAATAGT	480
AAAAGAGGTA	TAAAATGGCT	TTAACAGAAC	AAAAACGAGC	ACGCTTAGAA	AAACTTTCTG	540
ATGAAAATGG	TATCATCTCA	GCTCTTGCAT	TTGACCAACG	TGGTGCTTTG	AAACGCCTCA	600
TGGCTCAACA	CCAAACAGAA	GAACCAACTG	TGGCTCAAAT	GGAAGAACTG	AAAGTCTTGG	660
TAGCAGATGA	ATTGACTAAA	TACGCTTCAT	CAATGCTTCT	TGACCCTGAG	TATGGACTTC	720
CAGCAACTAA	AGCTCTTGAT	GAAAAAGCTG	GTCTTCTCCT	TGCTTATGAA	AAAACAGGTT	780
ATGACACAAC	AAGTACAAAA	CGCTTGCCAG	ACTGCTTGGA	TGTTTGGTCT	GCAAAACGTA	840
TTAAAGAAGA	GGGTGCAGAT	GCAGTTAAAT	TCTTGCTTTA	CTATGATGTA	GATAGTTCAG	900
ACGAACTCAA	CCAAGAAAAA	CAAGCTTATA	TCGGAGCGTA	CCGTTTCTGA	GTGTGTGGGC	960
TGAAGATATC	CCATTCTTCC	TTGAAATCCT	TGCTTACGAT	GAAAAAATTG	CACACGCAGG	1020
TTCTGTACAA	TATGCGAAAG	TAAAACCACA	CAAAGTGATC	GGTGCTATGA	AAGTCTTTTC	1080
ACACCCACGC	TTTAAACATT	GATGTCTTGG	AAAGTTTGAA	AGTTCCTGTT	AACATTAAAT	1140
ATGTTGAAGG	CTCCCCTGAA	AGGTGAAGTG	GGTTTACACA	CGTTGAAGAA	ACCAGCAGCC	1200
TTCTTCAAAG	CGCAAGATGA	AGCAACGAAC	TTGCCATACA	TTTACTTGAG	TGCTGGTGTA	1260
TCAG						1264

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTGAACTGGA TTTTGCTACA AGGTCTGATT TGTCAAAGAG ATGCGAGTTA TGATATGAAG	60
CAGGATGATT TGGATAAGGT AGCAGATTAT CTCTTCAAAA CAGAAGAATG GACCATGTAT	120
GAGTTGATTC TTTTCGGTAA CCTCTATAGT TTCTACGATG TAGACTATGT CACTCGGATT	180
GGTAGAGAAG TTATGGAGAG GGAGGAATTT TACCAAGAGA TTAGTCGCCA TAAGAGATTA	240
GTGTTGATTT TGGCCCTCAA TTGTTACCAG CATGTGTTAG AGCATTCTTC TTTTATAAT	300
GCCAACTATT TTGAGGCTTA TACAGAGAAG ATTATTGACA AAGGTATTAA GCTTTATGAG	360
CGTAATGTTT TCCATTATTT AAAAGGTTTT GCCTTATATC AAAAAGGACA GTGTAAAGAA	420
GGCTGTAAGC AGATGCAAGA GACCATGCAT ATTTTGTATG TGTTAGGTCT TCCAGAGCAA	480
GTAGCCTATT ATCAGGAACA CTACGAAAAA TTTGTCAAAA GTTAATTTTC CCAAATAAGG	540
GAAAAATAA AAAGCTCCTT TCGGTTTTGA TACAATAGTT TCAAAATTTG AGAGGAG	597

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CGTGTTCCTCA GATGGCCGCA TCCATTTATT GAGCCAGACG TGTCCAACT CATCAGGGTT	60
ATCTTCGATA ACCAAACGAA TACGAGTGCT TCGTCGCCAC CAAGGTCTGG TAGTTGACGA	120
TGTTCAAAAG AGCCGTTTCG ACCAACTGAC ATTGGGCTAG AGGTCCTTCC ACCTGCACAA	180
TCGGTTCATT AGCAAAAACC AAATCCCCTT CTGGGCAGA ACGAACGGTC AACTCCAAC	240
TGAAATTGCG AAGGTAATCC AAGAACGCCC CATGATAACC AAGCGACTCC AAATAGGCTA	300
TATCACTATC TGAAAAACGC AAGTCTTCAA GATAGTTCAC AATCTTTTCC AAACCTGCAA	360
AAACCGCATA GCCGTTCTTA AAAGGCTGTT GCGGAAATA CACCTCAAAG ACCGCCTTCT	420
TATTGTAAAT CCCTTGATCA AAGTAAACCT GCATCATGTT GATCTGGTAC AAGTCCGTGT	480
GCAATGTCAA ACTATCATCT GGATACATAC TTTTCCTACT TCCTTAGCTA GAAACCCATG	540
AAAATTTTCA AGAACTTTCA TGTATTCCAA TAAATTAGTA CTATTATATC ACATTTTAGC	600
TGGATTGAGA AAAGAGTAAC AAG	623

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

CCATGTTGGT TCTCAACTAT GTTTATGCTG TTCCTTTGTA CGCTAAGTTT GCTAACTTTG      60
ATATTGGAAA AATTTTGGGA CTTTCCAAC TACCTAATGAC CATGGTATTA CCTTTTAACT      120
TGATTGAAGG TGTATCTTTT TCCGTTTCAT TCTGGTTGTT GTATGTTCTC TTGAAACCAA      180
CCTTAAACAA TTATGAGAGA TAAACAAACA TTTTAAATGA AGGGCAGTTT TGCCCTTTTA      240
CTTTTCGTTA TTCTTGGCTA CATGGTCAAA TTTTACCCTG AAACGCTGGT CAATTTTGAC      300
CAATCGATTC AGACTGCCAT TCGAGGAGAC TTACCAGATT ATTTGACTAT TCTTTTTCGA      360
GCCCTCACAC GTCTGATTGA TATCCAGATG ATTATCACTT GGGTTGTCAT TACAGCTTTT      420
GTCTTTTATC GTAAGCGATG GAAGATAGAA AGTTTCTTCA TGCTGGGAAA TCTGGCTTTG      480
GCAGGTCTTT TAATCGTGAC CTTTAAAAAT ATCTACCAGC GCCCACGGCC AGATATCTTA      540
CATCTGGTGG AAGAGAAGGG ATTTTCCTTC CCAAGTGGGC ATTCTCTGGC TGTAACCTTG      600
ATGGTAGGT

```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

CTAAAAAAGT TAACAAGTGT GCCATGCCGA GTTACATTGG TTCCAGCTTG GAGTTTACTA      60
AGAACAATTT GATTCAAATT GTTGGGATTA AGGGAAGCTA ATATAGAAGT TGTAGAAGTG      120
ACGACAGCGC CTGCAGGTAG TGTAAGAGGC ATGGTTGTTG AACAAAGTCC TAGAGCAGGT      180
GAAAAGGTAG ACCTAAATAA GACTAGAGTC AAGATTTCAA TCTACAAACC TAAAACAAC T      240
TCAGCTACTC CTTAAAAGCA GATGGATAAT CAAAATGAGT AATCAATCTT TGTCATGATT      300
TCATGGCAAA GATTTTTTTT GAGTCCAGAT TTGTGATAGA ATAGAGGGAG TTGATAAAAG      360
GAGGAAAGCA TGGAAGAATC AAAAGAATTA AATGCCGTCA TTGATGTGAT TATGCTAGCG      420
GGGACTATTC TCCTTAAAAG TGGCTCAGAA ATCCATCGTG TAGAAGATAC CATGATTCTG      480
ATCGCGCATT CGCAGGGGAT TGTGGATTGC AATGTCCTTG CCATGCCTGC CGCTATCTTT      540
TTCTCTATTG AAAATACCAA TATTTGCGCG ATGAACGCGT GACCTCCTCT TCTTATAACA      600
TCGAAAAAGT CTGCGATGTG AACCAGATTT CTCGTCAG

```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CTCCATATTT	CTTAGCCTTC	TCAATTAGGG	TCTTGAAGTC	TTCGACACCA	CCGATACGCT	60
TACCAATATC	AGCATAGTTC	AAGTGACCAG	AGTCATGGCT	GTGATATCCT	TAACTTTTC	120
CCAACCTTGA	GGGTTGTTCA	TAATGCTACG	ATAAGCAATG	GCACCATCTT	GCCAATCAAC	180
TTTCTTGCT	GCATTGGCAT	CTTCAGTGAT	AACAACCTTA	GCACTTGGA	GTTCCCTTCGT	240
GTATTCCTGGG	AAAACAATGC	CCTTATAAGC	TTTTTCCCAT	TGCCATTGAG	AGCTGTGGAT	300
TCCTACATAG	TTGGCATTTC	CGACTGTTTC	TTTATAAGCT	GTCAAACGAG	TCCAGTCATT	360
CGAACCACCA	CCATAGCTAT	TTTGAGAGTT	ACTCCAAACA	CCAGCAGCAA	GCTTATCTGT	420
AGAAACAAAT	CCATACATGT	AACCCTTAGC	CAATCCTTC	ATTGGATTGG	TTACATCGAT	480
ATGATCATCT	CCGCTGACAT	GCGTATTGTT	TGACATGGTT	GCCCCATCAA	ACTTAGCACC	540
AGTTTGATCA	CTAGAAACAG	AGACTAAAGC	ATTGCCGAGG	AACTAATAG	AAGAAAGTAG	600
TTTTCTTTTCG	TCATCAATCT	TTTGACCTGG	AGTGACTTGA	TTGTGGTTGA	CAATCTTGGT	660
CACATCAAAG	TGCAATTGAT	TGTCCACAAC	TTGCAAGCGT	ACTGTCATTT	CCGCATTGAT	720
TAAGTGAGCA	TCATCGCGAA	GCTTCATCAA	GTACTCTGCT	GTTGTCTCAT	TGATTTTTTT	780
ATAAGTGACT	TCAGGGGTGA	TTCGGTGGTT	ATTGATAAAG	ACTTGGTTGA	ATTGTTGCAC	840
CTGTCTTGGC	AAAGTATGTC	CATTCAAGGT	GTATCCCTTG	ACACGAAGGA	AGGCTTGGTC	900
AATTACTGCC	TTAAGTACCT	TAACTGGAT	CGTATCATAA	GTCACCTTGC	TATCGTCAAC	960
AACCGGACCT	GTTTCTTTCT	GGGCAGGGGT	ATCCTCTGGG	TTTTACCCTC	TCTGTGGCTA	1020
TCCGTTTCAA	CGCTTGAACA	ACTGGTCGCT	CATCGTCATA	AGAGCCCGCC	TTGAGAAAAA	1080
TCTTCTTCTC	ATTTCTAAGA	TGGTCATTGA	CCGCAGCTGG	TAGAGTCACT	GTGTCAAAGA	1140
AGATTGACAT	CCTTATTTGC	CTGGCATTTA	CCTGACCGTC	TGACTTGAAG	ACTGATAGAG	1200
AGACGGTTTG	TTGATCCTGT	TTCAGGAGCA	GCAACACGAC	TACCTCTATA	CCAAGTGCTA	1260
GTGTTGGAG	ATTTATACTC	CCAGAACCAG	CCATCCTTGT	CATAACCGAC	AAAAACATTA	1320
TTATTGGTAT	CTTTAAATTT	CAAGGAGACA	CCAAAGCGTG	ATTTGCCCTT	TTCAGAATCT	1380
TCTTTGAAGG	TTAAATCAAC	AGTTGCATTT	CCATTGTCAT	CAACGGTCAA	GCCCTTCTTT	1440
TCAAACAGAG						1450

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1474 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGTATTGCG	CCATGAAGGC	AATCAAAAGT	GGTATGCCGT	CTTGNTGAAA	ATCTCTTGGA	60
ATAAGCTGGA	AAAGGGCAGA	GAAGGACAAG	TGGAAGCAGT	CAACCTCAAG	CATGACCAAG	120
TAGCTAATTT	GCTTTCACAA	AAGGGGATTT	ATCCAGCCTT	CCATATGAGC	AAGCGCTACT	180
GGATTAGTGT	GTCCCTTGAT	GATACTTTAT	CAGATGAANA	AGTACTGGAA	TTGATAGAAA	240
AAAGTTGGAA	CTTAACCTCT	AAAAAATGAA	ATATTTTAAT	AATTTTCATG	AACCTTCAAT	300
TAGCTAAATA	TTCTTTACTG	AAGAAATTTT	CAGAAAATAT	AGGATTTACC	ACACCAGAGG	360
AATGTGGTGC	CATCTTCAA	TACCTGATTG	AGAATGTCAA	GACGGATCGT	CAGATCATCT	420
ATTCGCCTCA	CTGTCATGAT	GAATCCGAA	TGGCAGTGGC	AAATAGCCTT	GCTGCTGTCA	480
AGAATGGTGC	AGGACGTGTT	GAAGAGACTA	TCAATGGTAT	TAGGGAGCGA	GCTGAAAATG	540
CTGCTTTGGA	AGAAATTGCA	GTGGCTCTCA	ATATTGCGCA	AGATTACTAC	CAAGTAGAAA	600
CCAGTATTGT	CCTAAATGAG	ACCATCAATA	CGTCAGAAAT	GGTTTCTCGC	TTCTCTGGTA	660
TTCCAGTTCC	TAAAAACAAA	GCCGTCGTTG	GTGGCAATAC	CTTCTCCCAC	GAATCTGGTA	720
TTCACCAAGA	TGGAGTCCTT	AAAAATCCTC	TCACTTATGA	GATCATCACA	CCTGAATTGG	780
TTGGTGTTAA	GATTCCGCTT	GGAAAATTAT	CTGGTCGCCA	TGCTTTTGTT	GAGAAACTGA	840
GAGAATTGGC	CCTAGATTTT	ACAGAAGAGG	ATATCAAACC	ACTCTTTGCT	AAGTTCAAGG	900
CACTGGCCGA	TAAGAAGTAA	GAAATCACAG	ATGCAGATAC	TCGAGCTTTG	GTAGCTGGAA	960
CCATGGTTGA	AAATCCAGAA	GGCTTCCACT	TTGATGATT	ACAACTCAA	ACTCATGCAG	1020
ATAATGACAT	TGAAGCGCTC	GTTAGCCTAG	CCAATATGGA	TGGTGAGAAA	GTCGAATTTA	1080
ATGCGACAGG	GCAAGGTTCC	GTTGAAGCAA	TCTTTAACGC	TATCGATAAG	TTCTTTAACC	1140
AATCTGTTCC	TTTGGTGTCC	TACACTATCA	ATGCGGTAAC	AGATGGAATC	GATGCCCAGG	1200
ATCGGGTTTT	GGTCACTGTT	GAAAACAGAG	ATACAGAAAC	CATCTTTAAT	GCAGCAGGGC	1260
TTGATTTTGA	TGTGTTGAAG	GCTTCTGCTA	TTGCCTATAT	AAACGCTAAT	ACCTTTGTTC	1320
AAAAAGAGAA	TGCAGGTGAG	ATGGGACGCA	GTGTTTCTTA	CCACGATATG	CCTAGTGTGT	1380
AAAGGAGAAG	GCTATGGCAA	AGAAAATAGT	AGCTCCTAAT	TACGAGACCG	AATTGGCCCA	1440
CAAATCATGG	AGGCTGGTTT	AGAAGTTCTG	GAAG			1474

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

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CCATACGACC TGTTCCTTTC GGTAGAGCAA CTCCCAGTTG ACCAGTCAAG CCGACCGCTT      60
TGGCAATGTA NTCCATATTT TGTGAGATTG GCATGANCAA ATATTGCAAT GGATACAAGT      120
TATCACTCTT GATGTAAAGA AGGGCGTTGA ACCAGTCATT CCAGAAACCA AGAGCTGTCA      180
AAAGCGTGAT GGTGCGATA CCTGGTAGTG ACAATGGCAA ACAGATTGGA AAGAAAATCC      240
GAGCCTCACT GGCACCATCG ATACGAGCCG ATTCGAGAAT GGCTTCTGGA ATGGTCTTCT      300
TGAAAAAGA ACGCATCAAG ATGATATTGA ATGGTGAGAG AAGCATTGGA ACAATCGAAG      360
GCCCCAACAG TGTACCAAG CTGAAGTACA CGGGTCACCA TGATATAACC TGGTACCAAA      420
CCAGCGTTGA ACAACATACT GAGAAGGACG AAGATGGTAA AAAATCTGCG ATACTTAAAG      480
GTTGTCCGTG AAATAGCGTA GGCATAGGTT GTTGTGATAA AGACATTTGT CAATGTCCCA      540
ACTACGGTTA CAAAGACAGA GATGAAGAGG GCTTGTAGGA TTTTATCCTT AAAGTGTGCC      600
AAAAACTCAA AACCGTCTAA GCCAAATTGG GATGGAAGA AGCTATAGCC GTATTGGAGG      660
AGGCTTTTCT CGTCTGTCAC TGAAATAATG ATAACGAATA CAAAAGGTAG GATACAAGAG      720
AGGGCAATCA AACCCGAAAT GATACTGAAG AAGATATCTG CTTTCTTACT GAAGGAGTGA      780
ATGCCGACAT TATCAATTTT TTCTTTTATA ATTTTCTTTT TTGCCATATT CTCCTCCTTT      840
CTAGAACAAA GCTGAGTTTG GATCGACTCG TCTTGCAAGC AAGTTTGATA GGATAACCAG      900
AATCAAACCA ACAACGGATT GGTAAAGACC GGCTGCTGCA GCCATACCGA TATCTGCTGT      960
CTGAGTCAAA CCATTAAAGA CATATACGTC CAAAACGTTG GTTACATTGT AAAGCTGACC      1020
AGCATTGTGT GGGATTGTAT AGAAGAGACC GAAGTCTGCG CGGAAGATAT TTCCGACTGC      1080
AAGGATGGTC AATACAGTTA CAAGCGGAGT CAACTGAGGA ATGGTTACGT TGCGAATACG      1140
TTGCCACTTG CTAGCTCCGT CCACTGTCGC TGCTTCGTAG TAGGTTGGAT CAATTCCCAT      1200
GATCGTCGCA TAGTACATGA CACTGCTATA TCCAAAGCCT TTCCAAATAC CTAGGAAAAG      1260
TAGGAGATAG GGCCAGATGC CCAGGTCAGC GTAGAAATTG ACTTCTTTGA GACCAAGACT      1320
TTCCAATAGA TGATTGAACA CCCCTTTATC AATATTTAGG AAGGCATCTG TAAAGAACT      1380
AATGATAACC CAAGACAAGA AGTAAGGGAA CAACATAGAA GTTTGAAAAA TCTTCACCAT      1440
TCTCTTAGAA CGGAG

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1455

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

CTAAAAAGAC CAACTTGCC TTGCCGTCTT GAATGGCCTT GACCACCAAT TCTTCACCCG      60
ATATGATGCG CCCTGCTCGC TGAGCAAGCC CCAAGAGATT ACTTATCTTT TGCTTATTCA      120

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AGTCCCAACT CTCTTCTTTT CACTTTGTGA TCCACATAAG CGATCAACTC GTCATAAAAG	180
CTTCTCTCCA CTTCCATGCT AAAGCTGCGG TTAAAGACCT TCTTCTTTT CGCCTCTAGG	240
GCTTCTGCAT TGTCTAGTTT GATATAAGCG CCGCGGCCAT TGGCCTTGCC CGTAGGATCA	300
ATAAAGACTT GTCCTTCCTT GTTCTTGACA ATGCGGAGCA AATCACGCTT ATCAATCACT	360
TCGTTAGACA CAACAGACTT GCGCAAAGGG ATTTTCTTG TTTTCATCTT TCCCTCCTCT	420
AGCAGCTTTT ATTCTTCTAC AGTATCGTTT TCTACTTCCA ACTCTACTGA AGCAGCGTCT	480
TCCATGGCTT CAAATTCGCT ATAGCAGACT TGATATCGAT ACGGTAACCA GTCAAGTGAG	540
CCGCCAAGCG CACGTTTTGT CCACGACGAC CAATGGCAAG AGAAAGCTTG TTATCTGGAA	600
CAACCACCAA GGCACGTTTG CTGTCGTTT CATCAAAGAT AACTTGGTCA ACCCCAGCCA	660
GGAGCGATGG GCATGGTAGC ATAAATTCAG CTGGATCTGC CACCCACCTC CAAAACATCG	720
ATATTTTCTT CGATTGGTAC CATGCGGTCA TTTTTCATCG CGTAACGAG	769

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTCGCAAGGA CAAGGACTTC ACCGGAGGAC AATTTTTGGA GAGACCAGCA GCTGGTAATT	60
CGAACACCTT CTACCTCGAA TCCCTGTAGT TGACATTTTT TCAGCCAACT CTTGTGATGG	120
CACATCAATG TCCACCAATT CTTTAAACCA TTTATAAGAT ACAAGCATAA TTTAGTTCTC	180
CAGAATGACA GTTGTCACCT TAGTTCTTTT CCTTTCCTAT CATTTCAATA GAAGAATCCT	240
CTTCTTACCT TAATTTCTTT CTCAGTAACC AATCCGTATC TACTTTTTGA CCAACCATAA	300
AATGATGTTG GCTAAATTTT TCAAAACCAT ATCGGTTATA AAACGCTTGA GCTTTTGTAT	360
TATGCTCCCA AACACCTAGC CAAGCCCAAG AAAAAGTATT TTTTGTAGCA AGTTCAAGAG	420
CAAATTCAAA CAGTTGCTTA CCTAGTCCAA ATCCTTGGA TTTTGTAGC ACATAGAGGC	480
GTTGAATTTT AAAAGCGTCC TCTAATTCTC TCTCAGTTG AGCACTTCCC CAGTTGACTT	540
TGAGAAAAGC AGCTATCTCC TCCTCCTGCA TAATGAAATA GGTTTCAGAG TCAGGATTTT	600
CCAATCAGT TGACAAAGTT TTCAGACTAT AAGCCTCTT AAAGTATTCC TGTAAGTGCT	660
CTTCCGTATT ATCATACGCA AAGGTTTCAC GAAAGGTTG TTTGGCAATT TTAGCCAACA	720
CCTCAACATC TGCCATTTCT ACTTTTCTAA TCATTATTTA AACTGTTCTG AGAAGCGGAC	780
ATCTCCTTGG TAGAATCCAC GGATATCGTT GATTCCATAA CGGAGCATAG ATCG	834

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

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CTCGTAAATG GAATGTGGTC AGTAATTTTG GTAAATTTGC AGATCCTATG GCGGATAAGT      60
TACTAGTTAT GTCGGCTTTT ATTATGTTGA TTGAGTTAGG TATGGCTCCG GCTTGGATTG      120
TTGCAGTGAT TATCTGTCGT GAGTTAGCTG TGACAGGTTT AAGGCTTTTA TTGGTTGAAA      180
CTGGTGGAAC AATTTTAGCA GCAGCAATGC CTGGAAAAAT TAAACTTTT AGTCAGATGT      240
TTGCCATTAT TTTCTTGCTA TTACATTGGA CTTTGCTTGG TCAAGTTCTA CTTTATGTAG      300
CCTTATTTT CACTATCTAC TCTGGCTATG ACTATTTCAA GGGTAGTGCC TATGTATTTA      360
AAGGGACATT TGGTTCGAAA TGAAATCAAT AATTGATGTA AAAAATCTTT CTTTTCGCTA      420
TAAAGAAAAT CAGAACTACT ACGATGTGAA GGATATTACG TTTCACGTGA AACGTGGAGA      480
ATGGCTTTTC ATTGTAGGGC ATAATGGTAG TGGTAAATCA ACGACGGTTC GATTAATTGA      540
TGGCTTACTG GAAGCAGAAT CCGGAGAGAT TGTAATTGAT GGCCAACGTT TGACTGAGGA      600
AAATGTTTGG AATATACGTC GTCAAATCGG TATGGTTTTT CAAAATCCAG ACAATCAATT      660
TGTTGGAGCG ACTGTTGAAG ATGATGTTGC TTTTGGTTTG GAAAATCAGG GACTTTCTCG      720
TCAAGAAATG AAAAAGAGAG TGGAAGAAGC TCTGGCTTTA GTTGGCATGT TGGACTTTAA      780
AAAGAGAGAA CCAGCGCGTC CTATCAGGTG CCAAAGCAC GTGTGGCCAT TGCAGGTGTT      840
GTAGCCCTAA GACCAG                                     856
  
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(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

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TCCCCATCCC AGTGGGCAGC AGCATTAGTC TGTACTTCTG CGTCGTTGCG TTTTATTAGA      60
AGACTGATTT TGCTTTGAAC TACTTGAAGC TGTCGTTGTA TCCTGCGAAG TTTTGTCTAA      120
CTTCAGTTTC ATTTGCAGCG ACATGACTAG TTGCCAAGCC TAGTAAACAG AACTTGTCTA      180
ATCCAATTTT TGTTTTCAAT CTTTCCTCTC CTATAAAAAA TGTAACAGAC ATCTGAATGC      240
TGTTCCACCT AGCTTTTGCT ACTTACTGAT TATTTTACAA AGTCAAGCAA AGCCAAGAAG      300
CTTTCAGCTT CAAGTGACGC ACCACCTACA AGGGCACCGT CAACGTCTGG GCAAGCCATG      360
TATGAAGCAA CATTTTCAGG TTTAACAGAA CCACCGTATT GAACACGAAC TTTGTCTGCG      420
  
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ACTTCTTGAC CAAAGTCAGC AGCTACAACG TCACGAACAA CTTTACACAT TTTTGTGCA	480
TCGTCTTGTG AAGCTGATT ACCAGTACCG ATAGCCCAGA TTGGCTCATA AGCGATAACT	540
GAGGCAGCAA CTTGTTCAGC AGTCAATCCA GCCAATGCAG CAGATACTTG AGCACCTACG	600
AATTCAGCAG CTTTACCAGC TTCGTAAGTT TCAAGTGATT CACCACAACA GATGATTGGA	660
AGCATACCGT TCGCAAAGAT TGCTTTTGCT TTTTGTGTA CATCTTCGTC AGTATCATGG	720
AAGTAGTCAC GCGGTTCTGA GTGACCGATA ACAACGTAGT CAGTACCGAT TTCTTTCAAA	780
ACTTGTGGGC TAGTTTCACC AGTGAAAGCG ACCTGCATTT TCAAAGTAGC AGTATTGAGC	840
AGCAACGTTA AAGTTTGAGC CTNNGGCAAC AGCAAGNACA GTTGTCAAAT CAAGAGCTGG	900
AGCAGNGATA CCTGCTTCAA CAAGATCTGA TGAAGGAAGT TTTGATGCAA CTGCTTCAAC	960
GAATGNTCCA GCTTNTTGGG GATTTTGTG CATTTCACG TTACCAGCGA TAAATGGTTT	1020
ACGTGACATT TCACATA	1037

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GATTCTACAG GATCCATTTT ACTATCTTAC GCGCCGGGAA GTAGGCTGAG ACATAACCAA	60
GTAATAGAGC CAACAAC TAG AGTTCCTAAA ACAGATAAAA GATTTAATTC AAAAACCTTA	120
GTGATGGATG GGTAAAAGTG ACTTACAATC GCATTCGCCA AACTTCCCAC CCCTTGTGCA	180
ACCAAAAATG CCAGCAGCAA GCGGATGCCT ACAATCCAGA TAGCCTCGTA AATAAAAATT	240
CCTTTGACAT CACGATTCTG ATAACCAACT GCTTTCATGA CACCTATTTT CTTGGAACGT	300
TGCATGATAT TGATGTAAAT AATGATACCA ATCATAACCG CTGCTACCAC AATAGCTTGT	360
GATGAAAGCA CAATCAATAA TCCCTGAATA ACACGAATAA AGGTAATCAC AATATCAAGA	420
ACTCTCTGTT AAGAAAGCAC AGTATACTTC TTATTTTCT GTAATCTTC TGTACTACT	480
TTTGTCTGTG ATGGATCTTT GAGTTCCAAG ATAAAATAAG ATACAGCTTT CGTAAATCCA	540
GCCTCTTTCA AAATCGTTTC CATTGATGA GACAGCATGA AACTGTTGCT GTCCTCCATG	600
TCATCTTCAT CATTGATTAC ACGTACAATC TTCGTTTGAA ATTGAGCAAT CTTACTAGTT	660
TCGGCAGCAC TTTCTACAAT GCTGACTGAG ACTGATTTGC CAATAAGATC ATTAGCTGTC	720
AAATTTTTTC CTGTCTGTTT ATTCCAATTT TTTAGTAAAC TGCTTGAAT CGTTAATCCC	780
TGTTCAATTTG TATCAGTATA GAGGGATCCA GCCAACACTT TGTCCGTCTC ATTATTACTA	840
ACAGAGATAC TTGTATCATC ATAAAGACTC ACTACTTGAG CATAAGAAGC ATCGTTTGAC	900
TCAAATCCAT TTCTTGCCCA TCTTTTCTTG CCCATCTATA GTAATATTTG ACATGTTTAT	960
CCCAAAAGGA CTCTCCAAAT ATTTAATAGA TCGAGCCT	998

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

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CACATGTCGA CTAAGCCGTT AGAAATCAAG TGTATAGGCA GTTCATCATC TAATAGAGCG      60
TTGCGTCCGA AAGTCTATCC AGACACGGCT CTTTAAAAAC AAAAGGAGAA ATGATGCATA      120
CTTATTTGCA AAAGAAAATT GAAAATATCA AAACAACCCCT AGGTGAAATG TCAGGTGGTT      180
ACCGTCGTAT GGTTCGGGCT ATGGCTGATT TAGGATTTTC AGGAACTATG AAGGCTATCT      240
GGGATGACCT CTTTGCCCAT CGTAGTTTTC CCCAGTGGAT TTATTTGCTG GTTTCAGGAA      300
GTTTCCCTCT CTGGCTGGAG TTGGTTTACG AACATCGTAT TGTTGACTGG ATTGGGATGA      360
TTGTAGCTT GACAGGGATT ATCTGTGTAA TCTTGTATC GGAAGGTCTGA GCAAGTAATT      420
ATCTTTTTGG CTTGATTAAAC TCTGTTATTT ACCTTATTTT GGCCCTACAG AAAGGCTTTT      480
ATGGTGAGGT GCTGACGACA CTTTACTTCA CAGTCATGCA GCCAATTGGA CTCTAGTTTG      540
GATTTATCAG GCACAGTTTA AGAAAGGAAA AGCAGGAGTT TGTCGCGCGT AAAGTGGACG      600
GCAAGGGCTG GACAAAGTAT CTTTCCATTA GTGTGCTTTG GTGGTTGGCC TTTGGCTTCA      660
TTTATCAAGT CTATTGGTGC CAATCGTTCC CTTATCCGTG ATTCAATCAC CAGATGCAAC      720
CAATGGGGTA GGGCAAATCC CTCATGACAA GTCTGTTTAC CGTGAACAGT GGATATTCTG      780
GGCGGCTACC AATGTCTTTT CAATCTATCT CTGGTGGGGA GAAAGCCTGC AAATTCAAGG      840
GAAATATCTA ATTTATCTCA TTAACAGTCT AGTTGGTTGG TATCAATGGA GCAAGGCAGC      900
TAAGCAAAAT ACTGATTTAC TTAAGTAGGA AAAGATGTTT GAAAGTGCTG TTTTGAGATT      960
TCGATTAAAA CAGATATAGT TGATAATCAA GGATTTATAG TATGAAAAAG AGGATCGGCG     1020
GGTCCTCTTT TGTTGTTGAA AAGATAAAAA ACTCAGTAAC CTAGAAATAA GACAACTGAA     1080
GCTTTACTCT ATATTCAATT TTTAGGAATG AGAAGGTCTA GATAAAATTG GACAACTTCC     1140
TGGTCTGTGA AATCTTGACC TTTTGTGAGC CACCAGGTCA ATGTCTCGAT AAAGTTGGAC     1200
ACGACCAAGT GTTGAGGTA AGAAGTAGGC AGATTAGGTT GGGCTTCTTT TAAATTATCA     1260
G

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(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CTGATCATCT AACACAGAAG GGAACGTCTC ATCTATTCTT TGATCTGGTG GTAGGTAAC	60
GTTTCTTTGC TTTAGGATGT GGTTAGGGAG GTGAAGTCAG ATAAGTAGAT GGGCTTAATT	120
TGCCCCAAGTC CCACATCAAA GAATTATCGG CGAATCCAAG GTGCTCCTTT AATTATTTGT	180
AGATCTTCAG GAGCAAGGGA GACAACTTGC ACGTGTCCTAA CGTAACCTGA AAGGCGTGCC	240
TGTTTAAAGT GATTAACTTT TGTCACGATG CCTTTTGTG TTAGTTCGAT TTCTAGGGGA	300
ATGGATCCAG TTTTCTCTG AACGAGACCT GAACCATGAA ACTTGTGCCT CATCATCAAT	360
GAATGAGATT CTTTATCTGT TCGAGTTCGA TCGACTACAG CGTCAAGGCT AACAAATAGA	420
TAGCCTCTAT CATGTCTGTT TT	442

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAGCTGATGA ACGCTCCAAA GAATTTCGCA AATCATCAAA ACGGTACTTA ATCCCCCAA	60
CCAAATCGGC ATGACCTGGG CGAGGATGAG TAATTTTCCG CTGCTTTTA AGGCGGTCTT	120
CAATGTCTC CGCAGACATG ATGTCCAGCC ATTCTGGTG GTCCTTATTG ATGACATACA	180
TAGTAATAGG CGCCCTGTC GTCTTCCCGT GGCGAACGCC CGAAGTAAAG ACAACCTGGT	240
CATTCTCAAT CTTCATACGA CCACCACGAC CGTAGCCACC CTGACGGCGT CTAAGGTCCT	300
CATTGATATC CTCAGCTGTC AATGGAAGTC CAGCTGGAAT TCCCTCAATA ATAGCTGTTA	360
GACGGGGACC GTGTGATTCT CCTGCAGTTA AATATCTCAT AACTCTCCT TATTTTACCA	420
AGTAGTCTTT CATCTCTTCC AGAGAACTG GATGAATGGT CGCTGAACCA AGCTCTGGCA	480
CCAAGACCAA TTTCAAGGTG TTGCCACGCG CTTTCTTGTC ATGAGTAAGA GCCTGATAAA	540
GCTTGTC AAC TTCCCAATTT TCATAGTCAA CAGGCAAGCC GAATTTCTGA CACATCTCTG	600
TGATAGATTG GGTAATGCCA GCTGGCATGA GGCCTTTTTC CTCAGCAATC TTGGAAATCT	660
GTACCATTC CATGGCAACA GCCTCTCCAT GCATGACCTT GCCATAACCG GCAGTCGCTT	720
CGATGGCATG GCCAATAGTG TGGCCAAAAT TGAGGTAAAG ACGAATACCA TTGTCCAAC	780
CATCTTCAAC CACCATCTTG CGCTTCACCT GACAAGAATG TTCAATCAAG GTCTCTGCAT	840
GTTCCAAAAT ACTCTCAACA GAACCATCA GTCCCGTCAA GAGAGCCCAC AGTTCTGGAT	900
CCTCAATCAA GCCATACTTG ATAACCTCAC CCATCCCTTC AATCAACTCT CTTTTTCCGA	960
GGGTTTCAAG AACAAGTGA TCAATCAAAA CCCCATCTGG TTGGGCAAAG GTCCCCACCA	1020
TATTTTTCAGC AAATGGTGTG TTAACACCTG TCTTTCCACC GATAGAAGAA TCAACCTGAG	1080
CTGTCAAAC AGTCGGAATC TGAACAAAGT GAATACCCCG CATATAGGTA GAGGCTACAA	1140

ATCCCAGCCA GGTCCCAACA ACGCCACCAC CAAGAGCAAC GATTCCATCC GCTACGANTC	1200
NGAACTTGCT TGA TAGAAA TTCATACACT TTCTGAACCG TAGTTAAATT CTTTCTTTCT	1260
TCACCTTCTA AGAAGTCCAA AA	1282

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CTCAGCAGT TCTGTTACCA AAGACCGTTC AAAAAGCAAA CTAGCAATAC TTATAACTTA	60
TTAGAAATTC CTAATTTTAC CTGCTAAAC GAATACAGGT CACGATGCCA TCTGAGTCTG	120
TGATTTCCAA TTGGCTCGAT GTCATCCATT TGATTGGTAC GTCAACTTCT TGTGCTCGTT	180
GGGCAATCGT TAACAGTTCT TCTTTATGTG CAACTTCGAT GACATAGTAG GCTAAACCTG	240
GTAAGCCTTG CTTACGCGGA AGCCAGACCT TTTCCTTCCC CATTTCGTTAA CTGCTAAATG	300
ATGATGGTAA TCTCCAGCCG CAATCCAAT AGCGCCAGGC ACACTGAATT TATTCTCTAG	360
CCCTAACACC TTTTGATAAA ACTGGCTGGA CTTTCGACTA TCCTTGACGG AAAGATGAAT	420
ATGCCCCATT CTTGTACCTT CTGCCAGGAT AAAGGGCTCT ACTCTTCCC CCAACTCATA	480
AATGTCCTGC GCCGCAAGAG CCTCCGTCAC TCCGATAATG CGTCCATCTT CTCGAATATC	540
CCATGTGGAA ACTGGCTTAT CTCGATAGAG TTCAATGCCA TTTCCCTCCA AATCTTCCAA	600
GTAAATAGCT TCACTGTAAC CATGGTCTGC ACCGCCGACA AGAGGAATTT GCAAATCTGT	660
CAGATGTTTC AAGACATCAG CCAAAGCCTT GCGTGTGGGC AAGAGAATGG CCAAATGGTA	720
AAGACCATAA TGTTCCTCA CTTCTCCGCT CTTCTTGTGC TTGAATCAG	769

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

CTGGAGATTA TTGAGATTGC CCGTCAAAAC GATTTGATTA TTTTGGCGGA TGAAATCTAT	60
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GACCGCATGG TAAATGGACG GACATGTGCA TAACGCCTGT GGCGAGCTTG GCACCAGATG	120
TCTTCTGTGT CAGCATGAAT GGTCTGTCAA AATCCCACCG CATAGCAGGT TTCCGTGTGG	180
GTTGGATGGT CTGTCTGGC CCTAAGACTC ATGTTAAGGG CTATATCGAA GGGCTCAATA	240
TGCTGTCCAA TATGCGCCTT TGCTCTAACG TTTTGGCCCA ACAAGTCGTA CAAACTTCCT	300
TGGGGGGTCA CCAATCAGTC GATGAATTGC TTCTTTCCTG GTGGACGAAT CTACGAGCAA	360
AGAAATTTCA TCTATAATGC CATTCAAGAT ATTCCAGGTT TGTCTGCCGT TAAACCCAAG	420
GCGGGGCTCT ATATCTTCCC AAAAATCGAC CGCAATATGT ACCGTATCGA TGATGATGAG	480
CAGTTTGTCC TTGATTTCTT GAAGCAGGAA AAGGTTCTCT TGGTTCATGG TCGAGGCTTT	540
AAGTGGCAGG AACCAGACCA CTTCCGTATC GTTTACCTTC CTCGTGTTGA TGAGTTAGCC	600
CAAATCCAAG AAAAGATGAC TCGTTTCTTG AAACAGTATC GTAGATAGGG CTTGCATTGC	660
AAAAAGCTGG AAACATTTGC CTAGAG	686

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CTAAAAAAG TCAAGTAGAA AACGAATATT CTAATAACT TGCACGAAAT TATTTTTCAC	60
GAATGACTTC GACCTTATAT CCATCAGGGT CTTTGACAAA GTAATAGTTT GGTGCAGTTC	120
CTGGTAGACC ATTTGGCTCA GTCATTTCAT AGCCTTTTGT ACTGTGCTCT TGATGAAGTG	180
CCTCAAGATC AGGTGTACTG AGGGCGATAT GGGCAAACCC ATCACCACCC ACATACGGAC	240
CGTGATCGTA GTTATAAGTC AACTCCAACCT CATAGTCATC ACCCTCAAGA CCTAGATAGA	300
CAATCGTGAA GGCATGGTCT GGAAAATCTC TGCGACGCAA TTCTTTAAAA CAAAAGCAT	360
CTTGATAAAA TGCAATTGAT TTTTCAAGAT TTTCTACTCG TAAGCAAGTG TGTAGCATTT	420
TTGAAGCCAT ATCTTCTCC TTTATTTTAA AAAAGACTGG ACAATCCTGT TCCAGTCTCA	480
TCAGTTGTTA TTTACCAAGT TTTGCTTTAG CTGCATCTGC AAGAG	525

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTAGCTTGT	GTCCTCTCTT	CTCTACGAG	TGGCGGTTT	GATTATCGCC	TGTCCTTGTG	60
CCTTGGGACT	TGCAACACCG	ACAGCCCTTA	TGGTGGGGAC	AGGACGTAGT	GCCAAGATGG	120
GGGTTCCTCT	CAAAAATGGA	ACTGTCTTAC	AGGAAATCCA	GAAAGTTCAA	ACTCTTGTCT	180
TTGATAAGAC	CGGGACTTTG	ACGGAAGGGA	AACCTGTGGT	AACAGATATC	ATCGGCGACG	240
AAGTAGAAGT	GTTTGGGTTG	GCAGCCTCCT	TGGAAGATGC	TTCTCAACAC	CCACTGGCTG	300
AGGCTATCGT	TAAGCGAGCG	AGTGAAGCTG	GACTTGAGTT	TCAAACGTG	GAAAATTTTC	360
AGACCTTGCA	CGGGAAAGGT	GTTTCCAGGG	CGAATTAATG	GAAAACAAGT	TTTACTTGGA	420
AATGCTAAAA	TGCTGGATGG	CATGGATATT	TCTAATACTT	ATCAAGATAA	ACTAGAAGAA	480
CTAGAAAAAG	AAGCTAAGAC	AGTTGTGTTT	CTTAGCTGTT	GACAATGAAA	TCAAAGTTTT	540
GCCTTGCTTT	GCCAGATATC	CCTAAAGAAA	TGCTG			575

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTCAATAGCA	CCAATAGACA	GTTTCTTGGT	TACATCATAA	GCACCAGGTG	TTACCAAAGC	60
TTCAACAGCG	TGAGTCAGAG	CATCCATACC	AGTAGCAGCA	GTCAGGCCTT	TAGGTTTGGG	120
AAGCATGAGT	TCCGGGTCAT	TAACAGAGAT	AAGAGCAAGG	CTATTCTTGT	CAACCATTAC	180
CATCTTAACC	TTGCGTTCTT	CATCAGTAAT	CACATAGTTA	ATAGTGATTT	CTGCAGAAGT	240
TCCTGCCGTT	GTATTGATAG	CCACAACCTG	CAAGCCTTTT	TTAGCAGACT	TATGAAGCCC	300
TTCATAATCC	TGTGGTTTTT	CACCATTGTG	AGCCATGATA	GAAATACAAC	TAGCTGCATC	360
CTGTGGAGAA	CCCCGCCAA	GACTGATGAT	AAAGTCACAG	CCATGTTCTT	GCAAAGCAGC	420
TACCCCATCT	GTGACATTTT	TACAAGTAGG	GTTTGGCGTC	TACATCGCTA	AAGATGACAT	480
ATTCGATTCC	TTCTGTATCC	AGTGGTTTTA	AAACCTTAGG	TAAAATATCA	CTGCCTTCGA	540
TGTACTTATC	TGTCACCAA	AGTGCCTTTT	TATAGCCAAG	TTCTTGATA	TAAGGACCCA	600
CTTCATTTAC	AACACCTTTT	CCAATAAGGT	TGACTGCCGG	AACATAAAAT	GTAGCCATAT	660
AATTTTCCTC	CTGCGCCTCC	GCGCTATCTA	TTTAACATCA	TTATATTACT	TTTTGTATTG	720
GTTTTCATTT	ATTTGTGAAT	TGTTTAAACA	ATCTTTTAA	AAGGATAGGA	GGGACGTAAG	780
TTCACCTCCT	ATATAACAA	GGTTTATTTA	TGTAGTGGTC	CCAATAACTG	ACATGCACGA	840
TAGTCTGCTG	ATTCTAGATC	TTCTGTTCCT	AATAAGGACC	AATTTTATAG	TCTAAAGATA	900
TCTTCTTCGG	GTACATTATG	CATATTGACA	GGAATTCTCA	ACATAGAAGC	CAAGGTAATC	960
AAGTCTGCTC	CAATGTGTCC	ATATGTTATG	GCTCCGTGAT	TAG		1003

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

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CTAAAGTTTC TGATGAACTT GGTGGTGGAT CAATTACAGC CCTACCATT TATCGAGACAC      60
AAGCAGGAGA TATCTCAGCC TATATCGCAA CCAACGTGAT TTCTATCACT GATGGACAAA      120
TCTTCCTTGG CGATGGCCTC TTCAATGCAG GTATTTCGTCC AGCCATCGAT GCGGGTTCAT      180
CTGTATCTCG TGTAGGTGGT TCTGCACAAA TCAAAGCCAT GAAGAAGGTT GCTGGTACAC      240
TTCGTATCGA CCTTGCTTCA TACCGTGAGT TGGAAGCCTT TACTAAGTTT GGTTCGACT      300
TGGACGCAGC AACACAGGCT AAGTTGAACC GTGGACGTCG TACCGTTGAG GTCTTGAAAC      360
AACCTGTTCA CAAACCATTA CCTGTTGAGA AACAAAGTAAC CATTCTTTAT GCTTTGACAC      420
ATGGTTTCTT GGATACTGTT CCAGTAGATG ATATTGTTTCG TTTCGAGGAA GAGTTCCATG      480
CCTTCCTTTG ATGCTCAACA TCCAGAGATT TTGGAAACCA TTCGTGATAC AAAAGACTTG      540
CCAGAAGAAG CAGTCTTGGA TGCTGCGATT ACAGAGTTTC TCAATCAATC TAGCTTCCCA      600
ATAAGAATAG AAGTGTCAGA TGGCAGTGTC TCTAAATGAT ATTAAACAA AAATCGCCTC      660
AACAAAAAAT ACGAGTCAAA TCACTAATGC CATGCAAATG GTATCGGCTG CTAAG          715

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(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

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ATCAAAGAGC CTATGTGCAG GCTGGGGCAG GGATTNTCTA GATCTATCGC CAAAAACGAA      60
TACCAAGAAA CCATTAACAA AGCAAAATTT ATGACTAGAA TTGGAGAACT AAGACCATGA      120
TTTTATTGAT TGACAACTAT GATTCTTTTA CCTATAACTT GGCCCAATAC ATTGGGAATT      180
TTGCAGAAGT TCAGGTTCTG AGAAATGATG ATTCCAAGCT GTATGAAGAA GCTGAAAAAG      240
CAGATGGTCT GGTCTTTTCT CCTGGTCCTG GTTGGCCAGT TGATGCTGGA AAGATGGAAG      300

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ACATGATTTCG TGATTTTGCA GGCAAGAAGC CGATTCTTGG GATTTGTTTG GGCCACCAAG	360
CCATTGCAGA AGTCTTTGGT GGTAAGCTAG GTTTGGCTCC AAAAGTCATG CATGGGAAAC	420
AGAGCAATAT CAACTTTGAA GCGCCATCTG TTTTGTATCA AGGTATTGAG GATGGCCGTG	480
CGGTCATGCG TTATCACAGT ATTTTGATTG AGGAAATGCC AGAAGACTTT GAAGTGACAG	540
CTCGTTCGAC TGATGACCAA GCCATCATGG GGATTCAACA TAAAAACCTA CCGATTATG	600
GCTTCCAGTA CCATCCAGAG AGCATTGGAA CGCCAGACGG CTTGTCTTCT ATTCCGAATT	660
TTATCGAGGA GGTGTAAAG TGAGGAACT AGGATGAAAG AGATTATTGA AAAACTAGCA	720
AAATTTGAAA ATTTATCAGG TGTGGAAATG ACGGATGTCA TTGAGCGTAT CGTAACTGGG	780
CGTGTAAC TG AAGCGCAGAT TGCTTCTCTC CTCTTAGCTC TTAAGATGAA GGGGGAAACA	840
CCTGAAGAAC GCACAGCCAT TGCCCAAGTC ATGAGAGGAC ATGCCCAGCA TATTCCAAC	900
GAGATTCATG ATGCTATGGA CAACTGTGGT ACAGGTGGGG ACAAGTCTTT CAGTTTAAAT	960
ATTTCCACAA CTGCAGCCTT TGTCTTGGCT GGTGGCGGTA TTCACATGGC CAAGCATGGT	1020
AACCGCTCGA TTTCTTCTAA ATCTGGTTCC GCAGATTCCCT CNAACCTTGG GAATCAATCT	1080
TGACCTC	1087

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CTCTGCTTGC TTTTGTGCT TGGAATTTTG TCACCTTTTT TCTTTGCCCA CCTACTCGAA	60
ATGAAATTTT TTATCAACAT GCTGCTCCTA CTTTACAGG AGTTACGGCA TTTTGTATGT	120
ATTTTTTTTA TCCTGTGATT GCAGGTCCCA TTTTGAAGA CATGATTTAT CGTGGATTAG	180
TGATGACTGC TCTGGAAAAA GGAAAGAAAT GGGGGCTAGA TGTAATTGGT TCCGCTGTTT	240
TATTTGGGGT CTCGCACATT AGTAATCACG GTTGGGTCTT GACAGACTTT GTCTTCTATA	300
TGGGTGGAGG TCTTATATTT GCAGTCTTAT TTAGAATGAC AAAGTCAATT TATTGGCCTA	360
TTGGAATGCA TATAGTCTAC AATGGCATTG GTCAGCTTTT GATGTTACTG TAATTTTGGT	420
TGTTAGTAGT ATCGCGGTCT ATCCTTGGGG AAAGCTTCCC ATTTGAATTT AAGAAGGAGT	480
TGTGATGAAA GTATTTCTTC AAAATAGAGA TTTTAGACAA TTAACCATCA ACCAGTGGAT	540
TTCAACGCTT GGGGATACGA TTTTATATCT GGCCTTCCCTG AATTATGTGG CAGATACATC	600
TTTTGCCCCCT TTGGCGATTT TACTCATCAC GATTTTCAGAA ACCCTGCCCC AAGTTCTACA	660
AATCTTTCTG GGAGTTTGG CGGATTTTCA ACATCATCGT GTCTTGAAAT ACACAGTCAT	720
TAGTTTTCGA AAATTTTTCG TTTACTCTAT AGTGTCCTTA TCGCTTTCAG GGCAGTCTTT	780
TTCTTGTGTT CTAGTAACCT TTATTTGTCT GCTTAACCTC TTGTCTGACA CATTGAGTGC	840
TTTTTCAGGC GCCATGCTCA CTCCGATTTT CATTAGAATT ATTGGGCAAG ACCATCTGGC	900
AGAAGCTATT GGATTTAAAC AGTCAACTGT TAGTTTAGTG AAAACAACCA GTAATATCCC	960

AGGAAGAATC TTACTAGGCA TTCTATCCAT CCAGTTTATT TCCTTACTGA ACGCTCTTAC 1020
 CTTTTTAATC GCATTTTATG GTATCCTCTT CATAAAACT GACCTCTTGA AAGTAGAAAA 1080
 AACGATTAG 1089

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ATTCAAGGTT CATTGCGGGA CCAACATCCG TTCACTTTCA TTTGCCATCG GTGGATGGTG 60
 CCCTTCCAGG AAATGGAGGG TCGTGGTTAT GTCCTTTCGT CGTCTTCTCC GTCGTGCTTC 120
 TATGCATGGG TCAAAAATTG GGTATCAACG AGCCTTTCCT TTACAAAACG CGTTCCAACT 180
 GTTGGAAGAA TCATGGAAAG CTAATACCCA GAAGTGCTTG AGAAACGTGA CTTTATTGAG 240
 AAAATCGTTA AGAGGCGAAG AAGAATCATT TGCCCGTACC CTTCACTCAA GGTCAACACT 300
 TTGCCAAGG CATTGTAGCA GACTTGAAAG AAAAAGGTCA ATCTGTTATC GCTGGTTCAG 360
 ATGTCTTCAA ACTCTATGAT ACTTATGGGT TCCAGTTGA ATTGACTGAA GAAATCGCTG 420
 AAGAAGCTGG TATGACTGTA GACCGTGAAG GTTTTGAAGC AGCCATGAAA GAACAACAAG 480
 AACGCGCGCG TCGGTCAGCT GTCAAGGGTG GCTCAATGGG TATGCAAAAT GAAACTCTTC 540
 AAAACATCAC TGTAGAAAGT GCCTTCAACT ACAATGCTAG CCAATTGTCT TCTAAATTGG 600
 TAGCTATCGT GCGGACAAT GCAGAAGTAG AAGCTGTTTC AGAAGGAACT GCCTCTCTTA 660
 TCTTTGCGGA AACGTCATTT TATGCTGAAA TGGGTGGACA GGTAGCTGAC TACGGACAAA 720
 TCTTGGATGA GTCAGGTAAG GTTGTGGCTA CTGTGACCAA TGTTGAGAAA GCCCCAAATG 780
 GTCAAGCCCT TCATACAGTT GAAGTCCTTG CACCGCTTGC CTTGAACCAA GAATATACCT 840
 TGGCAATTGA TAGCAATCGC CGTCACCGTG TCATGAAAAA CCACACTGCG ACTCATTTGC 900
 TTCACGCTGC CCTTCACAAT ATCCTTGGA ACCACGCAAC ACAGGCAGGA TCTCTTAACG 960
 AAGTTGAATT CCTTCGCTTT GACTTTACCC ACTTCCAAGC TGTAACGCT GAAGAATTGC 1020
 GTGCGATTGA ACAGCAAGTC AACGAAAAA TCTGGGAAGC TCTTGAAGTT AAGACAGTTG 1080
 AAACGGATAT TGACACTGCT AAAGAAAATG GGAGATCGAA TTCCTGCAGC CCGGGGGGAT 1140
 CCACTAATTC TANANCGGCC GCCACCGCGG TGGAAGTCCA CTTTNTTTTC CCTTTAATGA 1200
 AGGTTAATTG CCNCTGGGG TTANCATGGC CCNACCGTTT CCCGTTTAA ATTGTATCCC 1260
 CCCNAATC 1269

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1243 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

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CCGTTGATAT AGGCTTGGGC ATTGCCACAG AACTTCTTAC CATCAATCTC AAGGTCATTA      60
CGGACCTGTG AACTCAGCTT TAACCCCGAG TTGAGCCAGG GTATTGATAA CCGGAGTTGA      120
GAAGCTCTTG AAGTCAAATG CTTATTTTCA TCTTCTTTGG AGATGATCGT GTAGTTGAGG      180
TTATTTAAAT CGTGGTAAAC AGCTCCACCA CCACTAATAC GGCGAACTAC CTCAATACCA      240
TTTTCGCGAA CATAATCACG GTTGATTCTT TCGATAGTGT TCTGGTGACG ACCAACAATG      300
ATAGATGGCT TGTTAATCCA AAGTAGGAAG ATTTGATCCT CATCCAAAAG GTGTTTAAAG      360
GCGTATTCTT CCAAGGCAAT ATTAAAAGCA GTGTCAATTG AATGATTGAT AATGTATTTT      420
ATGATATCCC TTTACTTTAT ATGATAGAGA CTGGAAATAA CCTTCCAGTC TAATCTATCT      480
TCGTTTATT TTTTCTTAGG TGAATGGATG GCCATTCTTA GAACATCTGC AAACGCTTCG      540
TACATCACTT CAAAGTAAGT TGGGTGTCCG TGGATGGTCT TCAGCATTTT CTCAACAGTG      600
ATTTCCATTT CGATGATGCT TGATGCTTCG TTTATTAATT CTGCGGCTGC AGGAACAATA      660
ATGTGTACAC CAAGGATTTT TCCGTATTTT TTATCAGCGA TAACTTTTAC GAAACCTTGA      720
GCTGCGTCAG ATGCAATAGC ACGACCGTTA GCAGCAAAGT TAAACTTACC GATGGCAACA      780
TCGTATTTCT CACGGGCTTG TTCTTCTGTC AAACCTACTG CTGCTACTTC AGGGAGAGTG      840
TAGATGGCTG CAGGAGTCAA ATTCAATTTG GCAACTGCAT GATTTCCCTT AAGGGCATTT      900
TCAGCGGAAA CTTACCCCAT GCGGAAAGCT GCGTGAGCCA ACATCTTAGT ACCGTTGATG      960
TCACCTGGTG CATAAATGCC TGGAACGTAA GTTTCCATGT ATTCATTGAC CTTGATACAA     1020
CCACGATCCA ATTCAAATC AACCTCTCCA ATACCTTCAA GGTCTGGCAT ACGACCAATT     1080
GAAAGAAGAG CTTTGCTTGC GATGATATTG TCTTTTCTTT CAACCTTGAT ACGAAGTTGA     1140
CCATTTTCTT CAATGATTTT TTGCAGTTTA GTACCAGTCA AGATGGTCAT TCCTTTACGC     1200
TCAAGGATCA AGCGAAGGTT CTTAGAAACT TCCGCATCCA TAG                          1243

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

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CTGATAGTGG AGACTATCTT GGGTATTCTA GGTAGTAGAG GTATCCATTT AGCAGTTCAA      60

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GGTTGTGAGC	ATGTCAATCG	GGCTCTCGTT	GTTGAACGTC	AGGTGGCAGA	GCAGTTTGAT	120
CTGGAAATTG	TCAGTGTCCA	TCCTACTCTT	CATGCAGGAG	GTTCGGGGCA	GTTGGCAGCC	180
TTTAAGTTTA	TGCAGGATCC	AGTTGAGGTT	GAATTTATCA	AGGCTCATGC	TGGATTGGAT	240
ATCGGAGACA	CTGCAATTGG	CATGCATGTC	AAGCATGTTC	AGGTTCCGAT	TCGCCCTATT	300
TTGAGAGAGA	TTGGTCATGC	CCATGTAACG	GCACTGGCTA	GTCGTCCAAA	ATTAATCGGA	360
GGTGCGCGTG	CGCACTATCC	GCAAGACGCT	ATTAGAAAGT	CTTGAGAATG	AATAAAGGAG	420
ATAAAAGTGT	TTAAAAAAGA	CCGTTTTTCA	ATTCGTAAGA	TTAAGGGAGT	TGTAGGCTCT	480
GTATTTCTTG	GAAGCCTTTT	GATGGCTCCT	TCTGTAGTGG	ACGCAGCCAC	CTATCACTAT	540
GTAAATAAAG	AGATTATTTT	ACAAGAAGCT	AAAGATTTAA	TTCAGACAGG	AAAGCCTGAC	600
AGGAATGAAG	TTGTATATGG	TTTGGTGTAT	CAAAAAGATC	AGTTGCCTCA	AACAGGGACA	660
GAAGCATCTG	TTTTGACAG					679

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

AGCTCTCTCT	CAGCCATTTT	TTCAATATCT	GCTACGATTT	GTTCCCTGGC	ATAGGGAGGG	60
TCTAAGAAAA	CGAGGTCAAA	TTCCCCAGAN	AACCTGTTC	AATGCCCTTT	CTGCATCCAT	120
TTTGAGGAG	TTGAAATTTT	CCAACCTCCT	TGGTCATCTG	GATATTTTCA	GCCACGGATG	180
GTCTGAGCCT	TACGGTCTCG	CTCCACCAAA	ACAGCACTGG	ACATGCCACG	CGATACTGCT	240
TCGATAGATA	AACCACCACT	ACCTGCATAA	AGGTCCAAGA	CTCGTCCCAC	TTCAAAGTAG	300
GGACCAATCA	TGTTAAAAAT	GGCTCCCCTA	ACCTTATCCG	AAGTAGGTCT	TGTTGTCTTG	360
CCTTCTAGTG	TCTTGAGGGG	ACGTCCCCCA	TAGATTCCTG	ATACGATTTT	CATACTGTTT	420
ATTATACCAA	ATTATAGACA	AAAAGAGAAA	GAAAACCGAA	CCTTGCGGTT	CGATTCTCTA	480
CAAAATATTT	TCGTAAGTAT	CGCGGACTTA	CTTGAGGCCA	AACACTTGTT	TGCACTTCTC	540
CGATGTGTCT	CTTGCGAAGT	AGGAACATGG	CCATACGAGA	TTGTCCAATT	CCTCCACCGA	600
TTGTCAATGG	GAATAGGCCA	TTCAACAAAG	ACTTGTGCCA	TTCCAATTCT	AAGCGGTCTT	660
CATCACCTGT	AATTTCCACC	TGACGTCTAA	GAGTTTCTTC	ATCTACACGA	ATTCCCATAG	720
AAGACAACCTC	AAAGGCTCCA	CCTAAAGACT	CATTCCAGAC	AAGAATATCA	CCATTTAGAC	780
CCTTGTAGCC	ATTCTCAGAC	TCGCTTGTC	AGTCATCATA	GTCTGGTGCA	CGTCCATCGT	840
GCGGTTTACC	ATCTGGCAAC	TCGCCACCGA	TACCAATCAA	AAAGACGGCT	CCAAATTCCT	900
TTACAAATCG	CATTTTCCAC	GTTCTTTAGT	GTCAAGTCTG	GGTAGCGTTC	TACCAATTCT	960
TCTGTATGGA	TAAAGGTGAT	TTGTTTTGGC	AAGATAGACT	CGATGTCATA	GCGGGCTTCA	1020
ACAG						1024

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

CTTTTTTATT TCACAACAAG TTCATAACGT GTCTTACTGG TGAAGGTTTG ACCAGCTTTA    60
AGAATGACTT GGCCTTTAAG GTCACGTGTA ATGGCATCTG GTAAAGCTTG CGCTTCAAGA    120
GCAATCCCAT TGTGCTGTAG CATTGGCTGA CCTCCTATGA TGACACTTTC ATCCACAAAG    180
TTTGCTGTGT AGACCACAAA GCAAGGAGCT TCTGTCTTGA AAAGCAGGAA GCGACCTGAA    240
TTTTGGTCAT AAAGGAATCC AGCATTGTCA TGGCCTGCAG GAAGGGCAAA TGGATGATCC    300
AAACCTGATG CCAGCTGGAT TTGCTCATCT TCTTCTGCAA AGATATCCTT CAACAAGGCA    360
CCATTGTAGA TGTGTTTGAC CACATCACGG TTGGCTTCTG GAGTTTTGGC AGGAACACCG    420
TCAGGAGCGA TTGAGTAAAT GCCCTCTGTG TTTAGTTGGA AGACATGACG GTCAATCGTC    480
TGCGTGAAAT CACCAGACAA GTTGAAATAG CTGTGGTTGG TTGGATTGAC CAGCGTATCC    540
TGATCGGTCG TTACCTTGTA GATCGAATTC ATGGAGGCAC CAGTTTCTTC CAAGTGATAA    600
CTGATCCAAA TCTTGAGATT TCCAGGGAAC CCTCCTGTCC CATCTGTACG CTCTGTGTAG    660
AGAGTCAAGC CATGATCGCT TACTTCTTCA ACTTCAAACA AG                                702

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(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

CTCAATATTT CTTGTCCCAA TGTTGACCAC TGTAATCATG GACTTTTGAT TGGTCAAGAT    60
CCAGATTTGG CTAATGATGT GGTGAAAGCA GCTGATTGGA AGCCTCGAGT GCCAGTTTAT    120
GTCAAATTA CCCCAGAGTGT GACCGATATC GTTACTTTGC AAAAGCTGCA GAAGATGCGG    180
GAGCAAGTGG CTTGACTATG ATCAATACTC TGGTGGGAAT GCGCTTTGAC CTCAAAACCA    240
GAAAACCAAT CTTGGCCAAT GGAACAGGTG GAATGTCAGG TCCAGCAGTC TTTCCAGTAG    300
CCCTCAAAC CATCCGCCAA GTAGCCCAAA CAACAGACCT GCCTATCATT GGAATGGGGG    360

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GAGTGGATTG	GGCTGAAGCT	GCCCTAGAAA	TGTATCTGGC	TGGGGCATCT	GCTATCGGAG	420
TTGGAACAGC	TAACTTTACC	AATCCTTATG	CCTGCCCTGA	CATCATCGAA	AATTTACCAA	480
AAGTCATGGA	TAAATACGGT	ATTAGCAGTC	TGGAAGAACT	CCGTCAGGAA	GTAAAAGAGT	540
CTCTGAGGTA	AACTGCAATC	AATCTGTTCT	TGATTTTTTA	TTAGTTTGTA	ATATGAATTT	600
AGGAGAATTT	TGGTACAATA	AAATAAATAA	GAACAGAGGA	AGAAGGTAA	TGAAGAAAGT	660
AAGATTTATT	CTTTTAG					677

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACGCATTTCA	TTCAACGGAA	ATGGAGACTA	CCCTTGGGTT	GGCGTAGGCT	TGCCAAAGTT	60
TTCTGGCTAG	TTCTGGCCCC	ATAGGGACCA	TATTGAACAA	AATCAGCTTC	ACGTTCACCG	120
TTTTGGTCTT	TGTAACGACG	GTTACACGCG	ATAGTTGCTC	GCGCTACCGA	CTTGTCATTG	180
TTGGTTTTGT	GCAATTCTGG	TGTAGACGTT	AAACGCCCAA	TCATGATAAC	TTTATTATAC	240
ATATTTTCTT	CCTCCTACTT	ATCTATTTCG	AGGAAATCAA	AAAAGTTACA	GAAATTTGTA	300
ACTTTTCGAG	GAAATTTCTT	ATTTTTTATG	AATCATGAAA	CCTGTCGCCT	GTTGATTGGC	360
CATAATGGTC	ATATCTGTAA	TCTGAACACG	GCGAGGCTGA	CTGGTCACAT	AGACTACTGT	420
GTCTGCAATA	TCCTGAGCTT	GCAAGGCTTC	TATTCCTTGG	TAAACGGACG	CAGCCCGCTC	480
TTTATCACCA	TGAAAACGAA	CAGTTGAGAA	ATCTGTTTCG	ACAATCCCAG	GCTGAATGGT	540
TGTCACCTTG	ATATCCGTTG	CGATGGTATC	AATTCGCAGT	CCATCCGAAA	AGGTCTTAAC	600
CGCAGCCTTG	GTAGCTGAGT	AAACAAGGCG	GGCACCCAGG	CATAGGCGGT	AGGATTCCTG	660
GCGGGTTGAA	CCCCATATTT	TGGATAAACG	GGGACCTTGG	ATTGAACTTT	TAACCATTGG	720
CTGGGCAAGG	AAACAGCGGA	GTAACCGCCA	TCAGAACCTT	TAACATTGGT	ATCCAACATG	780
GTCAACATAT	CCAACTCTCT	ATAGTCTTGA	TAGGGAGCCA	AGCCAAGAGC	CAGTCCGGCG	840
TTGTTGACCA	AGATATCAAT	CCTCCCTATC	GTTTCTAGAA	TATCAGAGCA	AACAGTCTTC	900
ACCATGACCA	TATCCGTCAC	ATCTAGTGGA	AAAGTCCAGA	CGGTTTGATT	TGGAAAGCTT	960
ACTGCAAACT	CCGACTTGAA	GGATTTCTAA	TCTGTCTATC	CGTCGTCCTG	TTAGAACGAC	1020
ATCCTCACCC	TGCTCCAGAT	AAGCACG				1047

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1165 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

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CTTGTTGGAT ATAAGGATTG CGAGTTGCAT AGCGAAGAAC AATAATCGCG GCAAATAGCC      60
CATAAAGAGA GGTAGAGGCG CCTGCTGCTA AGGATTTAGG ACTAAATACA AAAACAAAGA      120
GATTGCCCAT CATTCCTGAT AAAAGATAGA GAAAGAAAAA CTGCTTAGAA CCGAAAATCT      180
CATATACCTG CATTCCAAGA TAATAAAGTG AAAGCATATT AACAATGAAA TGTTCACACC      240
CAATATGAAC AAAAATGGCA GACAAGAGAC GCCAAACCTG CTCGGGAAAG AGGCGAATAG      300
CTGGACCATA CATGGCTCCA AATCGAAATA ATGTATCTGC CCTGTCAAAG TTTCCGCCTG      360
CAGTGACCAA CATTAGTAAA AATACCAAGG CCGTCACTAA GAGGAAGAAA CTCGTCACAG      420
GGTAACGTCT ATCAAAGATT TCCTTCATCA ATTAATACCT CCTGAACAGG AATATCATGG      480
TTTTCAGGTA TAAAGTCCTG AATTTGACAA GGATATATCG TACTCAAAGC ACGACCAGAA      540
AAATGTTCCA GATAGCGGTC ATAATAGCCT CCACCGTATC CTATCCGATA TCCTTTCGTC      600
GTAAAAGCCA GACCAGGAAC ATGAATCAAA TCAATCTTTG AAACATCCAC AACTTCCAAA      660
TCTCCCTGTG GCTCCAGTAA TCCAAAGGAA GTTTTTACCA ACTGTTGCGG ATCATAGACC      720
ACAAAGTCCA TCGCCCCCTT GGGATAGGTC TTAGGTGTCA AAACCCTCTT GCCGTCCTTC      780
AGCGCCTGCT CAATCAGTTC CCGCGTTTGA AACTCATGAG AAAAAGAGAG GTAGGTTGCG      840
ATGACCTTGG CTTCTTGATA AAAGGGGTGT TGTAATAATC GTCGGTTAA AGCTTGGTCT      900
ATAGCCTGTT TTTGTTCTTG AGATAAAGCC TTCATTTTAT GCAAGACTTG CTTGCGTAAT      960
TCCGATTTCA TAGACAAGCC CTCTATTCTG CTGCCTTCTT TTTCAGGAAA CTAGACACCG      1020
CAGCCACCCC AATAGCTAAG ACTTCTTCCT TAGGACTCAT TTGAGGGTGA TGAAGAGCGT      1080
AGGGACTATC GATACCTAGC CAAAACATCA CACCATCAAC CTTTGAAAGG AGATAACCAA      1140
AGTCCTCGCC TGTCATAGCA GGTTTC

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(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

CTGGGCGACC TTGAGAGTGG CTTTACTGGG GCTGATTTTG GGAGTTTGA TTGCCTGTCT      60
TATGGCTGTA CTCGATGGAT AGTTTGACTT GGCTCAATGA CCTGATTTAC CCTATGATGG      120
TGGTCAATCA AACCATTCCC ACCATTGCCA TAGCTCCTAT CCTGGTCTTG TGGCTAGGTT      180

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ATGGGATTTT	GCCCAAGATT	GTCTTGATTA	TCTTAACGAC	AACCTTTCCC	ATCATCGTCA	240
GCATTTTGGA	CGGTTTTAGG	CATTGCGACA	AGGATATGCT	GACCTTGTTT	AGTCTGATGC	300
GGGCCAAGCC	TTGGCAAATC	CTGTGGCATT	TTAAAATTCC	AGTCAGCCTG	CCCTACTTTT	360
ATGCTGGTCT	GAGGGTCAGT	GTCTCCTACG	CTTTTATCAC	AACAGTGGTA	TCTGAGTGGT	420
TGGGAGGCTT	TGAGGGGCTT	GGTGTTTATA	TGATTTCAGTC	CAAGAAATTG	TTTCAGTATG	480
ATACCATGTT	CGCTATTATT	ATTCTGGTAT	CGATTATCAG	CCTTTTGGGT	ATGAAGTTGG	540
TCGATATTAG	TGAAAAATAT	GTGATTAAAT	GGAAACGTTT	GTAGAATTAG	AATGTTTCTG	600
AAAAAGAAAA	GAGGAAATCA	AAATGAAGAA	AACATGGAAA	GTGTTTTTAA	CGCTTGTAA	660
AG						662

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGAATTCGAT	CTCTTAAAGC	CTATTATGGT	TAATCCAATT	TGTTTTAGCT	GCAGGTGGAA	60
TTATGAATGT	CGGATATGAA	AAAGCATTCT	TGATGCAGAC	ATCGTTAAAT	TTGCCAACTT	120
CTGAAATTAT	CTCGACATAT	GTCTATAAAG	TTGGTCTTGT	ATCAGGAGAC	TATTCTTACT	180
CAACAGCGGT	TGGTTTGTTT	AATGCAGTGA	TTAACGTAGT	ATTGCTTGTT	GCAGTTAACC	240
AAATCGTTAA	ACGCATGAAT	AATGGTGAAG	GAATTTAAGG	AGGAAAGTAT	GAAAAATTCTG	300
ATTATGGATA	CAAAATTGTA	TAGACGTATC	TTACTCTTAA	ATAAAATCAT	TATTGTCTTT	360
ATCGTTTGA	TGACTTTGCT	TCCTTTACTT	TATATCGTCG	TAGCATCCTT	TATGGATCCT	420
AAGGTTCTGG	TTAGTAGAGG	GATTAGCTTT	AATCCAGCCG	ATTGGACTGT	AGAAGGTTAC	480
CAGCGTGAT	TCAGTGACCA	ATCTATTCTA	AGAGGTTTAA	TCAATTCTCT	ACTATACTCT	540
TTTGGATTG	CAGCT					555

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CTCATAATCA TATTTTGGAT TCGCAAATTG AGGGAGTTAT TTCAACGGCC GATATTATTG	60
ACAAAGCTGG AATCACTCCA ATCGGAGTTT ATACGCACGA ACCACGTGAT CAGGTTCCGC	120
TGGTCATTAA GGAAGTGAAT GGTATCAAGG TTGCATTGTC AGCCTATTCC TATGGTTTCA	180
ATGGAATTGA GCAGTATATT TCTCAGGAAG ACTATAATCG TTATCTTTTA GATTTAAACG	240
AAGATAAGAT GAAGGCTGAA GTTGAACGGG CAGAGAAGGA AGCAGATATC ACCATTATCA	300
TGCCCTCAGAT GGGTGTGAG TATCGATTGG AACCAACTGA AGAACAAAA GCTCTTTATC	360
ACAAGATGAT CGATTGGGGA GCGGATATTA TCTTTGGAGG GCATCCTCAC GTTGTGAGC	420
CATCTGAAAC GGTGAAAAA GATGGAGATA AGAACTCAT TATCTATTCA ATGGGGAAC	480
TCATTTCCAA TCAACGAATT GAATCTATGG GAGATGAAGA GAATGCTAAG TGGACTGAAC	540
GTGGTGTCT CATGGATGTT CACCATCAAG AAGAATGATG GAAAAACAAC TATCGGAACA	600
GCTAAAGATC ATCCTACTTG GGTCAATCGA ACACCAAAGG GAACCTTTTC ACCAGAAGGA	660
TATCCCTTGT ATCATTACCA AACTTATATT TTGGAAGATT TTATAGAGGA TGGCAGTCAT	720
CGTGACCAGT TAGATGAAGC GACTACCGGA ACGAATTGAT ACCCTATAA AGAAATGAAT	780
GAACATGTGG GATTGAAGTG GTATTACTTT GAATCCCGAG GAAAGTCCTG ATGATTAAGG	840
TAATTGCGAC AGATATGGAT	860

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CTCATTTGCA AAATCAGGAA AAACGGATGG TAACGGCAGT CCGAAATGTT CTATCTAAGA	60
AACAAGAGGC TTTGAAAAAA TGCACTCAGT CTGTTATCTT TAGACAACCT GAGCGCTTGT	120
ATGACGGTTA TTTGCAACGC TTGGACCAAC TGCAACTGCG TTTGAAACAA AGTTTGCGAA	180
CTCGGATTTT TGATAACAAA CAATTAGTTC AAGCAAGAAC TCATCAATTA GTACAATTAT	240
CACCTGTTAC CAAAATCCAA CGCTATCAAG ACCGTTTAGG ACAGTTGGAC AAGCTTCTTA	300
GGTAGCCAAA TGGCGTTAGT TTATGACGCC AAGGTTGCTG AGGCCAAGCG ACTTTCGGAA	360
GCTTTGCTCA TGTGATAC TAGCCGAATC GTGGCGCGTG GTTATGCTAT TGTCAAAAAA	420
GAAGAATCCG TTGTAGATTG GGTGAGAGT TTGAAGAAAA AAGACCAAGT AACGCTTTTG	480
ATGCGAGATG GTCAAGTAGA ATTAGAGGTT AAAGATGTCA AAACAAAAGA AATTTGAGGA	540
AAATCTAGCA GAACTGGAAC CCATTGTCCA AAGTTTGGA AATGGTGAAA TTGCTCTGGA	600
AGATGCGATT ACTGCCTTTC AAAAGGGCAT GGTCTTGTC AAAAGAGCTCC AAGCTACGCT	660
GGACAAGGCT GAAAAGACCT TGGTCAAGGT CATGCAAGAA GACGGAACAG AAAGTGATTT	720
TGAATGAAAA AGCAAGAAAA ATTAGCTCTT GTCGAGTCGG CTTTGAAGA TTTTATGGAG	780

ACCAGCAGTT TGCCTCTAGT TTACGGGAGT CTGTTCTCTA TTCTATTCAT GCTGGTGGCA	840
AGCGTATTCG GCCTTTTCTC TTGTTAGAAG TTCTGGAAGC CTTGCAGGTT ACCATCAAAC	900
CTGCTCNCGC GCAGGTAGCT ACTGCCTTGG AGATGATTCA TACAGGGAGC TTGATTACG	960
ATGACCTTCC TGCTATGGAT GATGACGAGG ATCGAGAGAG GGCGGAAAAA CCAATCACAA	1020
GAAATCCGGT GAAGCTATGG CCATCCTAGC TGGAGATGCC TCATGCTTAG ACCCATATGC	1080
CTTGATTGCG CAGGCAGATC CGCCAAGTCA GATCAAGGTG GGCTCGATTG CCAACTCATC	1140
CCTTGCTTCA GGTAGCCTGG GTATGGTGGC AGGGCAAGTC TTGGATATGG AGGGCGAACA	1200
CCAGCACTGG TCTCTGGAAG AACTTCAGAC TATGCATGCC AACAAGACTG GGAAGTTACT	1260
AGCCTATCCC TTCCAACGCG GCAG	1284

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CCACTATCAA GCATCTCTCT TGCAAACCTT ATCGCACTAT CTCCATCACC TTTATAATAT	60
ACATGAATAG TCAATGTCAT CTTATATCCT CCAAAATCAT CCTTCAATTT TTA AAAACA	120
AGTTTAGATG AGGATCTAAA CTTGTTTTTT ATGAACTAAT TATCTAACGT TTCGCCATTA	180
CTTTCAATCA CTTCTTTATA CCAATAAAAT GATTTTTTCT TATAGCGATT TATAGTCAAT	240
TGAAACAAGA ACAAGACAAA AGCACCCATA AGGTAACTT TTGAGTGCTT TGAAACGTTG	300
ATATAATCGT ATTGATTAAC GTTTTGAGGC AACTGACCTT GTCAGGTTGC AGCCACATTT	360
GTAAGCGACT AAAGTCGCAA CAACTGTGTC AATTGCACCA ATTTAGTAAG AAAGTATAAA	420
AAAAGAACAC CCCGAAAGGT GCTCTGTTAT AAGTTATAGT AATCTTTTCG AATTAACGTT	480
TACTAAATTG TGATGCTTTA CGAGCTTTCT TAAGACCTGG TTTCTAACGT TCAACTTTAA	540
CGGGAGTCAC GTGTAAGAAG TCCTGCGCGT TTCAATGAAT CGCGGAAGTC TGGGTTTACT	600
TGAAGAAGGG CACGAGCGAT ACCATGACGG ATAGCTCCTG ATTGACCAGC GTATCCACCA	660
CCTACAACGT TAACGAAAAC GTCGTATGAA CCTACAGTTG AAGTAACTGC GAATGGTTGG	720
TTGATGACAA GACGAAGGTC AGCGTGTTGG ATGTACTCTT CAACATCTTT TTTGTTAACA	780
GTGATTTTAC CACTTCCTGG AACAAAGCCG ACGCGTGCAA CAGCGTTTTT ACGACGTCCA	840
GTACCTGCAT ATTGTGCTTG TGACATACTT TATTGTTTCT TTCCTTAGAT AAGTCCTGAA	900
ATGTCAAGAA CTTCTGGTTG TTGTGCAGCG TGAGTGTGCT CAGCTCCAAC AAATACTTTT	960
AACCTCATAC CTTGAGCG	978

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

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CTTCGGGTTG GGCAGCTTAT TTAAAGGCT TGCTCTCTCA ATACGGGATA GCCTTTCCTC      60
AGGCTTTAAA TGGTACCTTT AATCCTCAAG CAGGGACATT TGTGATTTA TTGCCTATTC      120
TTGTCTTGGT CTTGGTGACT TCGCTTGTTT TACTAAATGC CAAGGCAGCC TTACGCTTTA      180
ATTCGATTCT AGTTATTTTG AAATTTCCG CTTTAGCTCT CTTTGTATTA GTAGGAATTT      240
GGAATATTAA GTTGATAAT TGGAGCGGAT TTGCTCCTTA CGGTTTTTGG ACAATCTAT      300
GGAGCTAGCA CTGGTATTAT GGCTGGTGCG TCCTTGATGT TCTTCGGTTT TTTGGGATTT      360
GAATCCATCT CTAATGGGGG GTCGTAGAT GAAGTCAAGA CTCCTCAAAA AAATATTCCT      420
AGAGGGATTG TCTTATCGCT TTCTATCGTA ACCATTCTCT ATGCCTTGGT GACCCTTGTT      480
TTGACTGGTG TGGTCACTA TAGTCATTTA AATGTCGATG ATGCCGTTGC CTTTGCCCTT      540
CGTAGTGTG GATTAGTTG GGCAGCCAAC TATGTGTCAT TAGTGGCTAT CTTGACCTTG      600
ATTACAGTTT GTATTTTCGAT GACCTATGCC CTATCGCGTA TGATTTACAG TTTAGCAAGT      660
GACGGCTTAG TGCCTGCTGC CTTTAAGGAA CTGACGAAGA CTAGCAAGAT ACCAAAGAAT      720
GCTACTATTT TGACAGGTCT AGCTTCAGCA GTAGCAGCAG GAATGTTCCC ACTAGCCAGT      780
ATTGCAGCCT TTTAAATAT TTGTACCTTA GCCTAATTGA TCCTGCTGGC TTATGGTCTG      840
ATTCGCTTAC GGAAAGAAAA AGGAATGCCC AAAG                                     874

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(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

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CTAACCCTNG ACGGGGCCGC TATCATCAGT CAAACAGCTA AAAATCTTGT CTGCAAAAGT      60
CTCGATTAACTAGCTTTTA CAAAAGCCGT ATTTCTTGA ATAACCTTGA GATTGATCAT      120
CTTATCCATC AATTCAGCCG ATTCGATATT GTCTTCAGCC AGTTGCAGAC TTTTACGAT      180
TGATTTTGGC AATTCGTAGA CATAGGTGTT GTCTCTCAA GGAATTTTGA CAATACCTAA      240
CTCTTTGATA TCTCGGGATA CCGTCGCCTG AGTGGCAGTG ATACCTGCTT CTTTCAAATG      300
TTCTACAATT TCTTCTTGCG TGCCGATTG ATAATCTGTC ACCAATCTTC TAATTTTTC      360

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AAGTCTCTCT	TTTTTATCA	TTTTTAAATT	GACTATGCGC	CCTCTCTACT	GCTTCTTTAA	420
TCTCAGCAAG	AATCTGATTG	CTTGCTGACT	TTTCTTTTTT	CAAATACACT	AAAAATTCAA	480
TATTTCCATG	TCCACCTTGG	ATGGGAGAAA	AGTCCAAGCC	AAGGACTGAA	AAACTGCCTC	540
TACTGCCATA	G					551

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CTCTTACAGG	AAGAACTCG	TCGTGACCTT	GCTAAAGAAG	TGAAGAAGTT	CGGCGAAAAT	60
GCTAAAGTGG	CTGTCCGCAA	TATCCGTCGC	GATGCTATGG	ACGAAGCTAA	GAAACAAGAA	120
AAAGCAAAAG	AAATCACTGA	AGACGAATTG	AAGACTCTTG	AAAAAGATAT	TCAAAAAGTA	180
ACAGACGATG	CTGTAAACA	CATCGACGAC	ATGACTGCTA	ACAAAGAGAA	AGAACTTTTG	240
GAAGTCTAAA	AATAAACAGA	AAAACCTCAGT	TGGCATTGCT	GGCTGAGTTT	TATTTCGAAAG	300
AAGGAAATAT	GAATACAAAT	CTTGCAAGTT	TTATCGTTGG	ACTGATCATC	GATGAAAATG	360
ACCGTTTTTA	CTTTGTGCAA	AAGGATGGTC	AAACCTATGC	TCTTGCTAAG	GAAGAGGGCC	420
AACATACAGT	AGGGGATACG	GTCAAAGGTT	TTGCATACAC	GGATATGAAG	CAAAAACCTCC	480
GCCTGACAAC	CTTAGAAGTG	ACTGCCACTC	AGGACCAATT	TGGTTGGGGA	CGTGTCACAG	540
AGGTTTCGTAA	GGACTTGGGT	GTCTTTGTGG	ATACAGGCCT	TCCTGACAAA	GAAATCGTTG	600
TTGTCACTCG	ATATTCTCCC	TGTGCTCAAG	GAACCTGGC	CTAAGAAGGG	CGACCAACTC	660
TACATCCGTC	TTGAAGTGA	TAAGAAAGAC	CGTATCTGGG	GCCTCTTGGC	TTATCAAGAA	720
GACTTCCAAC	GTCTCGCTCG	TCCTGCCTAC	AACAACATGC	AGAACC AAAA	CTGG	774

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CCTGCTCACG ATAAGGTCTT TGATGTANAA GTTCTTGTTG AAGGTAAGAG CATCGGTCAA	60
GGCCAAGGTC GTTCTAAGAA ATTAGCAGAG CAGGAAGCTG CCAAAAATGC CGTTGAGAAG	120
GGGCTGGATT CATGTATTTA AAGGAAATCG AAATTCAGGG GTTCAAGTCT TTTGCTGATA	180
AGACCAAGGT CGTTTTTGAC CAAGGTGTGA CGGCAGTTGT TGGACCCAAT GGATCTGGAA	240
AGTCCAATAT TACAGAAAGT CTGCGTTGGG CTTTGGGGGA GTCTAGTGTC AAGAGTCTCC	300
GTGGGGGCAA GATGCCGGAT GTCATCTTTG CTGGAACCGA AAGTCGCAA CCGCTCAATT	360
ATGCTTCTGT AGTTGTGACT CTGGATAATC ATGACGGATT TATCAAGGAT GCAGGTCAAG	420
AAATCAGGGT GGAACGCCAT ATCTATCGTA GTGGAGATAG CGAATACAAG ATTGACGGCA	480
AGAAAGTCCG TCTGCGTGAT ATTCATGACC TCTTCTTGA TACTGGATTG GGACGAGATT	540
CCTTCTCTAT CATTTCCTCA GGCAAGGTTG AGGAGATTTT TAATTCTAAG CCTGAGGAAC	600
GCCGGGCTAT TTTTGAAGAA GCTGCAGGAG TTTTAAAATA CAAGACTCGT AGAAAAGAAA	660
CTGAGAGTAA ACTGCAACAA ACTCAGGATA ATCTGGACCG CTTAGAGGAC ATTATCTACG	720
AGTTGGATAA TCAAATCAAG CCTCTTGAGA AGCAAGCTGA GAATGCCCGT AAGTTTMTAG	780
ACTTGAAGG ACAACGTAAG GCTATTTATT TAGACGTTCT GGTTGCTCAA ATCAAGGAAA	840
ATAAGGCAGA ACTAGAGTCG ACAGAAGAAG AGAGTTGGCT CAGGTTCAAG AACTCTTGAT	900
GAGTTATTAC CAAAAGCGTG AAAAATTAGA AGAAGAAAAT CAAACTTCTA AAAAGCAACG	960
CCAAGATTTA CAGGCTGAAA TGGCCAAAGA CCAAGGCAGT TTGATGGACT TGACTAGTCT	1020
GATTAGTGAT TTAGAAAGAA AATTAGCCCT ATCGAACTG GAGTCCGAGC AAGTGGCCCT	1080
GAATCAACAG GAGGCACAAG CCCGTTTGGC TGCTTTGGAG GATAAGAGAA ATTCACTCAA	1140
CAAAGAAAAG TCTGATAAAG AAAGCTCACC AG	1172

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGTTATTCC TGCTGCAGGG CTGGGCACAC GATTTTGGCC TGCCACTAAA GCTTTGGCAA	60
AAGAAATGCT TCCAATTGTA GACCGCCCCA CAATTCATTT TGTCATTGAA GAAGCTTTAC	120
GTTCGGGTAT TGAAGATATT CTAGTAGTTA CTGGAAAGAG TAAACGTTCT ATTGAAGATT	180
ATTTTGATTG AACTTTTGAA TTGGAATATA GTCTTAGAAA ACAAGGAAAG ATGGAAC TTC	240
TTAAGTCAGT TAATGAATCG ACTGATATTA AAGTACATTT CGTTCTGCAA AGTTCACCAC	300
GTGGTCTTGG TGACGCTGTT CTCCAAGCGA AGTCTTTTGT TGGTGACGAT CCCTTTGTTG	360
TAATGCTTGG GTGATGACCT TATGGATATC ACCGACTCAA CTGCTGTACC TTAAACAAGA	420
CAATTGATGG ATGATTACAA CGCAACACAG GCTTCAACTA TCGCAGTAAT GCCTGTTAGA	480
TATGAAGAAG TTCTCCTAAT GGTGTGATTC TCCCCAGAAT TGGAAAGTTA GTAATGGCCT	540
CTATAGTGTT GATGCCTTTG GTTGAGAACC AAACCAGAAG AAGCGCCTAG CAATTAG	597

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

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CTCCCTAGTG TGGTAGATTA GGCTATTTTT TGGTATAATA AAAGTTATGG AAATCGAAAA    60
AACCAATCGT ATGGAATGCG CTCTTTGAAT TTTATGCGGG CGCTTTTGAC AGATAAGCAA    120
ATGAATTATA TAGAGCTTTA CTACGCTGAT GATTACAGTC TTGCTGAGAT AGCTGAGGAG    180
TTTGGTGTTA GTCGTCAGGC TGTCTATGAC AATATCAAGC GAACAGAAAA GATTCTGGAA    240
GATTATGAGA TGAAATTGCA CATGTACTCG GACTACATTG TCCGTAGTCA GATTTTGTAC    300
CAAATCTTGG ATCGCTATCC CAAGGATGAT TTTCTGCAGG AGCAGATAGA AATTTTAACA    360
AGCATTGATA ATAGAGAATA AGAGGAAGAA AAATGGCATT TGAAAGTTTA ACAGAACGTT    420
TGCAGAACGT CTTTAAAAAT CTACGTAAAA AAGGAAAAAT CTCTGAATCT GATGTCCAAG    480
AGGCAACCAA AGAAATTCGC TTGGCCTTGC TCGAGGCCGA CGTTGCCTTG CCTGTTGTAA    540
AGGACTTTAT CAAGAAAGTT CGTGAGCGCG CAGTCGGGCA TGAGGTCATT GATACACTTA    600
ATCCTGCGCA ACAGATTATT AAAATCGTTG ATGAGGAACT GACAGCCGTT TTAGGTTCTG    660
ATACGGCAGA AATTATCAAG TCACCTAAGA TTCCAACCAT CATCATGATG GTTGGTTTAC    720
AAGGGGCTGG TAAACAACC TTTGCTGGTA AATTGGCCAA CAAACTCAAG AAAGAAGAAA    780
ATGCTCGTCC TTTGATGATT GCGGCGGATA TTTATCGTCC ACCTGCCATT GACCAG      836

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(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

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CGGGTTTCAA ACTCTTCTCT TGTCTTGGGC AGACTGCGGT TCCGGAAGNC TTCCAGATAA    60
CGTTCAATTT CATCTAGCAA ATCAGAAGCA GGATTGGTCT GGCTCAGTTG ACCTGCAATT    120
TTTGAAAAGA GTTGCCTAA GATCAGGCTT TCACTGGCGG CAAGGTGACA AGTGTTAATC    180

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TGTTGGGCCA TGTTTCTCAG GGATACGACT TTGTCGTTGT CTCATCTCAA AGTAGTGGAT	240
ATGGTAGTCG GTCTGGTGAA AGAGGTGGTC AGAGTGATCC AAATAGACCA GTCTGAGGGC	300
TTCTTTCAAA AGCGTGTCTA ATTCTGCTAC CAGCTGTGCT CGGTTGCGTC CGTCTCCTCT	360
GGATAAATAG TATTTGAAGC GCTGGAGGAT ATCTTTTAAC TTTTCTTCCA CCAGCGTGTG	420
GTAGTGCTGG ATTTCCCTCT CTCGTGAAGG CATATAGAGA TTAACAAGCA AGGCAAATCC	480
TGTACCAATA GCAAAGAGAA GGAATTCATT GACTAGAAGG TCTGGAGAGG TTGACTCTTG	540
AACCAAGAGA TGGCTAACCA AAACAGTGCT TGGTGTGATG CCAATTTCCC AGCCCATCTT	600
GTAGGCTAAA GGAACGTAGA AGGCCAGATA GAGGCCGAGA CTCCAGATAT GAAATCCGCT	660
CAAGTGAAAA GCTAGAACAC CCGATAGCCC CGAGACCTAG AAGCATAGAA AAAAGACGAT	720
TGCGAGCCAG TTTTAAAGTA CTTCTACGCG TATCAGATAG GCTCAAGAGA GCGATCATTC	780
CAGCCGAAAC TGCTGATGAA AGATTGAGAA AATAAGCAAG CAGGCAGGCA AGACAGGTAG	840

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GGATGGAATT GTTAGCAAAT GCCAACAAAA TCATGGAAGG AAAAGTTGTG CTAAATTGGG	60
ATATCCAATA CCTTGGCTGG GGTGACTATG GTAAGGAAAA TGTCAGTTAT CAACATCATC	120
TGGTGAAAAC TATGATATCG CCTTTCGAGA TAACTATATT GTAAATGCTC AAAAAGGTGC	180
TTATGCTGAC TTGACAGAAT TGTACAAAAA AGAAGGTAAA GACCTTTACA AGGCACTTGA	240
CCCAGCTTAT ATCAAGGGTA ATACTGTAAA TGGTAAGATT TATGCTGTAC CAGTTGCAGC	300
CAACGTTGCG TCATCTCAA ACTTTGCCTT CAACGGAAC CTCTTGCTA AATATGGTAT	360
CGATATTTCA GGTGTTACTT CTTACGAAAC TCTTGAGCCA GTCTTGAAAC AAATTAAAGA	420
AAAAGCTCCA GACGTAGTAC CATTTGCTAT TGGTAAAGTT TTCATCCCAT CTGATAACTT	480
TGACTACCCA GTAGCAAACG GTCTTCCATT CGTTATCGAC CTTGAAGGCG ATACTACTAA	540
AGTTGTAAAC CGTTACGAAG TGCCTCGTTT CAAAGAACAC TTGAAGACTC TTCACAAATT	600
CTATGAAGCT GGCTACATTC CAAAAGACGT CGCAACAAGC GATACTTCCT TTGACCTTCA	660
ACAAGATACT TGGTTCGTC GTGAAGAAAC AGTACGACCA GCTGACTACG GTAACAGCTT	720
GCTTTCACGT GTTGCCAACA AAGATATCCA AATCAAACCA ATTACTAACT TCATCAAGAA	780
AAACCAAACA ACACAAGTTG CTAACCTTGT CATCTCAAAC AACTCTAAGA ACAAAGAAAA	840
ATCAATGGAA ATCTTGAACC TCTTGAATAC CAACCCAGAA CTCTTGAACG GTCTTGTTTA	900
CGGTCCAGAA GGCAAGAACT GGGCAAAAAA TTGAAGGTAA AGAAAACCGT GTTCGCGTTC	960
TTGATGGCTA CAAAGGGAAA CACTCACATG GGTGGATGGN AACACTGGTA ACAACTGGAT	1020
CCTTTTACAT CCAACGAAAA ACGTTACAGA CCAACCAAAA TCCGAAAAAT TCCTAAAGAA	1080
AAGAAATTTN GGGCAGAAAG CCTAAAAGAA TCCTCCCAG CGCCTTTGGA ATTTTATCCT	1140

TTTTAAATAC CTTGGAACAA TGTTGAAA

1168

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ACTTCTGGAG CAAGTGACAC GATCTTCATG AAACCACCTT CACGCAATTC ACGTGCAACT	60
GGGCCAAAGA TACGTGTTCC GCGAGGAGTT TTGTCTTCAC GGATGATAAC TGCTGCGTTT	120
TCGTCAAATT TGATGTATGA ACCATCAGCA CGACGAGCAC CTGATTTAGT ACGAACGATA	180
ACTGCTTTAA CAACGTCACC TTTTAAACC GCACCACCAG GAGTAGCTTG TTTACAGAT	240
GCCACGATAA CATCACCGAT GTTTGCAAAT TTACGTCCTG AACCACCAAG AACTTTGATA	300
GTCAAGATTT CGCGAGCACC GCTGTTGTCT GCGACTTTCA AACGAGTTTC TGTTTGAATC	360
ATTTACAGTTT TCTCCTTTCA GGTGTGATTA GATGATGACC GCTTCTTCAA CAACTTCTAC	420
AAGACGGAAG CGTTTTGTAG CTGAAAGCGG GCGAGTTTCC ATGATACGTA CGATATCACC	480
TTCTTTGGCA ACATTGTTTT CATCATGAGC TTTGTATTTT TTAGAGTAGT TAATACGTTT	540
ACCATAGACT GGGTGGTTAC GTTTGTGTTT AACTACAAC GTGATTGTCT TGTCCATTTT	600
GTCAGATACA ACACGTCCAA CAAGAACTTT ACGATTATTG CGTTCCATTG AAATTTCTCC	660
TTCCCTAGTC TATTATTTTCG CTTAGATTG AACTGTTTTG ATACGAGCGA TTTGTTTTTT	720
AACTTCTTTC AAGCGAG	737

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CAAGCAATTG GCGCAGTTGT TCATTTTCTG TCTTTAAACT TTCCACCTCA TTTGATTTAA	60
CTTCTAATTG GTAAAGCTGT TTCTTCAAAC TTTCAATTTT ATTATATGTT CGTGTCAAAT	120
GAGCCAAATC TGATTTGACA GAATCAAACC ACTGAAAAGG TTTTGTACA ACTCTATCAA	180

CCAATGAGAT TCCATCTCCT AATTTTGTCA CAATTGTACT TGAATAAGTC GTCGCTAAGA	240
GAGCTGACAC AAGCAGAACA GTGACAAAA CAATAATGAC ATATTTTGAT TTTTAAAAAC	300
GGTTCATATC CCTACCTTTA TATCAAAAAC TGTTACAGTA ACTTTTATC AATTCCTGAA	360
AGCTACTAAG ATTTTAAGAA AAATAAACAA CAACCAAGTA CGAGAATAAC AAGAATGGTC	420
AGCGTATCCT TTAGAGTCCA TTTCAATTGT CGGTATTGAC TTCTGCCTTT TCCACCCTGA	480
TAGCCACGCG CTTCCATAGC GATAGCCAAG GAATCTGCAC GTTTTAAACT TGTCGCAAAA	540
AGAAGAATCA AAATGGGAAT CATCGCCTTT ACTTTTGA CGATGCTTCC TTCTCCAAAA	600
TCCACTCCAC GAGGCTTTCT GTGCATTCAA AATCCGAGTC GTATCATCCA TCAAGGTTGG	660
GACAATACGC AAATCATAG ACAGCATCAA TCCAATTTCA TGAAGTGGAA CTTTCACACG	720
CTTTAAAGGT GCTAATAAAG	740

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ACCTTTGATA AAACAATCGA TTTACCCTTT GAGAATTTAA GCCTTCCTGC ACCTGAAAAA	60
TTTGATACTA TTTTGACACA ATTTTATGGA GATTATATGA CCCTACCACC AGAAGAAAAA	120
CGCTTCTACA GTCATGAATT TCACGCTTAT AAATTGGAGG ATTAGGATGC AATATTTAGA	180
AAAAAAGAA ATTAAAGAAA TTCAACTAGC CCTGCTGGAC TATATTGATG AGACTTGTA	240
GAAACATGAT ATTCTTTATT TTCTCAGTTA TGGAAACCATG CTTGGAGCCA TCCGCCACAA	300
AGGTATGATT CCTTGGGATG ATGATATTGA TATTTCCCTT TATCGTGAGG ATTATGAGCG	360
TTTACTGAAG ATTATTGAAG AAGAAAATCA CCCTCGCTAC AAGGTTCTTT CCTACGATAC	420
ATCTTCTTGG TACTTCCATA ATTTGCGATC GATTTTGGAC ACTTCTACTG TTATAGAAGA	480
ACATGTTAAG TACAAGCGTC ATGATACCAG CCTTTTCATC GATGTCTCCC ATTGATCGAT	540
TTACAGACTT GAACATTGTC GACAGAG	567

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CCTTGC GTGT AGCTTACTTC AAGGTT CACC ATCCTATTTA T TACTACTGT GCTTACTTCT	60
CCATTCGTGC TAAGGCTTTT GATATCAAGA CCATGGGTGC GGGCTTGGAG GTCATCAAGC	120
GCAGAATGGA AGAAATCTCT GAAAAACGGA AGAACAATGA AGCCTCTAAT GTGGAAATCG	180
ATCTCTATAC AACTCTTGAG ATTGTCAATG AGATGTGGGA ACGAGGTTTC AAGTTTGGA	240
AATTAGATCT CTACTGTAGT CAGACGACAG AGTTCCTCAT CGACGGGGAT ACCCTTATCC	300
CACCATTTGT AGCAATGGAT GGTCTGGGGG AGAACGTTGC CAAGCAACTG GTGCGGGCGC	360
GTGAAGAGGG AGAATTCCTC TCTAAACAG AACTACGCAA GCGTGGTGA CTCTCATCAA	420
CCTTGGTTGA AAAGATGGAT GAGATGGTA TTCTTGAAA TATGCCAGAG GATAACCAGT	480
TGAGTTTGTG TGATGAGTTG TTTTAAAAA TTGCTTAATA ATCTATTAA AGAAGCTAAC	540
GTATATCCAA TAGATTTACA TTAG	564

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 564 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

CGAAGTTATC TTGGTGGATG ATGTGCTCTA TACAGGTCGT ACCATCCGTG CTGCTATTGA	60
TAATATTGTC GGTCATGGTC GTCTGCGCG TGTGAGTTTA GCAGTTCTAG TCGATCGTGG	120
ACATAGAGAA TTGCCAATCC GTCCAGATTA CGTTGGAAAA AATATCCCAA CCAGTCGTTC	180
TGAAGAAATC ATCGTAGAGA TGACAGAACT TGATGACCAA GACAGAGTTC TGATTACTGA	240
AGAAGCTTAG AAAGTTAAAG GAGTAGCCAT GTCAGAAAAT CAACAAGCAT TGAACCATGT	300
GGTGTCCATG GAAGACCTCA CTGTTGATCA AGTAATGAAA TTGATCAAGC GAGGAATTGA	360
GTTTAAAAAT GGAGCCCAGA TTCCCTATGA AGACCATCCG ATTGTTTCCA ATCTCTTCTT	420
TGAGGATTCT ACACGGACAC ATAAGTCCTT TGAAGTCGCA GAGATTAAAC TTGGATTGGA	480
ACGACTTGAC TTTGATGTGA AAAC TAGTTC GGTTAATAAG GGGTGAGACA CTTTATGACA	540
CCATTTTGAC TCTGTCTGCT TTAG	564

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

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TTTAAGTTCC AATTGTAAAC TCACGTTCTT GAACCTGGTT CTCCATTTTC AGAGATTTCC      60
GGTGCAGGAT TTTTGGTGT CGCGAAACGA ATATTTCCAC GTCCACCACG ACCACCGTGG      120
GCAACGATAA ATTCTTGCCC ATGTTCAATC AAATCTGTTA AAACCTTGCC AGTCTCCGCA      180
TCACGAACAG TCGTACCTTG TGGTACTCGA ACTCTAAGGT CCTCAGCACC ACGACCATGC      240
ATCCCTTTGG TCATCCCTTT TTCACCAGAA TCAGCCTTGA AATGACGATT GTAGCGGAAA      300
TCCATCAAGG TACGTAGTCC TTCGTCTACA ACGAAGACCA CATTCGCTCC ACGACCACCA      360
TCACCACCCC AAGGGCCTCC ATTAGGGACA TATTTTTCAC GACGAAAGGC AACCATACCA      420
TCGCCACCAT TACCAGCCTT GACCTTAATC TTAGCTGTAT CTAAAAACAT ACTCATTATT      480
TCTTCTCACT TTAAAAAAGG GCTGGGAAAT CCCAGTCACT AAATTTTCTT GAATCTATTT      540
TATAGATTAC TGAGGGCACC AATTGCAGTT GCAAAAATTC CCAATAAACT TGCTACTAGC      600
ATGATAATCA CGATAAACAA GGTTATTTTC TCAACATAG TTTTTTTACG ATTTCCATTA      660
TCTCCAAAT GCCATTTTC TCTCCTTCCG TTACATTCTA TTTTCTATTA TCTTAGCATG      720
AATTGAG                                         727

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(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

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CTGTGATAAA GGCAAATGGA AGGAACTAGA TAAACTGGGA CTTAAAACCA GTAGCAATCA      60
TGTAAGATGA GTGTTCCAAA CAACTGGAAG CAAAGGAGGG CAACAGATAC AGGCATTCCC      120
AAAATCAATG GTACCAAGAT GGTCGCACCA AACATGGCGA AAACGTGTTG GAAGCTAAGG      180
AGAATTCCTT TTCCATCCGA AGGACGTTGG TCAACGTCTA GTAACAAATC AACAGTTGAT      240
TCTTGTTTCA TATAAACCTC ACTTTTGGGC ATCAGAAAAG AGCCCATAT TTTACAGCAA      300
TAGGCCCTCA GAGTAAGACT TCTCTAAAAT CTAGACTTTA AAGAGTTTCA AATATTTTGT      360
CGTCTTCGTC ACCTCAGGG ATGACATTAA AAACCTTTGC TTAGGATAGT ATAGCAGAAA      420
AAAATGATTT TGTAATCAT TTTTCCCGA GCCTAGAAAT AAAAGAGCGA GGCTGATTTT      480
GTAAACATTT GTTACTAAA AAATTTAAAG TGGGCGTTTA TTTGGCATA CAGCCTTACG      540
TGGATATTTA TTTGGTGTTC CTTTTTCTT TTCTACCACT GTGATATAGC GCGGATCTCT      600
ATTCCGTAGG GCGTACTGAG ATTGTCTTCG ACCTTACTAA AAAGGAGATT GAGGGCATTG      660

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TTAGCTTCTA ATAATTCCTC AGGCGCATTG ATGGCCTTGA GTGCCAATAG TTTGCCACCA	720
ACCTTAAGGT AGGGAATAGT CAATTCAGAT AGGACCTGCA TACGGGCAAC CGCACGAGCT	780
GTTACAAAAT CATATTGAGC ACGGAAGTTC TTGTCTTGGG CAAAATCTTC GGCACGTCCG	840
TGGTAGAAAT GAACTCCGTT CAAATCCAGT TCTTGAGCCA AGAGTTGTAG GAAGTTGATG	900
CGCTTATTGA GTGAATCAAT AATGGTCACA TCTAACTCCG GATAGAGAAT TTTTCATTGGT	960
AGACTAGGAA ATCCTGCCCC AGCCCCGATA TCAAGAAGTT TGATAGTTTC ATTGGGAATC	1020
AAACCTTGAA GAATGGGTGC AATCGAATCG TAAAAATGTT TGAGATAAAC T	1071

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GGAACGTCGC TATCAAATAG AAGCACAACA TATTGAGCGA ATTTTGTAGCC ATTTTGACGC	60
CGATATGGCT ATATTCCCTG AACTAGCTAC CAATATTCAG AGGTGAGCAA GAAACCAGA	120
GAATCAAACCT ATTGTTTTCA TCAAGTTGGA CTTTTCTATG GCCAACTATG ATATTTTCAC	180
TTCTCCACCT ACCAATAGTG GAATAGCTCC TGTGACTGTG ATTGTCAAGA AAAGTTATGG	240
TTTCTATACA GAAGCTAAAA CTTTTCATAC AACACGGTTC GGGACAATTG TATTACATTC	300
GAGAAAACAA AATATACCAG ATATCATTGC CTTCATACT GCTCCTCCTC TGCCAGGTTT	360
AATGGAAATC TGGAAGCAAG ACTTAAACAT CATTATAAT CAATTGGCTT CAAAATATCC	420
AAAGGCTATT ATTGCAGGTG ATTTTAATGC AACTATGCGT CATGGAGCAC TTGCAAAAAT	480
AAGCTCTCAT AGGGACGCAT TAAATGTACT GCCACCTTTT GAAAGAGGAA CTTGGAATAG	540
CCAAAGTCCA AAACCTTTTA ATGCAACAAT AGATCATATT TTATTGCCTA AAAACCACTA	600
CTATGTAAAA GATTAGACA TTGTAAGTTT TCAAACTCT GATCATAGAT GTATTTTAC	660
AGAAATCACA TTTTAATTAT TTTATATAAA ATCACCCTC TAGTGTTTAT AACTAGAGG	720
GGGAATTTGT ATCCTACTAT CGTTTAACGC ACTTCTGCAT TGACTTTTTC TTCCGAGAGA	780
CGCTTGGATT TTTTCCATGT AGCGTGCGAC TTCCTNCGTC CGTTAAG	827

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CAGGGGATGC	CAGTTGATTT	GCTTCAAGTT	GACTTGACTC	GTACTTGGGA	AATCCTCGGA	60
GAAATCACTG	GGGATGCTGC	TCCAGATGAA	CTCATCACCC	AACTCTTTAG	CCAATTCTGT	120
TTAGGAAAAT	AAGAAAAATC	CATGATCCTT	CATTCCGGTCA	TGGATTTTAT	TGTCTTTATT	180
AGTAATCTGG	TCTTAAGACC	CCTGTTACAG	TTGCCTTAGT	TGCTTCGTAG	TCGCCATCTA	240
CGACAACCTT	GATAATGCGT	TTGACATCTT	CTTCTGGTGC	TGGAACAAGA	GGTAGACGAG	300
TGGGTCCAGC	TTCAAATCCC	ATATAGTTAA	GAATTGCCTT	AACTGGAGCA	GGACTTGGAT	360
AAGAGAAGAG	AGCATTAAAC	TTAGGAATGA	ATTTACGCTG	AATTGCTGCG	GCTTTCTTCA	420
TATCGCTTTC	TGCAATGGCA	GTAAACATCT	CGTGCATTTT	ATCCCCATTT	GTATGAGAGG	480
CAACAGAAAT	AACCCCATCC	GCCCCAAGGT	TCATGGCATG	GAAAGCATCT	CCATCCTCAC	540
CTGTATAAAT	CAAGAACTCT	TCAGGCTTGT	GCTCAATCAA	GTTAAGCCAT	ATTAGCCAAG	600
CTAGTTACAT	TCCTTTGACA	CCCGATAATA	TTTGATGGT	CCAGCCCAAG	CGAAGCATGG	660
TTTCCTGGAG	TTCAATTCTGA	CAACTACACG	CCCCTGGAAT	GTTATAGATA	ATAATTGGTA	720
GGTCAGAAGC	ATCTGCAATA	GCCTTAAAGT	GCTGATACAT	CCCTTCTTGA	GAAGGTTTGT	780
TGTAGTAAGG	AACAATAGCA	AGCCCGAG				807

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CGTGCCTTGG	CCAATGATCC	AAAAATCTTG	ATTTTCAGACG	AGTCGCTTCA	AATTTCGGCC	60
CCTGGACCCT	TAAGACCAAC	CCAAGCAGAT	TTTGGCCCTT	GGTTGCAAGA	TTGAACCAA	120
AAATTAGGCT	TGACTGTTGT	CCTGATTACG	CATGAAATGC	AGATTGTCAA	AGACATTGCC	180
AACCGTGTG	CAGTTATGCA	GGATGGGCAT	TTGATTGAAG	AGAGTAGTGT	GCTTGAAATC	240
TTCTCAGACC	CTAAACAACC	TTTGACTCAA	GACTTTATCT	CAACAGCTAC	AGGTATTGAC	300
GAAGCCATGG	TCAAAATCGA	GAAGCAAGAA	ATCGTGGAAC	ACTTGTCTGA	AAACAGTCTC	360
TTGGTGCAAC	TCAAGTACGC	TGGATCTTCA	ACAGACGAGC	CACTTTTGAA	TGAATTGTAC	420
AAGCATTATC	AAGTAATGGC	TAATATTCTC	TATGGGAATA	TCGAAATCCT	CGATGGTACT	480
CCTGTTGGAG	AATTGGTGGT	GGTCTTGTC	GGTGAAAAAG	CAGCGCTGGC	AGGTGCTCAA	540
GAAGCCATTC	GTCAAGCAGG	CGTACAGTTA	AAAGTATTGA	AGGGAGGACA	GTAAGATGGA	600
ATCATTGATT	CAAACCTATT	TACCAAATGT	CTATAAGATG	GGTTGGTCTG	GTCAGGCAGG	660
CTGGGGAACA	GCTATCTACC	TAACCCCTCTA	TATGACAGTT	CTTTCCTTCA	TTATCGGAGG	720

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CTTCTTGGGG CTAGTGGCAG GTCTCTTTCT CGTCTTGACA GCGCCAGGTG GTGTCTTGGA      780
GAATAAAGTC GTATTCTGGA TTTTAGACAA AATTACCTCA ATTTTTCGTG CGGTTCCTT      840
TATCATCTCTC TTGGCAATCT TGTCACCACT TTCTCACTTG ATTGAAAAAA CAAGTATCGG      900
GCCAAATGCA AGCCCTTGTC CCACTTTCTT TTGCAGTCTT TGCCTTCTTT GCGGTCAGG      960
TGCAGGTTGT CTTGGCTGAA TTGGATGGCG GTGTCATTGA GGCGGCTCAA GCGAGCGGAG     1020
CGACTTTCTG GGACATCGTG GGTGTTTACC TATCAGAAGG TCTTCCAGAT TTGATCCGTG     1080
TGACGACTGT GACCTTGATT TCCCTTGTTG GGGAAACAGC TATGGCCGGT GCGGTTGGAG     1140
GCGCCGGGAA AAGCGGTTTG CGTTATTGGG CGCTCTTCCG CTTCTCTCGCT C              1191

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(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

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TTCAATGGGC CCTGTAAGGC TGCCAAAAAG AGAAACCAAT TAAAACCGCG CCAGCCGCCA      60
AAATCCTTGG GCATTTT TAG CCAGCATGGG AAAAGTGATA GTGACTGGCC AAATCCACCA     120
CATTTTCGAT AGCAGAATTG ATAATTTCAA AGGCTACCAC CAAGAAAATG CTCAATAGGA     180
GAAAGAGCCA TTCGATTCGT GACACCTGAA AACCAAAACC TGCAAGGATG ACCACTAGAG     240
CCGTCACTGC ATGTTTTCGC ATATTGCGTT CTTCTTGAT AGCAGTAAA ATCCCTGTGA     300
TGGCAAATTC TAAACTGGAT ATCAGGTCAC GATTTTTCCTA TTTTCGTTTA TTGTCTTGTTG     360
AGTCCATAGG CTGTCAAAAT TTCTTCTTGT AAACCGAACA TCTCCGCTTC TTCTTCCGGA     420
GTATAGTGAT CATAGCCGTT AATATGTAAA AAGCCGTGTA CTGCCAAGAA GCCCATCTCA     480
CGCTCAAAGC TGTGACCATA TTCTTCGGCC TGCTCATGAG CCTTATCGAT AGAGATGAAC     540
AATTCCCCAA TATAGGCATC AACTCAGAC ATCATCTCTG CCAATTCTGG ATTTTCAAGC     600
AAATCCTCTT CGTCAAAGGC AATTTCCAAT TCTGGTTTAT ACTCAAGGCT GATGACATCT     660
GTCGGACGGT CCGTGTACCG GT                                682

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(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CTACTTCTGT AAATTCTTTA TAAATGACAT TTCCATTTCT TTCCACAGTC ACCAGCATTT	60
CTGTTGGATT ATAATCCAAA TTAAATAATT CTTCAAAAAA CTTTATCTTT TCATGATAAT	120
CTGCAATGTC AGAAAGATTA TTTTATTAA CACTCATAAC ACTAGCCCCCT TATTTTTCAG	180
TAAACTCTCC GTCTACGACG TCATCGCCTG CGTTTCCTGT TGCTTGTCG CCTTCTGCTC	240
CTTCTTGAGC TTGTTGCGCT GCTGCGGCTT GTTCGTAAAG TTTCACAGCA AGGCCTTGAG	300
CTTTTTCGTT CAACGCTTCA AGTTTCGCTT TCATGTCGTC CAAGTTGTTG TCTTCTTGAG	360
CTTTCTTAAG GTCATCAAGG GCAGCTTGGG CAGCGTCACG TTCTGCGTCG AAGCCTTTAC	420
CTTCAGTTTC CTTGATTGTC TTTTCAGTCG CAAAGATTGC TTGGTCTACT TCATTACGAA	480
GGTCTACTTC TTCTTTACGT TTCTTATCAG CTTCAGCGTT TGCTTCGGCA TCTTTCATCA	540
TGCGGTCGAT TTCTTCGTCA GTCAAACCTG AGTTCGATTG GATGACAATA GTTTGTTCTT	600
TTTGAGTTCC AAGGTCTTTG GCCTTAACAG ACACGATACC GTTCTTGTCG ATGTCAAATG	660
TTACTTCGAT TTGAGGAATT CCACGAGGTG CAGCTGGGAT ATCAGTCAAT TGGAAGCGTC	720
CAAGAGTCTT GTTATCTGCT GCCATTGGGC GTTCACCTTG AAGAACGTGG ATATCAACGG	780
CTGGTTGGTT GTCTGCTGCT GTTGAGAAGA CTTGTGATTT AGATGTTGGG ATTGTAGTGT	840
TGCGATCGAT AAGTTTGTGA AATACTCCAC CCATTGTTTC GATACCAAGT GACAATGGCG	900
TTACATCAAG AAGGACAACG TCCTTGACAT CACCAGTAAT CACACCACCT TGGATAGCCG	960
CACCCATAGC AACTACTTCA TCAGGGTTTA CTGATTGTGTT TGGTTCCTTA CCAGTTTCAG	1020
CTTTAACAGC TTCAACAACG GCAGGGATAC GAGTTGAACC ACCAACAAGG ATAACCTTCGT	1080
CGATTTCTGA CAAG	1094

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CTCTGSGTTC CATTCTTGTG GCTGTAATAC TAGGAATTTT TCTAGGATTT TTCTGGCAAG	60
AACCGATTCA GAAAGAAAAT CGTCTGGCTT GTCATGAGCA TGATTTTCTT TAACTTGAGT	120
TCTGCAAAAA AAGTTTTTCA AGTCTTTGTG CAGGCCATTG ATGAATTTT TGATACGGGG	180
CGTTATTTGG TATTTGGCTG CCTCTTTGCT TCTATAATAC AGGTCTACGT TCCGACTCGG	240
ATTCTGACCT CTATCAGTGC GACCCCTCTT TTTGCCATCC TGCTCTTGAT GATTTTAGCC	300
TTTCTTCTTT CGCTCTGTAG TGAGGCGGAT GCCTTTATAG GTGCTTCTCT TCTCTCGAGT	360
TTGCGTTTGG CACCAGTTCT GGCCTTCTC GTCATTGGTC CAATGCTGGA TATCAAAAAT	420
ATTCTCATGA TGAAAAATTA CTTGAAAGCA CGATTTATCA GTCACCTTCAT AACAATTGTA	480

ACTCTTGTCG TCTTAGTCTA TTCTCTCTTG ATTGGAGTCA TCCTATGATT CGATTTTTAG	540
TTTTAGCTGG CTATTTTGAA CTGACTATTT ACCTCCATCT GTCGGGCAAA CTAAACCAGT	600
ACATCAACAT GCACTATTCC TATCTGGCCT ATATCTCCAT GGTGCTTTCT TTTATCTTGG	660
CTATCGTTCA ATTGTATATC TGGATGAAGC AAGTCAAAAC CCACAGTCAT CTGAACAGCC	720
GATTAGCCAA GATGACGAGT ATTTCTCTTC TGGCTATTCC ACTTGTCATC GGCTTAACTT	780
TCCCAACTGT TAG	793

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TTCTTCCAAT CCAGGAAGTN AACTTGTTCC AACCTTCTGC TAGTTTCCCA GAATCCATTC	60
TGCCNAATTT ATTAGCTCTA TTCTCTAATG GAGAAGCACC TGAAAGTAAC TGACTGGATT	120
TGTCTGCTAA TTGCCCAGAT CCTGATTGTA ATTAACCAAC TCCTGCTGTC AATCTAGAAG	180
ATTTTTGTGT CAAGGTGTTT GAGCCTGAAA CTAGTTGATC CAAACTACCT GTCAAGGTGG	240
CATTTTTTTC ACTTAGTTGA CTTGCGCCCT GAGAACTTT ATCAACACCT GTAGTATATG	300
CGTTTACACC TGATGCAATC GACTGACTGG CAGGAAGTAA TTTGCTAGTA ACATCTCCTT	360
GTATCTCTGT TAATCCACTT GACAATCCTA TCAAAGAAGT AGAAGTAATA GGTGATACCT	420
GATTAGATTG ATTTTTTAAA GTCGAAAGAT TAGAAGATTG ATTTTGTAAG TTTTCTAAAC	480
TTCCCTGTAA ATCTTGTAAT AAAGCGACAA TTGATTGAGC CGATTGAATA CTATCAGTTG	540
AATTTTGAGA TACAGAATCA CTTATCTCAG TTTGTTGCTC ACTTGTCATG GATTGATAAG	600
CTGCTGTCGA TTGAATATTG GATAATGTAG TTGTTTTTTC AGATAAATCA CTTGGTAAAG	660
TCACTACCAT ATAGTAATCG CCATCTTCCA ATCCCTTCTT TCCTTCCTCT TCATCTACAA	720
AATGAAAATC CAAGGTTTTA TTTTCTTTTA AATTGGACAC CATGTCTTTT CCTATTGCCA	780
TAGTATTACC ATTATAGGAA GCCTCTTTAT CATTATTTAC AACTGCCACA GGTAAGTCAG	840
ACAATTGCCC ATATGGCTCC CACATTGATG ACAAAAATAT GATATTGTAC AGAG	894

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CTATGGCAGA	TCTAGACCAT	CCTCATATCG	TTCGGATAAC	AGATATTGGT	GAGGAAGACG	60
GTCAACAGTA	TCTTGCAATG	GAGTATGTTG	CTGGACTAGA	CCTCAAACGC	TATATCAAGG	120
AACATTATCC	TCTTTCTAAT	GAAGAAGCCG	TCCGTATCAT	GGGACAAATT	CTCTTGGCTA	180
TGCGCTTGCC	CCATACTCGA	GGAATTGTTC	ACAGGGACTT	GAAACCTCAA	AATATCCTTT	240
TGACACCAGA	TGGGACTGCC	AAGGTCACAG	ACTTTGGGAT	TGCTGTAGCC	TTTGCAGAGA	300
CAAGTCTGAC	CCAGACTAAC	TCCGATGTTT	GGGCTCAGTT	CATTACTTGT	CACCAGAGCA	360
GGCGCGTGGT	TCTAAGGCGA	CTGTGCAGAG	TGATATCTAT	GCCATGGGGA	TTATTTTCTA	420
TGAGATGTTG	ACAGGCCATA	TCCCTTATGA	CGGGGATAGC	GCGGTGACCA	TTGCCCTCCA	480
GCATTTCCAG	AAACCCCTGC	CGTCCGTTAT	TGCAGAAAAT	CCATCTGTAC	CTCAGGCTTT	540
AGAAAAATGTT	ATTATCAAGG	CAACTGCTAA	AAAGTTGACC	AATCGCTACC	GCTCGGTTTC	600
AGAGATGTAT	GTGGACTTGT	CTAGTAG				627

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTATGCTAGC	GACAGCTATT	CTTGGTGTCG	TGATTGAGTT	TCTTGCTTAC	CGACCTTTGC	60
GCCACTCTAC	TCGTATTGCT	GTTTTGATTA	CGGCTATTGG	GGTTTCTTTC	CTATTGGAGT	120
ATGGAATGGT	CTATCTGGTT	GGTGCCAATA	CCCGTGCCCT	CCCTCAAGCG	ATTCAAACAG	180
TTGATATGA	TTTGGGACCA	ATTAGCTTAA	CAAATGTGCA	GTTAATGATT	TTGGCCATTT	240
CCTTGATTTT	GATGATTTTG	TTACAAGTCA	TTGTCCAAAA	GACTAAGATG	GGGAAAGCCA	300
TGCGTGCACT	ATCAGTAGAT	AGCGACGCGG	CACAATTGAT	GGGGATCAAT	GTAAACCGTA	360
CGATTAGCTT	TACCTTCGCT	TTGGGTTCCTG	CTCTTGCGGG	TGCGGCTGGT	GTTCTGATTG	420
CTCTTTATTA	TAACTCTCTT	GAGCCTTTGA	TGGGGGTTAC	TCCAGGTCTT	AAATCTTTCCG	480
TTGCCGCAGT	ACTTGGTGGT	ATCGGAATTA	TTCCTGGTGC	GGCTCTTGGT	GGCTTTGTGA	540
TTGGTCTATT	GGAAACCTTT	GCGACAGCCT	TTGGGATGTC	AGATTTCCGT	GATGCCATTG	600
TTTATGGAAT	CTTGTTGTTG	ATCTTGATTG	TCCGCCCAGC	TGGTATCCTT	GGTAAGAATG	660
TGAAAGAGAA	GGTGTAACG	ATGAAGGAAA	ATTTAAAAGT	TAATATTCTA	TGGTTACTCC	720
TTTTGTAA						729

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

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CCACAGATTN GACCCAAACA GTATGGTCTC CGATATGTTC AGAAATTGTT ANGATNGCGA      60
TTGGNAAGAT AGCGATGGTT CTGGACCAAA GTAAAGATTG TACTCTTTAA AGGCACCACC      120
TGTGCTAAAT GGCAAGTAGA AACCAGGAAT TTCGAACCAG TTGGCTTTAA GAACTGGTGT      180
AAAGTCAACC AAGCCAAGAG TTAGTGCGAA AAGGTAACCA CCGATAATGG CAAAGAGGAA      240
TGGAATGATT CGTAGGAAGC CTTTTCCTTT TGTATTGATA AAGGCAGCAA TTAGGAAAGT      300
AACAACGGCT ACCAGAGCAT TTTTCCAATT TCCGTCTGCT ACAAGACCTG CATTGGTAAC      360
AGCTGAACCT GCAAGTCCAA GACCGATAAC GATGATCATA GGACCGATAA TGATTGGTGG      420
CAAGAGTTTA TCAATCCATT TTGTTCTTAC AAATCGGATG CTGGTAGCAA CAAGGACATA      480
GACCAAACCA GTCAAGATAA CCCCTGTTTG GGCAGCAGAT ACATCCCCCC CCATTTCTTT      540
CATAGCCAGT GACATAG

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(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

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CTTAGTATCT AGAAAAGGAG AAATAAAATG GTTAAAGTAT TAGCAGCGTG CGGAAATGGA      60
ATGGGTTCAT CAATGGTTAT CAAGATGAAG GTTGAAAATG CTCTCCGTAA GCTTAATCAA      120
ACAGATTTTA CAGTCAATTC ATGGCCAGTG TCGGTGAAGC TAAAGGTTTA GCAGTAGGAT      180
ATGACATCGT AATCGCTTCT CTTCAATTTGA TTCAAGAATT GGAAGGGCGA ACTAATGGGA      240
AGTTAATTGG GCTTGATAAC TTGATGGATG ATAAAGAAAT CACCGAAAAA CTCAGTCAAG      300
CACTACAGTA AAAGGTTGGA GGGGGCTGGA CAGAACTGA GAGTTATCGT TTCTGTCCTT      360
CTCCCTCTTT AAATAAAGGA GGCAGATATG AATTTAAAAC AAGCTTTAAT TGACAACGAC      420
TCGATCCGAC TAGGTTTAGA GGCTAACGAT TGGAAGAAG CAGTCAAGGT AGCAGTAGAT      480
CCCTTGATTG AAAGTGGGGC AATTTTGCCA GAATTATTAC CAAGCTATCA TTGAATCGAC      540

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TGAAGAGAAT TATGGGCCTT ACTATATCTT GATGCCAGGT ATGGCTATGC CCCACGCTAG 600
ACCTGAAG 608

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CTGATTTCAC TTGGGTTAGA GCATAGCCTA CCGCTCTCTA GCCACCTCAA TATCAGCATT	60
GGTCCCTTAA TTCAAACCTG GCGTATCGGT TTTTCAGATG CCAAGGTGCG CCAGCCTCAA	120
AAAATTGAAT CGGTGCTGCC TCTAATCAAT CCTCATGGTA TCGAGTTAGA TTCTTCTACT	180
TCTACTGTGT TTTTAAACA GAAAGGAATG AAGATCGATC TAGGTTGTTT AGCCAAAGGA	240
TACAGTGCGG ATAAGGTTGC CCAATTTCTT AGGAAAGAGG GGGTGACTTC TGCTTGATC	300
AATCTGGGAG GGAATATCCT GACCATTGGA AAAAATCAGG CAAGAGGGGA TAACCCATGG	360
CAAATCGGGG ATTCAAGGAC CCAGCCAATC CTAGGGGAAA TCATTTAATG ACCATCCCTG	420
CTTGTCATA AATCTGTCGT GACTTCAGGC ATTTATGAAC GTCACCTGAC CGTCAATGGA	480
CAAGATTACC ATCACATTTT TGACAGTCAA ACAGGATATC CTGTTGAAAC GGAAGTAGCG	540
AGTCTAACAA TCATCTCTGA TAAATCAGTC GATGGCGAAA TCTGGACGAC TCGACTCTTT	600
GGAGAAAGAC CGGCTTCTAT CCTCTGGCAA GTCGAAAGTT TGGAGGGCAT CGAAGTCATC	660
CTCATCGATA AAGAAGGCCA CCTAAG	686

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CTCTGGCTAC GCTCAAGACG AACATGGTAA CTTTGACAAG TTCTGGAATG GAACAGTCTT	60
CCATATGGTA GGAAAAGACA TCCTTCGCTT CCACTCTATC TACTGGCCAA TCCTTCTTAT	120
GATGTTGGAT GTTAAATTAC CTGATCGTTT GATTGCCCAT GGTGGGTTTG TCATGAAAGA	180

CGGAAAAATG	TCTAAGTCAA	AAGGGAATGT	CGTTTACCCT	GAAATGTTGG	TAGAGCGTTA	240
TGGACTAGAT	CCACTTCGTT	ACTACCTCAT	GCGTAACCTT	CCAGTTGGTT	CAGACGGGAA	300
CCTTTACTCC	TGAAGACTAT	GTCGGTCGTA	TCAACTATGA	ATTGGCTAAT	GACCTTGGGA	360
ACCTCCTTAA	CCGTACGGTT	TCCATGATTA	ATAAGTACTT	TGATGGACAA	ATCCCTGCCT	420
ATGTAGAAGG	TGTGACTGAA	TTTGATCATG	TTCTTGCTGA	GGTTGCAGAA	AAATCAATCG	480
CAGACTTCCA	TACACACATG	GAAGCAGTTG	ACTATCCACG	TGCGCTTGAA	GCAGTCTGGA	540
CTCTGATCTC	TCGTACCAAT	AAATACATCG	ATGAGACTGC	ACCATGGGTC	TTGGACAAGG	600
ATGAAGCTCT	TCGTGACCAA	TTGGCAAGTG	TCATGAGCCA	CTTGGCAGCC	AGCATTCTGT	660
TAGTTGCTCA	CTTGATTGAA	CCATTTATGA	TGGAACTAG	TCGTGCAGTT	TTGACTCAAC	720
TTGGTTTGGA	AGAAGTTTCT	AGTCTTGAAA	ACTTGAAGTT	TGGCTGACTT	CCCAGCAGAT	780
GTGACTGTAG	TTGCCAAACG	AACACCTATC	TTTCCACGTC	TAAATATGGA	AGAAGAAATC	840
GCCTATATCA	AGGAACAAAT	GGAAGGCAAT	AAACCAGCAG	TCGAAAAAGA	ATGGAATCCG	900
GACGAAGTTG	AG					912

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTATTTTITA	TTGCTGCANT	ACTTTTCTTG	GCTTGGTACC	TTCAGCTGGA	CCAATGACAC	60
CTGCCATCTC	AAGCTCTTCC	ATGAGACGGG	TCGCACGGTT	AAATCCAACT	GACAAACGAC	120
GCTGAATCAT	GGATGGCACT	GGCTTTCTGT	GTTTCGATAA	CCAAAGACTT	AGCTTCTTCA	180
AAAAGCGGAT	CACCACCAGC	ATCTCCATCC	GAAAAATCTC	CTTCATTTTC	AGAAACCTCA	240
CCTGGATCAA	AACTCTCATC	GTAGTCTGCA	TCTGCCTGAG	TCTTGATGAA	GTTCACAATG	300
CGCTCAACAT	CGTCATCCGA	GATAAAGGAG	CCTATGGAGA	CGTAACTGGA	TGATTTTCAT	360
TAATCGGTTT	AAAGAGCATG	TCTCCTCGAC	CAAGAAGTTT	TTCTGCTCCA	TTTACATCCA	420
AAATCGTGAC	GGGAGTCTGT	TCCTGATGAA	ACCGCAAATG	CTACACGAGA	TGGAACATTG	480
GCCTTAATCA	AACCAGAGAT	GACATCAACA	GATGGACGCT	GAGTTGCAAG	AATCATGTGG	540
ATACCTGCAG	CACGCCCTTT	CTGCCCAGA	CGGATGATAG	CATCTTCCAC	TTCTTGGCTG	600
GCCACCATCA	TGAGGTCAGC	CAACTCATCC	ACAATCACGA	CAATGAATGG	TAGCGGAATT	660
TGCTTGTA	CTGACTGGGA	ATCGAACTCG	TCTACCTTGG	CATTAAAACC	TGCAACAGCC	720
CGAACTCCCA	CCTTGGCAAA	GAGTTCATAA	CGGTTTGCCA	TTTCATCCAC	AACCTTTTGC	780
ACAGCCCTGC	TGGCTTTGCG	TGGATTGGTC	ACCACTGGCA	ATCTAACAGG	TGGGGAATAT	840
CACTGTAGAA	CAGATAACTC	AACCATCTTT	GGGATCGACC	ACCCATCCTC	AGTAAATTTA	900
ACTTGATCTG	GTCTCGCCTT	CATGAGAATG	CTANCAATAA	TGCCGTTAAC	TGCTACTGAC	960
TTCCCTGAAC	CCGTTGAACC	TGCAACTAGC	AAGTGGGGCA	TTTAAAAAAG	GTCAAAAGCT	1020

CTTGCGGTTC CATTACAGC CTTCCCTAAA GGAATTTCCA AGAAATTTTC TGCTTCGTTT 1080
GCGATTGTTC CATAGTT 1097

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CTCTTGCAAC TGGCTTGATG AGAGACACTG CTTACCTATC AATGGGTAGT GTTTCGATGG 60
GGATTGGCGG TTCTATTGTA AATCCAGATT TCTTCCAAGA ATACTTAGGA ATGCGAAATG 120
AATCGGTAGA TATGACGGAG TTCACGCGCC GTATGGACCG TGGTATTTAT GACCCAGAAG 180
AGTTCGAACG TGCTATGGTT TGGGTAAAAG AACATATCAA AGAAGGGGGT TGACCGAAAA 240
TTCGTGAGGA TTTGATTCTT TCTAAAGAAG AGAAAGAAAA ACAATGGGAA TTTGTTATTA 300
AGATGTTTAT GATTGGAACG TGACTTAATG GTTGGTAACC CAAGACTTGC TGACCTTGGT 360
TTTGAGGAAG AAGCAGTTGG TCACCATGCT TTAGTAACTG GTTTCCAAGG TCAACGCCAG 420
TGGACAGACC ATTTTCCAAA TGGGGACTTT ATGGAACTT TCCTCAATAC TCAGTTTGAC 480
TGGAATGGTA TTCGAAAACC ATTTGTATTT GCTTGATTTT GCGACAGAGA ATGATTCAT 540
AAATGGTGTG TCTATGCTCT TTAATTATCT ATTAACAAAT ACTCCACAAA TCTTGCTGA 600
TGTGCGTACT TATTGGAGTC CAGAGGCTGT TAAACGTGTA ACGGGACATA CTTTAGAGGG 660
TTGTGCTGCA GCTGGCTTCT TACATCTAAT CAACTCTGGT TCTTGACAT TGGATGGTAC 720
AGGGCAAGCT ACTCGAAATG GCAAACCTGT TATGAAACCA TTCTGGGAGT TGAAGAAAG 780
TTGAAGTTGC AGGCTATGCT TGAAAATACA GACTTCCCAC CAGCAAACCG CGAATACTTC 840
CGTGGAGGAG GATTCTCAAC TCGTTTCTTG ACGAAGGGGG ATATGCCAGT AACAAATGGTA 900
CGTCTCAATC TTCTAAAAGG GGTGGTCCA GTGCTACAAA TTGCAGAAG TTATACACTT 960
GAATTCCTG AAGATGTTCA CCATACCTTA GATAATCGTA CAGATCCAGG ATGGCCAACT 1020
ACTTGGTTTG CTCCACGTTT GACAGGAAAA GGTGCTTTCA AGTCTGTNTA TGACGTCATG 1080
AAT 1083

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```

CTCTGTTATT AAAGAAGATA ACGCTGCTAT CCGTGGTATG ATCACAGCAG TATCTCACTT      60
AGTAACAGTT GAAGAAGTAA ACTAATGAAG TTTTAGGGGA TGTGCACTGT ACCATCCCCCT      120
AAAAC TAGAT ATAGTCATCT ATGATGACAT CGTATAGGCG AGTTGATGGG GGAGACAACC      180
TTTTCTCCCT TATCGGCGCT AGCATTTTAC AAAAGAGGAG AAAATAAAAA TGAAACTTCA      240
TGAATTGAAA CCTGCAGAAG GTTCTCGTAA AGTACGTAAC CGCGTTGGTC GTGGTACTTC      300
ATCAGGTAAC GGTA AACAT CTGGTCGTGG TCAAAAAGGT CAAAAAGCTC GTAGCGGTGG      360
CGGAGTTCGC CTTGGT TTTG AAGGTGGACA AACTCCATTG TTCCGTCGTC TTCCAAAACG      420
TGGATTCACT AACATCAACG CTAAAGAATA CGCAATTGTG AACCTTGACC AATTGAACGT      480
CTTTGAAGAT GGTGCTGAAG TAACTCCAGT TGTTCTTATC GAAGCAGGAA TTGTTAAAGC      540
TGAAAAGTCA GGTATTAAAA TTCTTGGTAA CGGTGAGTTG ACTAAGAAAT TGA CTGTGAA      600
AGCAGCTAAA TTCTCTAAAT CAGCTGAAGA AGCTATCACT GCTAAAGGTG GTTCAGTAGA      660
AGTCATCTAA GAGAGGTGAC CTATGTTTTT TAAATTATTA AGAGAAGCTC TTAAAGTCAA      720
GCAGGTTCTGA TCAAAAATTT TATTTACAAT TTTTATCGTT TTGGTCTTTC GTATCGGAAC      780
TAGCATTACA GTTCCTGGTG TGAATGCCAA TAG                                     813

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(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```

CTGTCGTTCC ATGCGTGCCA ACTGTTTCTA GCCCCATTTT CTCAAGGACA CGTGCCACAG      60
AGTCTCCAAC CGCAGGGGTT GGTGCCAAAC TCAAGTCCAC AATACCAAAC TCAACACCCA      120
GTCTCTCAAT GGGGCATTTG GACCAAACCA ATTGGACCGG ATACGGAGTG ATTTTAAAG      180
GCAGTTTTCT CAACTGGTTT TCGGCTTACT AACATCAAAG CTCTGTCCAC GAACTTTTTC      240
CAAAGCACGT TTCACCACAC CAGGACCAGA AACTCCGACA TTGATGATAA CATCTGCTTC      300
CCCAACACCA TGAAAGGCAC CCGCCATAAA TGGATTGTCC TCAACAGCAT TAGCGAATAC      360
AACCAACTTG GCCGCTCCCA TATCTGAAAG ATTTGCCGTT TCCTTGTATA ATTCGTCCCA      420
TATCTGCCAC AGCCGTCATA TTAATACCAG ACTTGGTTGA GCCGATATTG ACTGACGAGC      480
AGACCTTATC CGTCTCAGTC AAAGCGCGAG GAATGGAATT GATGAGAATC TCATCTCCCT      540
TTTGATAACC TTTTGTACT AAGGCAGAAA AACCACCAAT AAAGTCCACA CCAATCTCTT      600
TCGAGCCTT ATCAAGCGCT TTTGCCAGAA CCAAGTAGTCC GTCGCATCTG TCGCTGCCCC      660
AATCAGAGAA ATAGGTGTCA CCGATACACG CTTATTAACG ATAGGAATTC CCAACTCAGC      720

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CGCA

724

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```

CTCACGAAAA GCTTTTGTAG AAGTATCTGT ACGACGCAAG ATTGACAATT TGTGTTGAAT      60
CAGTGGGTGA TTAATAACTN CAATTTNCCC ATTGTGGGAA TTCCTTCTTT CAATTTATTC      120
TTCTTATTAT ACCAATATTA ACGGTTTAAA AATCTCCTAA ACCATNTATN TNNGATAATT      180
TTTACATTAG ATCAGCCTCT TTAAGAGCTG TCTGTACTGT CTCAAGTGGT AAATGGGTCA      240
ATTCTGTCCC TTTTCTTGA TAAAGGTATT GGGCGTAGTC GTCCATTCGG TACTGGTTGA      300
TATAAACCAC ACGCTTGCAG CCGACCTGAA GCAATTGTTT TGTACAGTTG AGACAAGGAA      360
AATGGGTTAC ATAGGCTGTA AAGCCTTTGG GAACACCACG CTCAGCACCT TGAAGGATAG      420
CATTGACCTC AGCGTGAAGG GTGCGAACAC AGTGGCCTTC AATGACCAA CATTGCTGAT      480
CAATACAATG CTCAGTCCCT GACACCGAAC CATTGTAACC AGTGGAATA ACCTTATTAT      540
CTTTTACCAG AATCGCGCCC ACTTTAGCAC GTTTACAAGT GGAACGATTC GCAATTAGTA      600
GGGCTTGGGC TGCAAAATAC TCATCCCAGG CCAGTCTTTT TTCAGTCATC TCTTTTCTCC      660
TTTTTCTCTA TTTTTTAAAA AATGGTAAAC CTAAATCTGC AATCTTTTCA G              711

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(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

CTGTGGGACC AGNTTCAGCT GGATATTTCA AAAACTAACT ACTTACGGGT GATTAATGCT      60
TTTACTCAAA TTGAAGCGGC TAAGGCTTAT TTATTTGCAA ACTCTGAGTT TTCGGGTGCG      120
GATTGGGATA CGAAAATTTC AAGGGATATT TTCTGGGAAG AATCTATGCA TGGTATCTAT      180
CCAGAGAATG TTGGGGTCAA TGCTAGACTC CTTAATGATG AAGCTGATTT TTTTGA CTAT      240

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CTAAATCATT CTGCGATTTT TACTGCGGAA CGTGATGGGC AGACCTATTA TTTTATCCT	300
ATTCAGGCTG GGGACTATTT GGCTACGCCT GAAATCCAAG CATTTGCTCT GAATGGGGAT	360
GAGGTTATTA TTTACCCCA AGAGAAGGAT TTTGAACTC ATCGTAGTTA CCAGTACCAA	420
GACTTAACGA CTCGAGGAAC AGTTGAGTTT CGTAGTGTGT GTACACAGCC ACTTGATAGG	480
ACTTTTGCTT CTGCAGCTTT TCACTTGGGA TTATTGGTTA ATTTAGACAA GTTAGAAGCT	540
TACTTAGAAA CAGCACCTTT TCTTTAAAGT ATTTGGTTAT GATTACAAGT TTTTAAGGAG	600
ACAATTTTCT AAGAAAAATC TTACAGATGA GGAAGAACT ACGATTATTG AATTTTCCAA	660
AGACTTACTC CTA TAG	677

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GTATTCGGAC GTTCGTTCTGA ACCGGCCTGG TTGTTTCGCC GGCTGCACAA TGGCATTTTG	60
GAAAATGAAT AAAAAGAATT TTATTCATCT TCNAAACGCT TAAGATTCTC ACACACCACA	120
GATGTGTTTT AAAATCATAA TATTCAATCC CTCTATTCCA GCTCGTCAAC GATAAACATG	180
TGAGCCATAT TCATNGCTTT TAGCAACGCC TTATATGGAT TGGTATCAGA TTCATAATCC	240
TTCATTACAT TTACATCTCC TAGCTTCACA AGTATTTATA TATCATACAT CCTCATCTTC	300
ATCCTTCATA TAATCTTTGG CAGCCCACTC CCACACAGGA AGTATCACCT CAAATACATC	360
TCTATCAAAC ATCGGGGAAT GGAATTCCTT GGGAGGCTCT CTATCTGTAG AGTAAAGCCC	420
AACTCCTTTA TCCTTCTTAA CTTGGGGAAC ATCTGTTGTG CCAAACATCA TATGGCTAGA	480
TTTCGGAGTT GGGGCTCAA GAAATATAGC ATTGACAAGC TGTCTCTAA TATTGGTAGA	540
AAGACTATCG GAACGGGGTT GTTGCAATAC AATACAAACC CCCATAGATA GAGACCTTGC	600
TTTTTGAGCA ACGATAGCAA CCATATTTTC AAAATCTTTT TTAGCTTTAC TATCCATCGA	660
AGCAACTATG AACTATATTC TTCTATTACC AAAAGTAAAG GAGGAAGGCC GAGGTCTATT	720
CCAATACTAT CAAATAAATC ACTTTTGTTA TAAATTTCCA TCCGCCTATT CATCTCGTTA	780
ATGTAGGGAC GCACGATTTT TAAAGGCATC CTCATTAGTT GTTCCATAAT TTTCTACCTG	840
GAAGACCAGA AAATTTTGAT AATTTATAAA TATCTGAAAG TTTTGATCA ATCACAATA	900
TTTTTGATG TCTCCCAATT ACGGTCTGAG ATATGAAACG AGTCAAGTAA TAATATGTAA	960
AAAATGATTT CCCAGCACCT GACGCGCCCG AGATAAGCAT TGAAAAGTTT TTTCTCAAAT	1020
CGATAATAAA ATCATCATAG ATTTTAATTT TCAAACATAT ATCTTCTTCC AGAGGGAGAG	1080
AGGTAATATG TAAACGTTCA GGCTGTCTGT ATACAAAGAC ATATTCAACA TGAGTAGCAT	1140
AAATTTCTTT ATATGATAAG	1160

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

CTGGATATGG GTTACACCCA AGTCTTTGAA ATAGTCTAGT TTTTCAATGA AGGCTTCAAA      60
AGTCCCAAAT GGTTTGGTCA AGTCTTTTGC AATGGCAGGA TCTGAAGTGA AGTCACGCAC      120
ATGAGCTTCG TAGATAACGG CGTCTTCACG AGTCTTGAAA TTGTGAATCT TATTTGGCCC      180
ATAAGGCCCC TTAAAAAGGG ATCTTGAGGG CCGAGTTGAG CTGGATCTAC AAAGGCGGCT      240
TTAGCCACTT TATGGGCATC GTCAATCTTG GCATCGTCGC TATCCAAGC AGCAAGAGAT      300
TTAGCGTAAG GATCGAGTGC AAGAACAGTT TTACCTTGAC GCTCGATTG GTATTGATAA      360
TAGTAGCCAG TGAAATCTGT GATTCCGAGT TTGTTGTGTC TGTCTAAAGT TTGTTTCCAA      420
GTTCTCTTTT CCCCTTTTTC GAGAGCGACA GTTCCAATA CTTTGTGTCAGG GTCATTCTTG      480
TCGTAGACAA CAACAGAAAC CTTATCAGCA CTTGGTGACC AAAGGGTCAA ATCAACTTGT      540
TTTCCTTCTT CTTTGTAGTC AAATCCAGT TTGCCATCAT AGATCGAATG CCTCATCTTT      600
CAGGCGCCAG GGGGATCCAC TAGTTCTAGA GCGGCCGCCA CCGCGGTGGG AACTCCAGCT      660
TTGTGTTCCCT TTANTGAAGG TTAATTGCCC CTTGGGGTAA TCCATGGTCA TANCTGTTTC      720
CTGTGTNAAA TTGGTANCGC NCAAAATCCN NNNAATANA ACCGGAACCT AAATTTAAAC      780
CCNGGNN                                           787

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(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

CTTGTTTTTA TTGGTAACTA TACTTTAATG CGATAATTGA TTGGACTTTT GTCAAGGAGA      60
TGTGTATGTT TGAAGTAGAA GAATGGCTTC ATAGTCGGAT TGGTTTGAAT TTTCGATCAG      120
GTTTGGCCCCG AATACAGCAA GCGGTGGATT TGTTAGGAAA TCCTGAGCAG TCTTACCCTA      180
TTATCCACGT AACAGGGACT AATGGGAAAG GATCTACCAT TGCTTTTATG AGGGAATTAT      240
TTATGGGGCA TGGCAAAAAA GTTGCGACCT TTACCTCCCC TCATATCGTA TCCATCAATG      300

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ACCGAATTTG CATTAAATGGG CAACCTATAG CAGACGCAGA CTTTATCCGT TTGGCTGATC	360
AGGTCAAGGA GATGGAGAAA ACGCTTCTGC AAACCTCCTGA CCAGTTGTCC TTTTGTGAAT	420
TGCTGACCTT GGTGCTTTT CTTTATTTTA GGGAGCAGGA GGTGGATTG GTTTATTAG	480
AAGTGGGAAT TGGTGGCTTA CTTGACACGA CCAATGTGGT AACTGGAGAG CTTGCTGTCA	540
TCACCTCCAT TGGGCTTGAC CATCAAAAAA CCTTGGGTGA TAGTTCCTAG AACCAATGGC	600
AAACCAGAAA GCTGGTTATT TTCAAGGCTG GTAAGAAGGC AGTGATTGCG AAATTGCCTC	660
CAGAAGCTAG GCTTGTCTGT CAGAAAAAAG CCGAATCTTT AG	702

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CCTGATAACT ATACCATGTG CGTTTTTCT CTTTCCCAA GCGGCGAAGC TCCATGGCAG	60
TCGCAATGGT ATCAATGCGT TTCTAGCGAG CTAAAAATCA AGGGCGTAAT AATGAGCAGA	120
TTGCCTTTGA TTCGTTGCAT AAGAGAAGCT TTCTTGGATA ATTCCATCCC ACGCGCCTCC	180
TGAGACATCT TGATAGTAAA GAATCTTCC TGCAAATCTG GAATATAGCG CAAGGTCAGG	240
CTGACAGAAT AAGCAATCTT ATAGGGCACA CCAATTTGAT TTAAACTGGA AGCAAACCTGA	300
CTAGGATGGG TTGTCATCAA AAAGATAATA GCCAGAGGAA TGGTGCAAAG ATACTTAATG	360
ACCAAATTTA GCAGATAAAA GAGCTCCTGG CTGGTTAGAG TGTAGACACC GATTCCCTGC	420
CAATCACAC TTCTCTCTCC ATAAAGTCCA ACCCCATACT CGGGAGAAAA GAGATAGACC	480
ATCAAAACGT TTAAAACGGC AAATACCGTC GCAAAAACGG CTACAAAGGA AACATCTTTA	540
AAGCGAATTT CTGATAAATA GAGGAGAAAG ACTGAAAAGA TGGCAATCAG CAAGAGCATT	600
CTGGTATCAT AGCTAATCAT GG	622

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:


```

CTTATATGGA GGGCTTATAA TGGCAGATCT AAAATTAATC GCATTGGACT TGGACGGTAC      60
CTTGCTGACT ACTGATAAAA GGCTGACGGA TCGCACCAAG GCAACTTTGA AAGCTGCGCG      120
TGATCGTGGT ATCAAGGTCG TATTGACAAC TGGTCGTCCC TTAAAAGCCA TGGACTTCTT      180
TCTCCATGAG TTAGGGACTG ACGGTCAGGA AGATGGAGTA TACCATTACT TCTAACGGTG      240
GTTTGGTTCA GAAAAATACA GGTGAAATCC TTGATAAAAC AGTCTTTTCA TATGCTGATG      300
TGGCACCCCTT GTATGAGAAA ACAGACAAAT TATCACCTGC CACTTGATGC CAATCTCAGA      360
AAGAACAGTT TATCAAATCC AATCGGACCA AGAAAAGTCTT TATGCCAAAT TCAATCCAGC      420
TTTGACTTTT GTTCCAGTTG ACTTTGAAGA CCTGTCTAGT CAAATGACCT ACAACAAATG      480
CGTGACTGCC TTTGCTCAAG AACCTTGGA TGCAGCCATT CAGAAGATTT CTCCAGAATT      540
GTTTGACCAA TATGAAATCT TTAAATCAGG TGAAATGTTG CTAGAGTGGT CACCAAAGAA      600
TGTTCATAAA GCAACAGGTT TGGCAAAACT AATCAGCCAT CTTGGAATCA ACCAAAGCCA      660
AGTTATGGCC TGTGGTGACG AGGCCAATGA CCTTTCTATG ATTGAATGGG CAGGTCTTGG      720
TGTCGCTATG CAAAACGCTG TTCCTGAAGT AAAGGCAGCC GCAAATGTAG TAACGCCGAT      780
GACCAACGAT GAGGAAGCTG TCGCCCGGGC TATCGAACAA TATGTGCTAA AGGAGAACTA      840
AGATATGGGA TTGTTTGACC GTCTATTCGG AAAAAAGAA GAACCT      886

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(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

CTATGAGACC TAACACAATT ATTCTACCAA AAATTCAATT AAAAGTCAAT TCTCTATTTA      60
TGGTAGGGGA ATCCCTGCTG AATCGTAAAA GCGCGATAGA TTTGTTCAAC AAGAACTAGT      120
CTCATTAAGT GATGAGGCAA GGTTAGGCGA CAAAAGTGA CAGAAAGATT GGCTCTATTT      180
TTTACAGATG ATGACAATCC TAAACTTCCC CCAATAATAA AAGTAAGAGT AGAAATCCCT      240
CCTTATAGAA GTTTCTTCTA ACTGCTTACT AAATCTTCTT GAGAAGAAAG TTTTCCCTTC      300
AATGGCTAAC ACAATAACGA AATCACGGTC AGCAATTTTT GATAAAATTC TCTGACCTTC      360
TATTTCTAAA ATCTTTTGAT TTTCTGATTC ACTGGCCTTA TCTGGTGTTC TTTTCATCTGA      420
TAACTCAATC ATTTCAAATC TAGCAAATCT AGAAATTCGT TTTGAATACT CTGCGATACC      480
ATCTTTTAAA TACTTTTCTT TCAGTTTCCC AACTGTTACA ACTTTAATTT TCATGACTCT      540
ATTCTAACAT ATTCTCTATT TTTTCACATC TTATTCACAA AATAAAAAAT AGATTTCAAT      600
TAAGAAAATC ACAGTTTCAA AAGAGTTATC CACAGTTTGT GTAAAACCTT TGTGTTTAAG      660
TTATAATTAA G

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671

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

CTGGGCTGAG TTTTCCAGAT ACAAATACTG CAACCGCAAC TGCAATCCCC CAACCCATAG      60
TAATCACAAT CCAACCTGCA CTGTTGCTCT TGGTTTTTGG AAGAACCACA CCTGCAACAA      120
CACCATTTC TAGAAGAATC AGGATTAAAG TCCCTAAAAA TTCTCCAAAT AATTCACTCA      180
TCATTTTCT GTCTCCATTA AAAAGAAGGG GCGGGCGACA AGGATTGCTA CCCTCCACCT      240
CTTTTATTT TTCTTAATTT TTTAATTCTG CTAAGTCGTT TTGAGCAAGA GCTGCTTTTA      300
CATCAGCAG GTAAGTTGCT TTTTCTTCTT CTGTCCAGTC ATAGAATCGT CCCATTTCAT      360
CCAAACTGG CTCAACGATA CTATCCAAGC TATCAGCAT AAAGAGCATG TGATTGGTAC      420
GACGAAGAAG GAAGTCAACT GGGCTAAGAG TCAACTCATT GCGCATTGCA TAGTGAAGGG      480
ACAAGGTGTC TGCCAAGCTA AGACCTGGCG CTTGTTCCAA G                    521

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(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

CTGGAATAAC ATTATAACGA CCAGTCATGT ATAATGGAGT TTGTTCTCTA TCAGTATTTA      60
CGTTTACAAA GAACTTACCA TTTCTTTTAT TTGAATAGTC TCCATGTATG AATACTTTTG      120
TATCCTCAAG TACTTTTCTT TGGATGCTCC TGGATGCGCT ATTACATATC TAAAAAATTC      180
TTTTATTACT TCGCTAAAGA GTAAGCTTTC TTTATTATTT ACACCATAGG TATAAGCTGG      240
GTGTTCAAAA TTATAAACTA CACCTCCATT AAGGTAAACC CCTAAAGCTT CTTCTCCTAG      300
CATAGACTCT GGTTCAGTCA ACCATTGTCT ATCTCCTTGA CTTTTTCCGA TATTACCACT      360
TGCAAACAGT TTCCATTAC CTGTCTCATA CCACTTCCAA GTATCCATCA AACCACCCCA      420
TTGATAAGTA TGATTTGAAA GCCAAAGTCC CTTCAATATA CTTTCTGTAG TTGAATCATT      480
TCCCTCAGCA GCAGGTGTAT TTTTGAACAT GAAAATAAGG TTCTTCCAGT ACTTATCAAC      540
AGATTCTGTA AATGCTATCT TACCGTTTTT TCCAAATGCT TTTTCTATTG CAGAACCATT      600

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ATTTTGTTCA	GCCGGGGCAT	ATAAAATATC	CTCCATTTTT	AGCTGATACT	TTTAAGTAAT	660
CTGCCGCCTT	ATTTTCAATA	TCATTTGCCC	AAATCCAATA	ATTCTCTGTA	CTGAAAATAC	720
CATGCAAAAT	TGGATATTTT	TGAT				744

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTGAAATTTT	GGAAGAAAAA	ATCGGTGTAG	ATACAGTCCA	AAAAATAGGA	CGCATCTTGA	60
TTTGTTTTAA	ACAATCTAGC	AAGAAAGAAA	ATCGCAAGAT	TTCTAAGAAA	GTCAAAGAAA	120
TCTAAGATCG	AAACTCCAAA	TAAGTGTTTT	TATAGAGAAA	TAAAGGGGAC	TAGCCTATGA	180
CAATCGAACT	ATTGACTCCC	TTTACCAAGG	TAGAGTTGGA	GCCAGAAATC	AAGGAGAAAA	240
AACGCAACA	AGTTGGGATT	TTAGGGGGGA	ATTTTAACCC	TGTTTACAAT	GCCCATCTCA	300
TTGTTGCGGA	TCAAGTACGG	CAACAGTTGG	GACTGGATCA	AGTTCCTGCTC	ATGCCTGAAT	360
ACCAACCTCC	TCACGTTGAT	AAAAAGGAAA	CCATCCCTGA	ACACCATCGT	CTCAAGATGC	420
TTGAGTTTGG	CAATTGAAGG	GAATTGAAGG	CCTAGTCATT	GAAACCATTG	AGTTGGGAGC	480
GCAAGGGTAT	TTCCTACACC	TACGAAACCC	ATGAAAGA			518

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTTGCTTNGN	GGCTCGCTTA	CTTNGACCCA	CGTCGCTATG	ACTTGGCAGC	AGTTGGTCGT	60
TACAAAATCA	ATAGAAAAC	TCAATGTAA	AACACGTTGT	GTTCAACCAA	ACCATTGGCA	120
GGAGCCATTG	GTAGACCCTG	AAACTGGAGA	AATCTTGGTA	GAAGCTGGTA	CGATTATGAC	180
TCGGTAGCGT	GATTGAAAGC	ATTGAAAGCC	ATTTGGATGG	CGACTTGAAC	AAGATTGTCT	240
AACATCCCAA	ACGATGCAGC	CGTTGTGACT	GAGCCTGTTG	TTCTTCAAAA	ATTCAAGGTT	300

GTTCCTCCAA CTGATCCAGA TCGCGTCGTA ACGATCATTG GTAATGCTAA CCCAGATGAC	360
AAGGTTTCGTA CGGTGACTCC TGCAGATATC CTTGCTGAGA TGAGCTACTT CCTCAACTTG	420
GCTGAAGGAC TTGGCCGTGT AAATGATATC GACCACCTTG GAAATCGTCG TATCCGTGCG	480
GTTGGTGAAT TGCTTGCCAA CCAAGTACGT TTGGGACTTT CTCGTATGGA ACGTAATGTC	540
CGTGAACGTA TGTCTGTTCA GGACAATGAA GTCTTGACAC CACAACAAAT TATCAATATC	600
CGTCCTGTAA CAGCTGCGGT TAAAGAATTC TTTGGTTCAT CACAGTTGTC ACATTTTCATG	660
GACCAACACA ACCCGCTTTC TGAGTTGTCT CACAAACGCC GTTTGTAGCC TTAGGACCTG	720
TGTTGTTGAC TCGTGACCGT GCCGGATATG AAGTACGTGA CGTGCACTAC ACTCACTATG	780
GTCGTATGTG TCCAATCGAG ACACCTGAAA GGACCTAACA TCGGTTTGAT CAATAACTTG	840
TCATCTTTAC GGACACTTGA ACAAATATGG TTTTGTTCAC ACACCA	886

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 791 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CTCTCTTGAT GGCTGAACAT GCGCCAAATG CTAAGATTAC AACTATTGAT CGTAATCCAG	60
AAATGATTGG TTTTGCCAAG GAAAATTTTG CCCAGTTTGA CAGTCGCAAG CAAATCACTC	120
TCCTAGAGGG AGATGCGGTG GATGTCTTAT CTACACTGAC AGAGTCTTAT GATTTCGTCT	180
TTATGGATTG TGCCAAGTCT AAATACATCG TCTTTCTGCC AGAAATCCTC AAACATTTGG	240
AAGTTGGTGG TGTGGTTGTC TTGGATGATA TTTTCAAGG TGGTGATGTT GCCAAGGATA	300
TTATGGAAGT CCGTCGTGGT CAGCGAACCA TTTATCGAGG CCTTCAAAAA TTATTTGATG	360
CAACCTTAGA CAATCCAGAA CTCACCGCAA CATTAGTGCC TTTAGGAGAT GGTATTCTCA	420
TGCTTCGTAA AAATGTAGCA GATGTTCAAC TGTCTGAAAG CGAATGATTT TCAGAAAAAT	480
TTAAGAAAAA ATAGTAAAAT AGATAGAGTA ACACCTATCT CAAAGGAGTA GACATGAAGA	540
AAAAATTATT GGCAGGTGCC ATCACACTAT TATCAGTAGC AACTTTAGCA GCTTGTTTCA	600
AAGGGTCAGA AGGAGCAGAC CTTATCAGCA TGAAAGGGGA TGTCATCACA GAACATCAAT	660
TTTATGAGCA AGTGAAAAAC AACCCCTTCAG CCCAGCNAGT CTGTGTTAAAT ATGACCATCC	720
AAAAAGTTTT TGAAAAAACA ATATGGCTCA GAGCTTGATG ATAAAGAGGT TGATGATACT	780
ATTGCCGAAG A	791

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CCAACCTCTTG AATCCGATTA TTTAAATTAT CAAAATCAAA GATTGTTGTT TCAGAGAAGA	60
TTTTTGGGTC CGGTGAGAAG TGAACAGTTG TTCCTGTTTT ATCCGTATCT CCAACTATTT	120
CAAGTTATGC GACAACATGA CCACGACGGT ATTCTTGGA ATGAATCTTA CCATTTTGT	180
GAACATGAAC GTCTAATTGA GTGGAAAGGG CATTAAACAAC TGACGACCCC ACCCCGTGAA	240
GACCACCTGA AACCTTGAT CCACCACCAC CGAACTTTCC TCCAGCGTGA AGGACTGTAA	300
AGACGGTCTC AACAGCAGGA CGGCCTGTAA ATTCCTGAAT ATCGACTGGG ATACCACGCC	360
CATCATCCAC AACAGTAATC GAATCATCTG GCTCAATAAA AACTTGAATA TGGCTGGCAA	420
ATCCTGCCAA GGCCTCGTCA ATTGAGTTAT CAACAATTTT CCAGACTAGA TGGTGAAGAC	480
CTTCTTTTGA AGTTGATCCA ATGTANATCC CTGAACGCAT NCGAANAGCC TCTAAGCCCT	540
CTAAACTTG AATTTGACTG GCATCATAAT CCTGTGCCTG CAGATTTCTG ATTTCTCCTG	600
TCATCTAATG CCTTTTCTT ATATGTCTAA TACTTGTCTC AAATTCACGA TACTGGTAAA	660
CAAGTGGGTA TCAAGTCCTG CAGCTTGACC TGCTTCGATA TCAATCNG	708

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

TTTAAATTTT TTNTATGNNC TCCTACTACG CGGTGACTAG CATCATAAAC TGTAGTATCC	60
ACTAGACCCC TCTAAAGTAT CAACTTGGTA ATCCAAGAAC ATGCCATCAT CACTTAAAC	120
TTGTTTTTTA TCTGTATACA TTTGATGAAT TTTAAAATTA TATGATGGAT AGCCTGTGAT	180
AGTCACAGTT ATTCTGTCA AATTTTTTTG ACTAGTAGGA AGACCCAAAG TCCCTAATTT	240
TGCACCAATG GGCTCTTCTA GAATTAATAA AGCCAAGTCA TATTCCCTTG CATCCTTAGA	300
ATTTAAATTT CTAAATTCCT TCAAATAACA AACTTCCTTT ACTTTGATCT TTCCAATAG	360
TTCTTGACTT GGACTAACAG CCGGAAGAAC ATAAATATCA TCCGCTTCTT TCCCATAGTC	420
ATGTCTGTAG TTAGTTGTGA GCCCGCTGGT AATTAACACA TTATCTTTAA TAAATTCGC	480
ACTTCCCTC CCTTCTACAT TCATTCCATC GGCTACTCCA TAATACTTAG ATAAAACCAT	540
AG	542

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1028 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

CTCGTTACCC AGAGTTCGCT CAACTTGAAG GGCAACTTAA AGGGNTTGNG CAATTGAAAA    60
AACACGGAAT TGAAGGTGTA GTTGTATATCG GTGGTGACGG ATCTTACCAC GGCGCTATGC    120
GTTTGACTGA ACATGGCTTC CCAGCTATTG GTCTTCCAGG TACAATCGAT AACGATATCG    180
TTGGTACTGA CTTTACAATC GGTTTTGACA CAGCGGTTAC TACTGCCATG GACGCTATCG    240
ATAAGATTCG TGATACATCA TCAAGTCACC GTCGTACTTT TGTAAATCGAA GTTATGGGAC    300
GTAACGCTGG TGATATCGCT CTTTGGGCTG GTATTGCAAC TGGTGCTGAT GAAATCATCA    360
TCCCTGAAGC AGGCTTCAAG ATGGAAGATA TCCTAGCAAG CATCAAAGCT GGTATGAAT    420
GTGGTAAAAA ACACAATATC ATCGTCTTAG CTGAAGGTGT GATGTCAGCG GCTGAATTTG    480
GTCAAAAAC TAAAGAAGCT GGAGATACAA GCGACCTTCG TGTAACAGAA CTTGGACATA    540
TTCAACGTGG TGGTTCTCCA ACTGCGCGTG ACCGTGTTTT GGCGTCACGT ATGGGTGCAC    600
ATGCTGTTAA ACTTCTTAAA GAAGTATCGG TGGTGTTGCG GTTGGTATTC GTAACGAAAA    660
AATGGTTGAA AATCCAATTC TTGGTACTGC AGAAGAAGGG GCATTGTTTA GCCTTACTGC    720
AGAAGGTAAG ATTGTGGTTA ACAACCCGCA CAAAGCCGAT ATTGAGCCAA GTCTTCTGGA    780
CCATTTTTTT GTAGATACTC ATCAGGATCC AAGTTATCAG GCATGCTAAC GATTTGCACA    840
GGCATATCAC CAATTTTCATC CAATGCTTTC AATATCGCGG CTTGCCCAGC CTTATCTCCA    900
TCGTAAACAA GAACCAATTT CTTGGTTAAC CTTTTCAGAT GCTCAACATG CTCTCGACTC    960
AAGGCCGTTC CCATCGACCC ACAGCATTTT CGATTCCACC CGATAGGCTG CAATAACATC   1020
CATGAATC                                     1028

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(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTGAAGAAAA TCAGTAAACA AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT	60
TTTGGACAGG AAAAAGACGG TAGTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG	120
CAGGGACAAA CACTATCGGG CGCTCATGAT CTCTTGGACA GCCTCATTGA GCGTGATTAT	180
AACTTGATG CTGCGACAAA TGGCATTACT GCCATTGAGA CAGGACGTTT GGCTCAATCT	240
GGTCTAGCAC CTTATTTCOA TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG	300
GATGCTCTTT TTTATGAAAA GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACG	360
CTGATGATTG GAGATTCTCT AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC	420
ACTATCTGGT ATAATCCTCA TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA	480
GTCTATTCTT ACCAAGACTT GCTGGATTGT TTAGATAAAA ATATTCTTGA AAAGATCACG	540
TTTAAAGGAG ATTAG	555

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

CTCATAACCG TTCAAGNCGN TATCGTAAGC AATGGCACGA ACCTTAGCCA AATCACCTTC	60
TAATTCGTGA GCAGTCTCTT CCTGTGGAAG TGTGAATGGA TGGTGGGCGC TCATGTAGCG	120
GCCTTCTTCT TCAGACCATT CAAAACATCG GCCAGTCAAC CACCCAAAGG AAGTTGAACT	180
TATCATTATC AATCAAGCCA AGCTCTTTAG CAATACGTCC ACGAAGGGCA CCCAGTGTG	240
CATTAGCCAC TTCAAGCGTA TCCGCCACAA AGAGAACCAA GTCCTTATCT TCAAGAGCAA	300
GCGCTGTTGT CAATTCTTCT TGGATACCAG TCAAGAACTT GGCAACTGGT CCGTTTAATT	360
CTCCATCAAC CACCTTGACC CAAGCAAGAC CTTTGGCACC ATACTGTTTG GCTACTTCCG	420
TCATCTTGTC GATGTCTTTA CGTGAATAGT TGTCCGAGT CAAGGGCTCG AGACCGTTGA	480
CCACAATCGC TTTTACAGCA AGTGCTTCTG AAAAGACTTT AAAGTCTACA CCTTTGACCA	540
CTTCTGTCAA GTCCTGAAGC AACATGTCAA AACGAGTATC TGGCTTGTC GAACCGTAAA	600
GAGCCATAGC ATCATCGTAT TTCATATGAG GAACGGTAGC GTTACTTCAA TGCCTTTTGT	660
TTCTTTCATC ACGCGCGCGA TCAAGCCTTC TGTAAATATCT TGGATTTCTT GCTCAGTAAG	720
GAGATTCCAA GTCGACTCAG TAATTCAGCT GCGGCTCTCC ACGC	764

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

CTGTATGAAC AATATAGGAA CGTCTCCGGA TAAACTCCTT GGATTAATGG AGTTTCTTTT	60
GGCATGGATG AAACACCATT AAAGGAAATT CATAATATGT CCTGCCATAA AGGTTACATT	120
GTTTTCTTTA CACGCATCTA CCATCTCGCG ACAATCTTGA TAAGAAAGCG GCAATTGGTT	180
TTTTCAACAG AAAACATTTT TACCATGCTG TGCAGCCTTA ATAACCGGTT CCTTATGAAG	240
ATTATTTGGG AGTTGCGACG ATAACACAAT CTACTTCATC GCTAGAAACC AACTCATCTA	300
AGGAACTTGC TACTTTTGCT CCCAATTCTT CTGCAATCGC CTCTGCATTA TCTGGATCAT	360
AGAGAAGAGT AATCTCTGCT CCATCATTCT TTTGCATATA GCGAGCCAAT TCAGCTCCAA	420
AATACCCTGC TCCAACAACA CCGTATTTAA CCATGTTTTT TCTCCTTTAT TTTGTTAAAT	480
CATTAATTC CAAATCTATA TACTGAACTA CATTGCTTAA ATGCAATTCA TTTCTCGACC	540
ACGAATCATA TTTTCAAAC AGT	563

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

ACTATTGAGT CACTTTGGGA AGCGAACATG GAGTATATTT CTCCAGAAAA TGCCTTGGAT	60
AGTCGTAACC GTCAATGGAA GATTACTCA AGAACTTGA TTTCACCACC AACTTCCTC	120
GGGGCAAATG CTCATGTGGA AGACTCATTA GTGTAGACG GATGTTTCGT TGAGGGGGGA	180
AACTGGTAAA ACATTCTTAT CCTTTCAAC AGGCGCGGCA AAGTTTCGCG AAAGGAGCGG	240
GAAGTCCCTT GGATTTCACT TATCATGGAG TGGAGCTATC ATTGGTCAAG GAGCTAAGAT	300
TAAACGTGCC ATTATTGGTG AAGGTGCGAT TATTTCTGAC GGTGTCGAAA TTGATGGAAC	360
AGATGAAGTA CAAGTTGTAC GATATAATGA AGTAGTGGG GTAGCAACAG ATGAAGATTG	420
ATAAATATTC TGCCATTTTA GGAAATACAG TTGGTTTTCA CAATATGTCG ACATTGACGG	480
ACCACCGTCC AGTAGCAAGT TTGCCATTTG GTGGGAAATA TCGTTTGATT GACTTCCCGC	540
TTTCAAGCCT TGCTAATGCA GGTGTTCGTA GTGTCTTTGG TATTTTCCAG CAGGATAATA	600
TCAGCTCAGT ATTTGACCAT ATTCGTTTCA GACGCGAGTG GGGCTTATCA ACCCTTCTTA	660
GTCATTACTA CCTAGGAATT TACAATACCC GTGTAGAAAG TTAGTACAGT TGGAAAAGAA	720
TACTACCAAC AG	732

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

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CTCGTGTGAT TTTTTCGCCT ATAAATAATT TTTATCAGCC TGATATATAA TATATATTAT    60
GCAAGTGATT GGAAGTGTGA TAAACTAATA TAACAACGAA AATCTTATGA GAGAATAAAG    120
CTTTATCTTA GATAAACTTA GGAATCAGGA TTTTATAAGA TTTTCCAATA ATATTAGTGT    180
CAATAATAAG AAAAGAGGTA TCTTATGACA ACATTTACTA TCCATACAGT AGAGTCAGCA    240
CCAGCAGAAG TGAAAGAAAT TCTTGAAACA GTAGAAAAAG ACAACAATGG CTATATTCCC    300
AACCTAATCG GTCTCTTGGC CAATGCCCCG ACTGTTTTAG AAGCCTACCA AATTGTCTCA    360
TCTATCCACC GTCGCAACAG CCTGACACCC GTTGAGCGTG AAGTGGTGCA AATCACGGCA    420
GCCGTGACCA ATGGTTGTGC CTTTCTGTGT CGCAGGTCAC AACACCCTTT TCCATCAAAC    480
AAATCCAGAT GAATGATGAC TTGATTCA                                         508

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(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

CTGAACCCGT ATTAATAAGG GCATCCAACC TGGAAATGAT CAGCCAAAAT TCGCCACACA    60
ATTCATAGCA GACATGACCT TACCAATTCC ACTTCTACA AGAACGACTT CATGAGAAGC    120
AATGGTTCCT GTATGATAGG TATTCCCCAA AACCACTTGC TCCTGGGCAT TATCTAAATG    180
CTGGACCAGA TAAGCCAGTT CTTCTGGCAT AGCAGCAATA ATTCTATTTT TCATTTCAAT    240
TCCTTTTCTA TTACAAAAGT TTCATTGCTA AAACAAGCAA AATCAAGAGA AAGATGACCG    300
CAAATAAGAT TTTATTCAAC TTAGAATTGA AGACATTTCT CTTGGTATTT TCAATACGAC    360
GGCTTTTATG AATAGATGGT TCGACCTGAA TCTTCAAGGT TTCTGGCTA AAACCATGAT    420
CCTTAGGATT GGCATAACCA AAACGGGAAG AAGAGGTTGG TAAAATCTTA GTTTCCTCAT    480
TATCATCTAG CAAAGGAGAG CACCGTTGAA ATTTTTTCGC CTCTATTAG                    529

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(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

AGCTTATTTT GATAGAATGA TTAAAACAAA ATCTAGAAAG GGAATCTATG TTACACAACG      60
CATTTCCTTA TGTACAAGG AAGTTTTCAT AATCGATTGT CATCTTCCTG ATTATTCTCC      120
TTATGGCGAG CTTGAGTTTG GTCGGCTTGT CAATCAAGGG AGCTACTGCC AAGGCTTCTC      180
AGGAGACCTT TAAAAATATC ACCAATAGCT TCTCCATGCA AATCAATCGT CGCGTCAACC      240
AAGGAACGCC TCGTGGTGCT GGGAATATCA AGGGTGAAGA CATCAAAAAA ATCACCAGAA      300
ACAAGGCCAT TGAGTCTTAT GTCAAACGTA TCAACGCTAT CGGAGATTG ACTGGATATG      360
ACCTGATTGA AACGCCAGAA ACCAAGAAGA ATCTCACTGC TGATCGTGCC AAACGTTTTG      420
GAAGTAGCTT GACGATTACA GGTGTCAATG ACTCCTCTAA AGAAGACAAG TTTGTCTCTG      480
GTCCTATATA AACTAGTCCA AGGAGAGCAC TTAACCAACG ACGACAAGGA TAAAATCTTC      540
TCTTCGCACA AGGACTTGGC AGCCAAACAC GGCTGGAAAG TAGGGGACAA GGTTAAACTG      600
GACTCTAATA TCTACGATGC AGATAATGAA AAAGGAGCCA AGGAAACAGT TGAAGTGACA      660
ATCAAGGGAC TCTTTGATGG TCATAATAAG TCAGCAGTAA CCTACTCACA AGAACTTTAC      720
GAAAACACAG                                     730

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(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

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CTGACATGGT TTAAAGAGAT TTTCAAAGAG TATCGGCCAT GGCCCCTGCC TGCAAACAT      60
ACATCTTGTG ATAAGTTCCT CCCAGAGCCA AGAGTTCCTC ATGGGTTCCTA CTCTCGATAA      120
TGCGTCCCTT ATCCAAGACA TAGATGCAGT TGCGGTCTTG AATAGTAGAA AGGCGGTGAG      180
CGATAGCAAT AGTTGTTCGG CCCTGTCTCA TCTTCGCCAG AGAAGCTTGA ACCAAACTTT      240

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CTGTTTCAGA GTCAATATTG GCTGTCGCTT CATCCAAAAT CAGGATTTTA GGCTGGCTGG	300
CGACTGTTCT AGCAAAGGCA AGAAGCTGGC GCTGCCCAGT AGAGAAGCTC GAACCACGCT	360
CGGAAACAGG GGAGTCGTAC CTCTGAGGAA GTTCTTGAAT AAAGGAATCT GCATCCACAA	420
AGGCTGCCGC AGCCTTGAAC CTGCTCATCA CTGATTTCTT GGTACATGGC GAAATTGGAC	480
TTAATAGTTC CCTTATAGAG AGGTCCTGCA GAACCAAACC GATGTTTTTT CTCAG	535

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CGGTTAAATC GAAGGAACAA TCGCCATCAG GATAACAGCT ACCCACCCTA GCGTATCTTC	60
CAGAAAATGC AGACTCAGAA TAGACTCATT CTTTGTCTTT CCCTTACCAA CCACCAGACT	120
CGCTAACAGA TTGATAGTAA TCGCAATAAT TCCTAACCAG AGAATCCCCT CATCATTGAC	180
TGGTTGCGGA TGCAAAATCT TCGTGACATT TTCCAAAATG ACTAGAACAG AGCCTGTTAC	240
GAGAATCACA GCTGTTACCA AGGCTCCTAG CAGGCTAAAT CGCTTATAGC CCAAGGTGTA	300
CTGATTGTCT TCTTCACGAT TGGAGATTGT TTCTAGAAAA GCTGATATTC CAATTGCAAT	360
CGCATCTCCC AAGTCATGCA CAGAGTCAGC AAGAACAGCG CTAGAACCAA ATACTCCACC	420
TGCAATAAAC TCAACAATGG CATAAGTCAA ATTTAAGAAA AAAGCCACCC AAACAGCATA	480
TTTTGCCTTC ATATTTCTCA TTCCTTTGTT ATAATAGATT TATGAACACC TTGTTCATTA	540
TCATTATCCA CTAAACTCA AAGAAAGGAT AGAAGCAAAA CGTCAGCTTT ATTCAAGTTCT	600
GAACAATTTG CCTTAAGTGT CCATATGACT AACATTGACC GCCGTATCAG CAAAACCAAA	660
AAAGCCATCT ATCAAGCTTT TATACAACCT TTGAATGCTA AGGGCTACGA GGCCACTACT	720
GTTTCAGGATA TCATTGATCT CGCAGATGTG GGACGATCCA CCTTTTACTG TCACNCTATG	780
AGAGTAAGGA G	791

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

CTCAGGCGAT TACTAATTAC ATGACTTCTG CCTCAAACCTT TAATGTCGAT GAGGCTAGCC	60
AATTCATTCA ACAATTTACA ATTACAAAAC AAATCGAACA AGTAGAAAAA CTATTAGAGG	120
AGTAGCATGG AAAGTGCATT AATTAGTGTG ATTGTGCCAG TCTATAATGT GGCGCAGTAC	180
CTAGAAAAAT CGATAGCTTC CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT	240
GTTGATGATG GTGCAACAGA TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT	300
GACAGGGTGT CAGTGCTTCA TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG	360
ATGAAGCAGG CTCACGGGGA TTATCTGATT TTTATTGACT CCAAATGATT ATATCCATCC	420
CAAGAAATGA TCCAGACCTT ATATAACCAA TTAATTCCAA GAAGAATGCC GGATGTTCCA	480
AGCTGTGGTG TTCATGAATG TCTCTGCTAA TGATAAAACC CC	522

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TCGGAACAGG GGATAATTTT CATTAATAAA ACCCAAAATT TTTTCATGGA GGTAAACTTT	60
TCATAACCTT TTTTCAAGGA AAAAATGGCA ACCTACTAGC TAATAAACAA GGAGCTTTTA	120
GTGGAAAATT CGGTATAAGG TAAACTATA CCCTAACCAA TTGAAATAGC TATTAGCGAC	180
TTTCTCTGAA ATATGGTATG ATAAAGGATA TACAAGGAGA TAAATGAAT AATAATTTAC	240
TGGTATTACA ATCAGACTTT GGTCTGGTTG ATGGTGCGGT ATCGGCTATG ATTGGAGTGG	300
CTTTAGAAGA GTCTCCAACC TTAAAAATCC ATCACTTGAC GCACGATATC ACGCCTTATA	360
ATATTTTGA GGGGAGCTAT CGTCTCTTTC AGACGGTGGA TTAGTGGCCT GAGGGAACGA	420
CGTTTGTATC GGTGTGCGAT CCAGGTGTCG GTTCGAAACG TAAGAGTGTA GTTGCCAAGA	480
CTGCACAAA ATCAATACAT TGTCACGCCA GATAATGGGA CGCTTTCCTT TATCAAGAAA	540
CACGTTGGCA TTGTAGCCAT TCGTGAGATT TCTGAGGTGG CCAACTAGG	589

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

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CTGAGTGAAG AAAAGTACCA CCACGAGAAA TGATGTCTCC TACTGAAGCT GCATCTAGGG      60
GATGAATTTT ACCGGCAACC ATACCAGCAT ATCCGTCATA GATACCAAAC ACTTCCATTC      120
CTTCTGAAAT TGCTTGACGA ACAACTGCAC GGATAGCAGC GTTCATACCA GGTGCGTCTC      180
GGCCACTAGT CAAAACAGCA ATACGTTTCA TATTGGTTTA TGCTCCTTTT TCTTTTAACA      240
TTCTTTCTTG ATTATATCAC ATTTGATTTT AAAATTCTTC TATTTTCCGT ATTTTATAGCG      300
ATAAATCGTT TTCATAACGA TTTCATTCAA TTTCTCCTCT AATTCATTGG ATTTAGCTAC      360
AAAATGATGG GGAGAAACGA TGGTTTTCTG TTCTCTTCA TACCGGATGA TGACTGGGAT      420
TGGGCCTTTA AATTGTTCTA AAATACGTGA AATTTCTTGA TCCGATTCAT GATTTTTCAC      480
CTGTATCCAA AAGCGTTCAG CAACTGCTTC TCTTATTTCT TGTGCAATCA TTTGCAAACG      540
GCCATCACGT GATTGTATTT TTCCTTTTAC ATAGTAGAAG GCTCCCTCTT TTATTTCTCTG      600
TCCAACCTGA CGATATAAGT CTGAAAAGAG AGTGACATCC AATTTTCTCT TACTATCATC      660
TGCCTGTAAG AAGGCCATAT TTTACCCTT TTTGGTACGA ATCACTTTTA TTTTCTGAAC      720
TTCAACCAAT                                     730

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(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

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TGTGATATCT TNTGCTTNGA AGGNACCTAA CGTGGCGGCT GTCGCTCGAA ACCAAGCGGT      60
CATCTCCGAG GAGAAGGTAT TCTCCTTCTG GGAACAGTAA AGCTAAAGTT GGTGTTGTAG      120
TTGACATCAA CNGTGAAGGC TTGGGCTTTT TGAGCGATAC TTCTAAAGAA AGTTCCTTTA      180
TTTCCTTCAA AGCCCTTGCC TGAGTAAGTG CTTTGGAGTT TGTCATCCTT GAAGCGTTTG      240
ATATAGTCTG CTAGATAAGG CTCGTCCGTT TCTTTGTCAT TGGATGTAGG AGTTTATTCA      300
TTTTTCGTAA CGAATGGTGT CGCCAGGCAT TCCAATCACG CGCTTGACGA TGTCTTATT      360
GCCATCTTCC TCATGGGCCA CCACGATATC AAAACGGTCA ATAGGAAGGT GTTTTACAAC      420
GAAGAGAATT TCGCCATCCG CTAGGGTCGG ATCCATGGAA TGTCTTCTA CGCGAACATT      480
GCTCCAAAAA AAGATACGAC TTAAAGCTAG TAATGACAGA ATTAGGAGGA ACAGTCCCCA      540
CTCTTTTAAG AAATTTTAA ATGAATTCAT AACTTACCTT TCTAAGCGTT TTTTCGCTTT      600
TTCAGTGTTT TTAAAGTGCA ATTTGGCGCA GAAGTTGAGT CCCTGCATAC CATAGGCTTG      660
CAAAATCTGG CTAGCCACCT TGTCAGAAGC CGTCCAGCT CCACTTGGA GCTGATAACC      720
CAGTTCTCGT CCCAGATTTT CAAGATTTTC CAGAAAGAGA TCACGCGCAA TGACAGAAGA      780

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AACTGCGACA GACTAGTATT TGCCCTCAGC CTTTCTTCT AAG

823

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CTTCTAAAAA GTCAGCATAC TGCTTTTCGC TAATATCCAT AAATTCAGGA TCATAGAATG	60
AAAAGGCTTG GTCTAACTGG CTGTAGGAGT GTCATGGCCT TGGCATAGTA CTCTTGATAC	120
TTAGCTTCAC GTGTATCCTG GTCATTCTTC ATATGAGCAT AAACGTAAAG CTTCTCCATC	180
TGGCGTTCCA TTTCAAGAGA AAATTCAGTG ATTTCTAGTA GGTTATCCGC ACTATCCAAG	240
AGATGGCCTT CATACTGGGC TACTGTCTCC AATTGTTCTG TTAAATCTTT TAAGGCTTCT	300
TCCCAAGCCT GGTCAGTTGG GTAGATCGTT GATAGATCCC ATGTATCTTT TTCATTTATT	360
TCATTTCTTT GTAATACCAT TAGATTCCTC CATCCTTTCT ATTCTACCAT ATTTTCAAG	420
AAATATTGCT GATAAAAGGC TGGTGGATAA AGCTTTTGCC AATCATTTTG AGGATTTTTT	480
GGGTAATAAG GTATAAAGT GCTGAATAAT AA	512

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTAATAATAA CGATTTTATG ACCAAGATGG TCATGGTCTG ATTGAGTGAG CCCGCGATAG	60
AGTCGAAGAG TCGAATGGCT GAAGCATTTG GGACAACGCT GGACACCGCA GATTGATTCA	120
TAAGCAAGCC CGCCTGACTT TCGATACTAG TTGCACTGGT ATCCCTTAAT GAGACCAGAT	180
AAGTGTGGC TTGGGGTAGC TGTCCGTAAA GTTGCTCATA GCTAGCCTGA CTCATATAAA	240
TAAAGTGACC AACGTAGTTC TCAGTAATAG CAGCGACCTT TAGTTCCTGA CCTTCAATTT	300
ATAAAGTCTG CCCAACCTTG ACACCTGCCA GCTGGGCGAG TTTAGCTGTA ATAACGATGC	360
CATCTTTTAA TGTGAGCTCC TGCTGATGAT GTTGAAGATG GATAAAGGGA GTCAAATCTT	420

.CCTTCTCTAT CATCATAAGA GTAATGTTTT GAAGACCAGC CTTGCCTTTG AAATCCTTGT	480
CTAGCGTTTT AGAATAGATT TTCTGGTAGG CTAGTATCTC CTGCCCTTTC AACACTTCTG	540
CTAG	544

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTGGCTTTGT TTGATGAAAA AGATCAGTTT GTCCAAACAG TGACCATCGC TAGCCACCGT	60
AAACAGAAGA ACTTTGACAT TATTAAATTC AAAGATATGT ACCATATCAA TACTATCGAA	120
AAGTACAAGG GATACAGTCT CAAGGTCGCT GAGGAAGATT TGAATGACCT AGACGATGGT	180
GAATTTTACT ATCACGAGAT TATCGGTTTG GAAGTCTATG AGGGTGATAG CTTGGTTGGA	240
ACCATCAAGG AAAATCCTGC AACCAGGTGC TAATGATGTC TGGGTGGTCA AACGAAAAGG	300
CAAACGTGAT TTGCTTTTAC CTTATATCCC ACCAGTGGTT CTCAATGTTG ATATTCCAAA	360
TAAACGGGTC GATGTGGAAG TCTTAGAAGG GTTAGACGAT GAAGATTGAT ATTTTAACCC	420
TCTTTCCAGA GATGTTTTCT CCACTGGAGC ACTCAATCGT TGGAAAGGCT CGAGAAAAAG	480
GGCTCTTGGA TATCCAGTAT CATAATTTTC GAAAAAATGC TGAAAAGGCC CGTCAAGTTA	540
GATGATGAAC CCTACAGAGG CGGTCAGGGC ATGTTGATCA GAGCACAACC TATTTTCAAT	600
TCCTTAGATG CTATTGAAAA GGGAAATCCG CGCGATATTG TCCTCGATCC TGATGGAAAG	660
CAGTTTGATC AGGCTTATGC TGAAGATTTG GCTCAAGAGG AAGAGCTAAT CTTTATCTGT	720
GGGCACTATG AGGGTTATGA TGAGCGCATT AAGACCTTGG TAACAGATGA GATTTCCCTG	780
GGCGAGTATG TCCTCACTGG TGGAGAATTG GCAG	814

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

CTATATTGTA NACTTTCTGA TCAAATTGAC TAGGTAAAAT CACCCCATAG GCTGTCAGAG	60
TCCCACTTCC ACTTCCTGCG TAGCCCATAT CTCGCTGGA GAGGATTTCA GCCGAATCCA	120
CAAAACCAGT AATGGTATAA GTATGGTCTT TTAAAGAGGA ATGACCCTCT TCTTTTCTT	180
TAAACTAAT CTCCTGTCCC ACGCTGTATT GGCCTTGCAA ATGAGTGGCC AAAGCGATTT	240
CCTTGCTGA CTGAGGAAGT CATCCCTTTC TTAGCTGAAA GGTTGAAATT CGCTCTGGTT	300
TGGAGTACAG CCGAATGGCA TCCTGCCCAT TATCCATAGT CACATCTGTC AAATAGCCAA	360
ACTCGACCTC TGCGCCCTCC GTCTGTTTTA GTTCTTCTTG GTATGCTTGA TCCAAGCCAT	420
AGTTAGACAT GACTGCCAAA TCCAAGGTTT GAGCAGTTGT TAAATAAGCA TTAGCTGTCTG	480
TCTCCATGTT GGGACTGGTT ACTTTGAGGC CTACTAAGGC TAGAGATCCC AACATCATCA	540
GGATCAAGAT GGATAAAAAA CGCCCCTTGG AGCCTGTGAA GGACTGAATT AAGTCCTTCC	600
AATAAGTTTT TCGCTTGATC ATGCTAGTAC TCCAACTGT CAATATCCTG AGGATGCTGG	660
TTGAGCACCA CATCCTTGAC ACTGGCATCG TGCATATGAA TCACGCGATC AGCAATGGGC	720
GCCAAAG	727

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CTCAAAAAGC AGTAAAGAAA GAAGAAAACA GTCCTTTTGC TGGCTTACAA GGACTATTTG	60
ACGGAGATGA ATAATGATCT TGTCAAAAAA ACGAGCACGA AAGGTGCTAG AAGAAATCAA	120
TGCCCTATTTC CAAGATGCCA AGCATAGTAA AGGTAATTTT ACCAATCATT AAGATACTCC	180
TGGGAGCGGT AATGTAATCA GCCCAGAAGA CAGATGCAAC GGTAAATAAG ACCACACCAG	240
GTCTCTTTGT TGTATATCCA ACACCCCAA ATATGTATGT AGCGACAGAG AGAGAGATTG	300
CTAAACATAT TTCTCGCTTG GGATGGTATC GGAATAAAGA TAAATTCCTT AAAAAATGTG	360
CCCAACAGTT AGCTAAACGA TTTTGATGGT CAAGTCCCTC AGACACGTGA AGAATTGGAG	420
AGTTTGCCAG GTGTTGGTCG CAAGACAGCC AATGTTGTCA TGAGTGTAGG ATTTGGGATT	480
CCAGCCTTTG CAGTGGATAC TCATGTGGAG CGTATTTGCA AACACCACGA TATTGTGCGA	540
AAATCAGCGA CGCCACTTGA GGTGGAAAAG CGGGTCATGG ATATCTTGCC GCCTGTTTCAG	600
TGGTTAG	607

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

CTCATAGTAT TCCTCTGTTT CTTCTTTAAT CCGGATAGGC AGTCAATCCT GAAAAGACAG	60
AGGCACTCCC CCTTTTAAAT CTTTTTCCTT ACAATTCAGC AAGAATCGCT TTAAGCAAGC	120
CTTTGAAATC ACCTTTAACA CGTTCAGTCA CTTCTACAAC TTCTTCGTGA TTGAGTTCTT	180
CTTGGAACC AGCCGCAAAG TTAGTGATAC ATGAAATTCC CAGAACTTTC AAGCCAGAGT	240
GGGCTGCCAC GATAACTTCA GGAACCGTAG ACATACCAAC TGCATCTGCT CCCAGTGTCT	300
TATAGGGAAC GAATTTCTGC TGGTGTTC TAAGTCGGAC CAGTTAACTC CGATATAGAC	360
ACCTTTCCAT CAAAGCTTGA ATATTAAGTT TTTTGTAGA	398

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

CAGTTCAACT GGTGCAAAT GCAAGAGCCA AAACCCGCAA ATCCTTCTGG GCAGTTCTAA	60
AATAGCTGGG ACACTCTGCA ACTGGATCTG CATCTTTTCT CTATCCAAAT TTCAAAGCCT	120
GCTGACTGAA ACCCGATAAA ATCATGTGGG CCGCAAACAA CTCCTGACTG ACTGTATCGT	180
GCAAATCCCG AGCAATTGCG TTCCGTTCTT TCTCGATGAT TTCCTCTTCA TGAGCAAGGC	240
TATGATTTTC AGCTTTTGA AGAGCTTCTG TCAAAAGGTT AAGTTTACCT GATAAGGACT	300
TGAAACTGGC ATCCAAATCT GGATCTGCAA CCTGAACCAC TTCTTGCCCT GCCAATAAAC	360
GCTTGAGATT AGCCTGCATT TTTCTTAGAG AAAGTCTTTC GATCCCTCGC CAAAACAGGG	420
CTAAGAGACA GGTATGGAC ATGCTGAAAA CCAACAATAA AAAGACAAAT TTTTCTGTTC	480
TTTCGACATC GTGCAAAAAG ATAGACCAGT CAAAATCAAG TATTTCCAGC AAG	533

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CTACCAAGAG AGCCAGAATA CCCATAGAAT AGCTATAAGG TTTCAGTCAG AAAGGCTACA	60
ACTTGCAATCA GACCATTTAA AGCCCCATGA GTTTGGTACA AAGGCAATCA AGATAAAGAT	120
ACTTGAGAAG AGAATAACAG GCATACCTGC AATGAAACCA TCACGAATAG CACGAAGATA	180
GATATTACGA GATAGTTTTT CAAAGAAAGG CTTTCCTTTC TCGATAAATG CAATTAGTTT	240
ATTCAATTATT TAACTCCTCT CTTGTAGAGT TCAATTAAAT GATGCATCAA ATCTTTTAAC	300
AAGATAGTTG TCATTAAAGTG GTCTTGCCCA TGCATCATGG TTACACTATA AGCCAAGTCC	360
TCACCTGAAG CTTCTTAGT CAATACACTT GTTTGCGCGT GGTGAGCCTC TGCAATACAG	420

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CTGTCTTTGA AAAGGAAGGT AAAGTCTTG AAGCCAGCG TTTGAAACAG CGGACAGAGT	60
ATGATATCGA AATGTTGCGT GAGATGGGCT ATACCAATGG GGTGAAAAT TATTCTCGCC	120
AACATGGATG GACGGAGCGA AGGAGAGCCT CCTTATACGC TTCTCGACTT CTTCCCAGAT	180
GATTTCTTGA TTATGATTGA CGAGAGTCAT ATGACCATAG GGCAAATCAA GGGCATGTAC	240
AATGGAGACC GTTCGCGTAA AGAAATGCTG GTTAATTATG GTTTCCGTTT GCCGCTCTGCT	300
TTGGACAATC GTCCTCTCCG TCGGGAGGAG TTTTGAGAGT TCACGTTTAT CAGATTGTTT	360
ACGTTTTTCAG CGACACCTGG TGACTTATGA AAATGAACAG ACCGAGACAG TGATTGAGCA	420
AATCATCCGT CCAACGGGAC TCTTGATCC AGAGGTGGAA GTCCGTCCGA CTATGGGACA	480
GATTGATGAC CTCTTGGGTG AAATCAATGC CCG	513

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TCGCAGACAA	ACCAAGGATG	ATATGAANCC	ATTCAATCTC	TATGAAGCAA	GTTGAAGCCA	60
AGGAAGAAGA	GCAAGAGCAG	GCTGAACGAG	AAGCTGAGAG	TAAGAAAGAA	CCTTACATCT	120
ACTACATCCT	TTCTTTTGCT	AAGTTGGCTG	ACTTGGTAGC	TTTGGCCAAG	ACAGTGACTT	180
TTGAAATGGA	AACTTCTGAA	CTCTACAAAA	TGAACGAGCG	CTATTATGGT	CTCTTTGACC	240
GATTGTAGTG	GACTATTGTA	AATCATCCAA	CGGCCCATAT	CCAGCTTGGC	TCTGATGGCC	300
CGAAATGCGC	GAGTTTGCAG	ACGATAGTGA	TATCAGTCGC	TCAGTCTTAC	AACAGTATGG	360
TCAAGTCTTG	ATGAGTCACG	ATGCAGTGCT	CAATCTGCAA	AAATCGGCTA	ATCCTTTCTG	420
GAAAGCTNTN	TTMNNATTTT	AANANNAGCG	AATCGTCTGA	TCCNTTTTTT	CTTTTTNTAC	480
TGATATAGTG	ATTTACTATN	ATANGAATTT	TCACAANNTT	CTGTTATAAT	GGCTATATTN	540
AAAANTTTTCG	ANGAGATAAN	TATNACNNTT	CANATTGCTT	TNCTTTGATT	TGGTTNNNTT	600
GCAANTGGTG	TGCCTTNCCT	CCNTNNANGG	ANAATGGAGG	ACTANTCATT	NCCNTCCGCN	660
CNTTCANATA	CCCAANTTGC	TNTTGTATTN	GTCCCNGATC	ATCATNACTT	CNCTCTCTTG	720
CTCNCTCCNC	GGGAATGATT	TTTNCTTTGT	TCCCATCGTT			760

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

CTGGTGAAAA	AGAATTCGCG	CTTGGACTTT	CAAACGTGGT	ATGAAGGCTC	CTCAAGCAGC	60
TGGTATTATC	CACTCAGACT	TTGAAAAAGG	CTTTATTTCGT	GCAGTAACCA	TGTCATATGA	120
AGATCTAGTG	AAATACGGAT	CTGAAAAGGC	CGTAAAAAAA	GCTGGACGCT	TGCGTGAAGA	180
AGGAAAAGAA	TATATCGTTC	AAGATGGCGA	TATCATGGAA	TTCCGCTTTA	ATGTCTAAAA	240
ATTAATAAAT	GGTGTCAATT	AGGTTGGAAA	AAAATTCCAA	CCCTTTTGGC	TTTGTAAAGG	300
AAAAATAAAT	GACCAAATTA	CTTGTAGGCT	TGGGAAATCC	AGGGGATAAA	TATTTTGAAA	360
CAAAACACAA	TGTTGGTTTT	ATGTTGATTG	ATCAACTAGC	GAAGAAACAG	AATGTCACCT	420
TTACACACGA	TAAGAATATT	TCCAAGAATT	CG			452

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

ACTTTTCCCA CAACCAGAGG GCCCTAGGAT GACAACAAC TCCCTTTTTT GATTTCTAGA	60
GAAAGTCCTT GGAGGATGGG ATTGTCTCCG AAGGATTTGT TTAGTTCCTT GATTTCTAAG	120
ATAGTTTCAG ACATTTAGTT GCTCCAATGT TTTTCTAAGT GAGTGGATAG TTTGGAAATA	180
GGGTAGCAAA CTGCGAAATA TAAGACTAGA ATGGTTCCAT AAACCCAAAA TGAACCAGTT	240
GGGATGGTCA GCGGATTGCT ATCGATGATT TGTTGTCCAA CTTTGGTCAC TTCCACAACC	300
CCAATCAAAA CAACTAATGA AGTGGTTTTA ATCATCCGAG TGACAAGATT GATAGCCTGC	360
GGTACCAGTC TTCTTAAGAC TTGTGGGATG ATGATGTGGT ACTAAAGTNG AACATTAGTC	420
AAGCCGAGTT GCCTGTCCAC TTTTCAA	447

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

CTCGTGCTCC ATAAGGGAAA TCTCGATGGC TGACACGCCC GTAAAGGTCG CATCAAAGCG	60
ATCTTGAACC GACTCAGGAG AGGCGCCATT GTGCAATTCT AACAAAATAT CCCGTAGGAC	120
ATGAATCCGT TCATCTGTCA TTAGTCTAAT CCAATCACTT CGTAGCCATT CGCTTCCAGT	180
GTGCGTACAA TCTTGTCAT AGGAGTTCCT GCTAGCTTAG AACCTGTTT AAGTGATACT	240
TTACGACCAA CTGTATTGCG CATTAAAGGA TTGGCAAGGG GTTTAAAACC CAACTCCACT	300
AGAATTTCCA AGACTTCTGG ATGCTTGTC ACCACTTCTG CAACAGGAAT TGACACATCG	360
ATGATATTGT CCATGACGAC CTCCATTGTA TGTCTAATA CTCAATGAAA ATCAAAGAAC	420
CAACTAGAAC TTG	433

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

CTTGTCATGT TTTAGCTGGA AATTTGAAAA AGGTAGCTTC TACCATGTAT TTGTTGACAC	60
CAGTGAATGT TATTGTAAAT GTTGAAGATA TCCGTTTACC AGATGAAGAT CAACAGGGTG	120
AGTTCGGTTT TGATATGAAG CGAAATAGAG TACGATAATG ATTTTTTTAA TTCGTATGAT	180
TTATAATGCA GTGGATATTT ACTCCCTGAT TTTGGTAGCC TTCGCTGTCA TGTCTTGGTT	240
TCCAGGTGCC TACGAATCCA GTTTAGGTCG TTGGATTGTA GCGTTGGTGA AACCAGTGCT	300
TGCTCCCTTG CAACGCCTGC CTTTACAGAT AGCGGGTCCT TGATTTATCT ATTTGGGTTT	360
GCGAATTGTT TTGGTTCGAT TTTTAGGAAA AAAACCTAGT ATGCGTTTTC CTGGCGAATG	420
AATAGGAATG AATAAAGGAT TTATCCAGCA TTTCTCCCAT AGAAGAATTC GTCCATTTC	480
TTGACAAGGG AAATGGAATG GATAAAGAAG G	511

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CTCTTCAATA CGGTCAATCA ACTTCCATGA CGCACCAACC TCATCCCAGT GGCTAAAGTT	60
AGTTGAGTTG TTATTTAGGA CATCATAAAT CAATTTCTCG TATGGTTCTG GAGAAGCACC	120
AGTTGCAGTC GCGTCTGTAC GATAATCAAG TGAGTTAGGA GCCAAGTTAA ATTCTTCTCC	180
TACTTGCTTC CCATTTAGGC TAAGAGAGAA GCCTTCTGTT GGTGAATAT AGATGGTCAA	240
AATATTTGGA GCAAGTGGTT CTCCAAATAT AGAATCCATT TGTTTAAAGA CGATGTTGAC	300
ATGACGTTTT TTCCTTTTTC AGTCAGTCGT TTACCTGTAC GGAAAAAGAA AGGATCTAAC	360
ACCACGGAAT CGATCGCTGT CTACAAAGAA GGCACCAGAT GTAAAGGTTT CAGTTGTTGA	420
TTCTGGATTC ACATTTGGTT CGCTACGATA AGAGATGTAT TTCATGCCAT CAATCTTACC	480
AGAGCGGTAT TGTCCACGGA TAAAGTGTTT TTTGAGTTCT TCATCAGTTG GATGATAGAA	540
GTTTTTAAAG ACTTAATCTT TTCAGCACAA ATCTCGTCTT TTGTGAAG	588

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

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GANAACACAA CCAGAGTCAG CAATAATCTC CANGNCATAG AAATACTCCA TCTTTGTCAG      60
TCATACATCG ACNAAGGTTT TGTCTCTCCN ACAATTATGT CATGAAAACC CTTGAAACAA      120
AAGCATCATC CGTCTGTGGT GACAAGTAGA AAGGAAAATG TCATGTCTGA ACGTAGAATC      180
TCTGAAAAGT CTCTCGAAAA TCTCAAAAAA TCAAACCAAG AATCCNATNT ATTAACCAAA      240
GAAGCCAGGG ACACACGCCC TCGGGCAACT ATTGGAAAAA AAGGAAATGA CCAAGATTAG      300
TATTTATGAA TTGGTCAAAC GAGCAGGTGT TTCGCGTGCG GCCTTTTATC GCAATTATGA      360
CTCCAAAGAG GAAATTTCAG AGAGCGTATT TAAACGAACT GTCCACAATA TTATGGAACA      420
GATGCATCAT TACGATTTAA AGACAGACCT TTATGTGGTT TGCTTCACCT TTTCCGGGAG      480
GCCAGAAAGG AAGCTAGAGT AATTCAATTG GCCTTGGATT ACCATCTGGC AAAAATCTTT      540
GTCCAAGCCA TGCAGGAATT TATAGAAAAA TACCATGGGA AATCGAAAGG CGTCAG      596

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(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

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CTTGTCATGA ACATTGAAA CTGGGTCGCT TGTGATTGA ATCTGAAGCA AAGGCAAGTG      60
GCAATTCTGA ACCGGTCCAT TGGTCAGAAA TGTTTGACACC TTGCTCAGTT TGAGCAGATA      120
CGCGAACATG AAGTTTAGTT GTTAATTGAG TACCTTCTAA GCGACCATTA ACTGTAAAGA      180
CACCTTCCTT AGCGTATTGC TCTGGACGAA TCGCATCCCA TGCAACCTTA GCTGATGAAA      240
CGTGACCATT TGAATCATAT GTCCGAACAC TTTCTGGTAA TTGTGGTGCT TCTGCGATTG      300
GAGTTGTCAC ACTGACTTCT TCAACTGAAA CGATACCGTC TACAGAGACT TTTGCACGCG      360
CTTCAAGGTC AATTCCTTCA ACTTTACCTA GTACTTCAAA TGTGTGATAG GAGTCTACTT      420
TGTCTTTCGG AATAGCTTGC CAAGTGAAGT TATGAGTTTT AGGGAAACCT TTGTCATACT      480
CAACTGTTAC TGTGCTGGA AGACTTGGTT CCTGATGCAA A      521

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(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

TAGAATGATG CTCTGCTAGC AGGATTATTC ACGCTACAGG TCACCAGAGC TTTCTTGATG	60
TTCTTTTCCT TAGCAACTTG CAAGCCCTGA CGGAGAGTTC TTTTGCATAA CCCTTGCCCTC	120
TTTCAGATGG ACGGATGGAG TAGCCAATGT GCCCACCTTC TTCTAGTAGA AAGTTACTGA	180
GGCGCAACCG GAGATTAAGA AATCCAAC TGTTGACCTTT CTCAGAAAAA GCCACTAACT	240
GAATTGCAGG AAGCCATCCT TCAGGCAGAT TAATCCCCAT TTCCTGTTCC TGATTGCTTT	300
CCAACCACTC TTCATACACA AAATTCTCTG TATCCCCAAA TCCTCCATCA TGGGCTGATT	360
GGCTCTTTTC AAATCTGTG ATCATATCTA AAACAGCTTT CTTATCCGCT AATCTTGGTC	420
TGCGTAATTC CATCCTTACC TCCACTATG AGAAAAGCGA GAGCTGGCTC TCACCTTTAT	480
TTTTCTTGT TCTTGTTTAA AAATTGTTCT CTGAAGCTAA GCAAGCGTTC TTTCTTACCA	540
G	541

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCTGCTCCTT ATCTTTCAG TAATTGGCGT TTTAGTGGCC TTGATAGCTC AATTTTACTC	60
AGCAAAGGCA GCAGTAGGTT TTGCTAAGGA ATTGACAAAC GATCTTTATC GTCATATTCT	120
TTCTTGCCC AAGGACAGCA GAGACCGTCT GACAACTTCT AGTTTGGTTA CTCGCTTGAC	180
TTCGGATACC TACCAGATTC AGACTGGTAT CAATCAATTC CTGCTGTCTC TTTTACGAG	240
CGCCCATATA TCGTTTTTGG TGCCATTTT ATGGCTTATC GAATCTCAGC TGAGTTGACT	300
TTCTGGTTCT TAATCATGGT TGCCATTTTG ACCATTGTCA TTGTTAGGGT TATCTCGATT	360
GGTCAATCCT CTCTACAGTA GTCTCAGAAA GAAAACCGAA CCAACTGGGT TCAGGAAACC	420
CCCCACCAAT TGCAAGGGAT GCCGGGTTAT TCCGTGCCTT TGGTCAAGAA AAACGATAGT	480

TACAGC

486

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```
CTACTCAATG ACGACCAGCA GTCATAACAT CAGCAACACT AATTCCCTTG CCACCTTCTT    60
GCCATCCACC TTCAAGTTGA TGAGCAGCAA CAGCACCACC CCATAAAAAT CTATCTTTAA    120
AAGTAGTCAT CTTTTTTCCT CCTGACTTTG ATACTCTTAT TATAAACCTC AAACCAAAG    180
ATGAAAACGC ATTCTTTTTC CTTATTGTTA AGGAAAGAAG TAATTTTAA TGGGAAATAG    240
AACAAATATCT TCTTGATTC TCGTAATGAT ATCTTTACGA TTTTCAATAC TTCCAAACTA    300
CAAAACTCT CACAATAATT CTAATCCCT GTGCTATAA ACGACTTATC GCTTCTGGC    360
ATCCCAGAAAT CATCCTCTAT ATAACGTTCA ACTTGCATCT TGGCAAGTGA TATTTTTC    420
TTAAATCTAA GATTTCTGC ATTGTCTTG ATTGATGATG CTTATCTAAA GCTTCTTGAT    480
TTATCCACTG ATCAATAAGG AGAATAGTTC CCTCTTTTC AATGGTAAA AAATATTCGT    540
ATTCAAGTT ACCTTTTGA TTTCTAATTT CTCAACAAG G                    581
```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```
ACTCCTTGT AATTTTAC TTTCTTCTT TTATGTGTTT AAGATGATCT GGATGGTCAA    60
TCTCTAAATC AAAAATCTCT GGAATAGAAC TGTAGTGGAT AATGCACTTG ATACCCAACT    120
GATTCATTTT TTGTATGAAA GAAGTATTCA GATAGCCTGC TACAGCAAAA TCAATCTTGT    180
TCTTCTTGC TTTATCCTGC ATATCTCTTA GCATATCTAA CATTATTGGA CTTTCCATAT    240
CATGCCATTG ACTGTTCTC ATAGTCGCAA AAACAAAGGA AGTCAAATCA GTCACTCCAA    300
CTACAATCTT TGAAATGCCC GTTCCAGTA TACTAGATAA GTCAAATAC GCTGACGGTA    360
```


ATTCAATCAT CGTTCCGACT TTCCCAGTAA AACCCCTGCTG AGGCAATACT GTAATAA

417

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

CAATCCGATC CCTGAACTCA CTCCTGTAAT GAGAAAACGT TTAGTCATGC AATTCTAACC	60
CAATCCGTTG CCAAACATC ACAAACCTGTC GGGCTCCAAC ATGGGAAAAA CCTTCTCCTT	120
CGCCAGAAAC GTTGATTAGG AAATAAGGTG TCATTTCAAG TGCAAGCCCA TTTTGCTCGA	180
TGGTATCAA GAGTTGGACA TAGTTTTCCG CACCTCCCCA ACCAGTTCGT ACATATTTCC	240
TCTTAGCCTT TAACCCAGGC AGGATCTCTT CAAATGTCAT GTTTTCCTCC TTTAATTCTA	300
CATTCTTCAT TTAATTATAG CAAAAACCA CTTTATACGG CTTTTGGAC TGTGAGTTAT	360
TCAAACCTGG CTAATTACTT ACGGGCAAAT TATCCCTGC AGGCAAGATT AAATTCATA	420
CCATTCTTTT CTTGTTAAGC TAAAGTTT	448

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CTACTTGAT TGCTGGAAT GGTATAAGAT GAAATCTAC AAGTCACTAA TTTTCATATA	60
ACCAAAAAAC GAACAGGCTC TTTTCTGTT ATTCAGAAGA GAACTTGTC GTTTTATCT	120
TGATTTTCTT AAAAAGCTCT ATATACATAG GGATTTCTG GTTTATCGAC TTTGGTAAAG	180
CTGTCGATTT CCAAGGTTGG AAGGTTTGT TTGAGTTCTT TATGGTAGTG ATTGACCAGT	240
TTTCCTTTGG CTGAAATCCA AGTGTGTTT TCATACTGCC GGGTATTGCC CTTGGTCAGC	300
AATCCATAGA CACCAGAATC TGCGATGCAG TGAATAATGC CGAAGCGGAA CAAAAATTGG	360
CTATTGGCAT GACTGGGGTC ATTATAGACA AAGCCTGTTG AACTGGATTG TCTTAACCCT	420
CAAATTCATC TGGGATAGTC GTAGATAGCC TCCATGACCT CCCATATAGT TTTCAATTAGT	480

GATCTGAATA CTATCTTGGG ATAAGTATTT ATCCGCCGCC GTTCGCATTT CCTTTTCATA 540
GGCTGATTTT GAAAAATAAG AACTGGTATC TGGTTTCAA TATTGGCTTG TCGTCCCTTC 600
GCTTGTNTGA ATGGCTAGAT CCGTTCCTTC CGATAGGGGG AAATGATAAC CTTTAGCAGA 660
AACGGTCTGA GAATCCAAG 679

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CTGCTATCAA GACAGTATTA CCGCTGAAAG AAACAGCTTC ACTAAAAAGG CGCAATTGAA 60
AAATAAGACG GGATCACGAA CTCCCGTTTT TCTATAAAAG AAAGGAAATG GGATGAAAAA 120
ATTAGTCTTT GTCTGTCTGG GAAATATTTG CCGTACCCCT ATGGCCGAGT TTGTTATGAA 180
ATCAATGACA GATAACTACG AAATCCAAAG TCGAGCAACT TCCTCTTGGG AACATGGCAA 240
TCCGATTCAT AAGGGGACTC AGGGAATTTT TCAAGAGTAT GAGATTCCTT ATGACAAGAA 300
CAAGACATCG CTTCAGATTA GTAAGGAAGA TTTTGAAGCC TTTGATTATA TTATCGGAAT 360
GGACGCTTCA AATGTTTCCG ACTTACGTCA GATGTGTCCA GTACACTGTC AAGATAAGAT 420
TTACTCATTT TCATCTGAAA GTGTTCCAGA ACCTTGGTAT ACAGGGAGAT TTTGAAGAAA 480
CCTATCGACG TGTTCAAAGA AGGCTGTCAA CTTGGTTAGA A 521

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

CTAAACGAAT TTCCATCTTT TTTCCTCATT TCTGACTAGT TTCTCCCATC ATAGCATAAT 60
TTAAGTATTT CTACAAGCAG TTAAAACTTG ACTTTGTGTT TTTGTTATTT TATAATCTAG 120
TTATCAAAAC TATATAAAAA GGAGTTGAAA ATGAAAATA CCTTTTCCTA CCCAAAATGG 180
GCAGAAATTC CAAACATTGA CCTCTATCTG GACCAGGTTT TGCTCTATGT CAATCAGGTC 240

TGCGCCCCCTA TCTCTCCTAA TAAAGACAAG GGCCTAACAG CATCTATGGT CAACAATTAT	300
GTGAAAAATG GTTACCTGAC AAAGCCTGAC AAAAAAAAAAT ACCAACGCCA ACAGATTGCC	360
CCGTTTGATT GCTATCACAA CCCTCAAGTT CTGTATTTTC CTATTCCAAG AAAATAGCCC	420
CAGACACTTA ATACTCCTAC AAACCTCAAG CCAAGTTTCC AGAACCAACT CCTACGAAAG	480
CCTTTGTTGG AACTATATGA ACCCAGAATT GACCC	515

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

CTTGTTGGAT ACAATCTTTG AAGAAACACA AAAGGGAGAT GACTAAGATG AAACGATGGA	60
TAGCATTAAA TAAGATAGAA TTTCTATTGA CCAAACGGCA ATCAGTCTAT TATTTATTAT	120
CAGTAGGGAT GCCGACAGCC TTCTATCTAT TCTTTTCTAG CATGTACCAG GATACTCCAG	180
GTGGACCCGC GAATTTTATG CGTGATTATC TTATCTCCAT GACTGCCTTT TCTATGATGT	240
CGACAGCTAT CTTCTCATTT CCAGTTGTTT TACATACCGA CAAGATGAGC AACTGGCAGA	300
AAACATTACG TCATAGCCCT GTTAATATGG TAGAATATTA CCTATCAAAG ATAACAGTAT	360
GCTGGGTGTA TTATTTGGTT TTCCATTCTT GGTGGTTTTT CCTCAGTTTG GGCTTTTTGT	420
TAGAAGGTGT TGGACTTGTT CTCTAACAAA GA	452

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TAACTCTGCT ATAATGGATT TATTCCTTTT TGTGTTTACA CAATTTATTT TATACTACCA	60
AAAAACAAG GTCAGGATTT TGTCCTGAC CTTTGACAAC TTTACCGATT CTTTAGTTCT	120
ACATAGCGCT TGTACCAAAT GTTACATAG GCTTCTGAGA AAGGACCACG TCCATTGTTA	180
ATCCAATCAA CAAGAATTTT GACATGTTCT TTAAATATAT AGTCCAAGTC ATCAGAATAA	240

```

TTCATTTTGC GTTTGTGACG CTCGTACTCT TCAACGTCCA AGAGACGTTT TTCCCCATCT 300
GTAAAAATTT TAACATCCAA ATCGTAATCA ATATACTTCA GTGCTTCTTC ATCCAGATAG 360
TAGGGGCTAG CCATATTGCA ATAGTAAGAA GTCCATTATC ACGAATCATG GCAATGATAT 420
TAAACCAATA TTTCTTGTGA AGTAAACAAT AGCCGGTTCT CGAGTGACCA ACGACGAACA 480
TCACTTTTCGG TAACAATGTA TGATCGTTGA CCCAATAATG GCGTTTCTGT TGTTTTAATA 540
CCATTGGTGT CCGCCAAGTC CGTGAAATC C 571

```

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```

Met Glu Lys Cys Tyr Thr Asp Val Thr Glu Phe Ala Ile Pro Ala Ser
 1             5             10             15
Thr Gln Lys Leu Tyr Leu Ser Pro Val Leu Asp Gly Phe Asn Ser Glu
      20             25             30
Ile Ile Ala Tyr Asn Leu Ser Thr Ser Pro Asn Leu Glu Gln Val Gln
      35             40             45
Thr Met Leu Glu Gln Ala Phe Thr Glu Lys His Tyr Glu Asn Thr Ile
      50             55             60
Leu His Ser Asp Gln Gly Trp Gln Tyr Gln His Asp Ser Tyr His Arg
      65             70             75             80
Phe Leu Glu Ser Lys Gly Ile Gln Ala Ser Met Ser Arg Lys Gly Asn
      85             90             95
Ser Gln Asp Asn Gly Met Met Glu Ser Phe Phe Gly Ile Leu Lys Ser
      100            105            110
Glu Met Phe Tyr Gly Tyr Glu Lys Ser Phe Gln Ser Leu Lys Gln Leu
      115            120            125
Glu Gln Ala Ile Ile Asp Tyr Ile Asp Tyr Tyr Asn Asn Lys Arg Ile
      130            135            140
Lys Val Lys Leu Lys Gly Leu Ser Pro Val Gln Tyr Arg Thr Lys Ser
      145            150            155            160
Phe Gly

```

(2) INFORMATION FOR SEQ ID NO:264:

263

MISSING UPON TIME OF PUBLICATION

Thr Pro Pro Phe Glu Ala Thr Ile Lys Asp Gly Trp Val Ser Asp Val
 100 105 110
 Val Ser Lys Met Ile Lys Ala Leu Arg Ser Gln Leu Ser Met Gln
 115 120 125

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Ala Glu Ile Gly Ala His Ala Gln Asn Gly Glu Arg Val Leu Thr
 1 5 10 15
 Gly Asp Glu Leu Ile Asp Phe Val Asn Asn Lys Leu Phe Lys Glu Leu
 20 25 30
 Lys Gly Ala
 35

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met Trp Met Ala Ala Phe Phe Gly Met Ala Thr Lys Tyr Ala Glu Gly
 1 5 10 15
 Leu Leu Ala Ile Lys Tyr Arg Thr Lys Asp Asp His Gly Ala Val Ala
 20 25 30
 Gly Gly Pro Met His Tyr Ile Leu Leu Gly Met Gly Glu Lys Trp Arg
 35 40 45

```

Pro Leu Ala Val Leu Phe Ala Val Ala Gly Val Leu Val Ala Leu Leu
 50                               55                               60
Gly Ile Gly Thr Phe Thr Gln Val Asn Ser Ile Thr Glu Ser Ile Gln
65                               70                               75                               80
Asn Thr Thr Thr Ile Ser Pro Ala Ile Thr Ala Leu Val Leu Ser Val
      85                               90                               95
Phe Val Ala Ile Ala Val Phe Gly Gly Leu Lys Ser Ile Ser Lys Val
      100                               105                               110
Ser Thr Thr Val Val Pro Phe Met Ala Ile Ile Tyr Ile Leu Gly Thr
      115                               120                               125
Leu Thr Val Ile Phe Phe Asn Ile Gly Lys Ile Pro Gly Thr Ile Ala
      130                               135                               140
Leu Val Phe Thr Ser Ala Phe Ser Pro Leu Ala Ala Val Gly Gly Phe
145                               150                               155                               160
Ala Gly Ala Ser Val Arg Met Ala Ile Gln Asn Gly Val Ala Arg Gly
      165                               170                               175
Val Phe Ser Asn Glu Ser Gly Leu Gly Ser Ala Pro Ile Ala Ala Ala
      180                               185                               190
Ala Ala Lys Thr Asn Glu Pro Val Glu Gln Gly Leu Ile Ser Met Thr
      195                               200                               205
Gly Thr Phe Ile Asp Thr Leu Ile Ile Cys Thr Leu Thr Gly Leu Thr
      210                               215                               220
Ile Leu Val Thr Gly Val Trp Ser Gly Asp Leu Asn Gly Val Ala Leu
225                               230                               235                               240
Thr Gln Ser Ala Phe Ser Thr Val Phe Ser His Phe Gly Pro Ala Leu
      245                               250                               255
Leu Thr Ile Phe Leu Val Leu Phe Ala Phe Thr Thr Ile Leu Gly Trp
      260                               265                               270
Asn Tyr Tyr Gly Arg Thr Leu Phe
      275                               280

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met Val Gln Val Gly Thr Thr Leu His Lys Glu Gly Val Ser Ala Phe
 1 5 10 15
 Asp Arg Phe Thr Asn Glu Leu Lys Ala Ile Met Val Glu Lys Gly Tyr
 20 25 30
 Glu Ser Leu Glu Asp Phe Arg Gly Lys Leu Arg Tyr Ile Asp
 35 40 45

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Lys Lys Tyr Phe Ile Gly Gly Leu Gly Ser Asn Ala Tyr His Ser
 1 5 10 15
 Lys Asp Phe Leu Gln Glu Leu Asp Ser Gln Val Tyr Phe Leu Asn Pro
 20 25 30
 Tyr Glu Lys His Leu Arg Asp Glu Thr Glu Leu Lys Ser Trp Phe Lys
 35 40 45
 Asn Glu Ile Val Glu Glu Glu Ser Ile Cys Leu Ile Gly His Ser Ile
 50 55 60
 Gly Gly Asp Leu Ala Arg Tyr Phe Ala Ser Glu Phe Glu Glu Val Lys
 65 70 75 80
 Lys Leu Ile Leu Leu Asp Gly Gly Tyr Leu Asp Leu Asp Lys Ile Leu
 85 90 95
 Pro Leu Asp Thr Glu Leu Glu Glu Thr Lys Asn Tyr Ile Lys Ser Gln
 100 105 110
 Ile Ile Ser Asp Leu Asp Val Leu Thr Ser Lys Glu Lys Ser Glu Ala
 115 120 125
 Lys His Trp Ser Glu Asn Met Glu Lys Ala Val Arg Gln Ser Tyr His
 130 135 140
 Trp Asn Val Glu Tyr Asn Arg Tyr Glu Leu Ala Ile Asn Tyr Glu Asn
 145 150 155 160
 Ile Glu Ala Ile Leu Arg Leu Arg Arg Lys Ile Gln Ala Phe Lys Arg
 165 170 175
 Glu Val Gly Asp Thr Leu Phe Ile Ser Pro Arg Tyr Pro Asn Glu Ala
 180 185 190
 267

Thr Trp Arg Glu Glu Ala Leu Lys Glu Leu Pro Asp Tyr Phe Asp Thr
 195 200 205
 Ile Phe
 210

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met Lys Leu Glu His Lys Asn Ile Phe Ile Thr Gly Ser Ser Arg Gly
 1 5 10 15
 Ile Gly Leu Ala Ile Ala His Lys Phe Ala Gln Ala Gly Ala Asn Ile
 20 25 30
 Val Leu Asn Ser Arg Gly Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe
 35 40 45
 Ser Asn Tyr Gly Ile Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp
 50 55 60
 Phe Ala Asp Ala Lys Arg Met Ile Asp Gln Ala Ile Ala Glu Leu Gly
 65 70 75 80
 Ser Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu
 85 90 95
 Met Leu Lys Met Thr Glu Ala Asp Phe Glu Lys Val Leu Lys Val Asn
 100 105 110
 Leu Thr Gly Ala Phe Asn Met Thr Gln Ser Val Leu Lys Pro Met Met
 115 120 125
 Lys Ala Arg Glu Gly Ala Ile Ile Asn Met Ser Ser Val Val Gly Leu
 130 135 140
 Met Gly Asn Ile Gly Gln Ala Asn Tyr Ala Ala Ser Lys Ala Gly Leu
 145 150 155 160
 Ile Gly Phe Thr Lys Ser Val Ala Arg Glu Val Ala Ser Arg Asn Ile
 165 170 175
 Arg Val Asn Val Ile Ala Pro Gly Asn Asp
 180 185

(2) INFORMATION FOR SEQ ID NO:271:

268

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```

Met Val Met Gln Arg Leu Leu Leu Lys Ile Phe Pro Thr Asp Asn Asn
 1             5             10             15
Val Val Trp Lys Leu Phe Val Pro Leu Leu Arg Asn Pro Lys Ile Leu
      20             25             30
Phe Leu Asp Glu Pro Ala Ala Gly Met Asn Pro Gln Glu Thr Ala Glu
      35             40             45
Leu Thr Glu Leu Ile Arg Arg Ile Lys Asp Glu Phe Lys Ile Thr Ile
      50             55             60
Met Leu Ile Glu His Asp Met Asn Leu Val Met Glu Val Thr Glu Arg
65             70             75             80
Ile Tyr Val Leu Glu Tyr Gly Arg Leu Ile Ala Gln Gly Thr Pro Asp
      85             90             95
Glu Ile Lys Thr Asn Lys Arg Val Ile Glu Ala Tyr Leu Gly Gly Glu
      100            105            110
Ala

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```

Met Thr Arg Tyr Ala Leu Leu Val Arg Gly Ile Asn Val Gly Gly Lys
 1             5             10             15

```

Asn Lys Val Val Met Ala Glu Leu Arg Gln Glu Leu Thr Asn Leu Gly
 20 25 30
 Leu Glu Lys Val Glu Ser Tyr Ile Asn Ser Gly Asn Ile Phe Phe Thr
 35 40 45
 Ser Ile Asp Ser Lys Ala Gln Leu Val Glu Lys Leu Glu Thr Phe Phe
 50 55 60
 Ala Val His Tyr Pro Phe Ile Pro Glu Leu Phe Phe Thr Glu Ser Arg
 65 70 75 80
 Gly Leu

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Glu Gln Phe Leu Asp Asn Ile Lys Asp Leu Glu Val Thr Thr Val
 1 5 10 15
 Val Arg Ala Gln Glu Ala Leu Asp Lys Lys Glu Thr Ala Thr Phe Phe
 20 25 30
 Ile Gly Arg Lys Thr Cys Pro Tyr Cys Arg Lys Phe Ala Gly Thr Leu
 35 40 45
 Ser Gly Val Val Ala Glu Thr Lys Ala His Ile Tyr Phe Ile Asn Ser
 50 55 60
 Glu Glu Pro Ser Gln Leu Asn Asp Leu Gln Ala Phe Arg Ser Arg Tyr
 65 70 75 80
 Gly Ile Pro Thr Val Pro Gly Phe Val His Ile Thr Asp Gly Thr Asn
 85 90 95
 Gln Arg Pro Leu Ala Asp Ser Ser Met Ser Ala Gln Glu Ile
 100 105 110

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```

Met Tyr Leu Ile Leu Pro Phe Cys Val Pro Gly Ser Phe Asp Arg Lys
 1           5           10           15
Val Leu Val Gly Arg Pro Asp Val Lys Gly Arg Glu Ala Ile Leu Lys
      20           25           30
Val His Ala Lys Asn Lys Pro Leu Ala Glu Asp Val Asp Leu Lys Leu
      35           40           45
Val Ala Gln Gln Thr Pro Gly Phe Val Gly Ala Asp Leu Glu Asn Val
      50           55           60
Leu Asn Glu Ala Ala Leu Val Ala Ala Arg Arg Asn Lys Ser Ile Ile
      65           70           75           80
Asp Ala Ser Asp Ile Asp Glu Ala Glu Asp Arg Val Ile Ala Gly Pro
      85           90           95
Ser Lys Lys Asp Lys Thr Val Ser Gln Lys Glu Arg Glu Leu Val Ala
      100          105          110
Tyr His Glu Ala Gly His Thr Ile Val Gly Leu Val Leu Ser Asn Ala
      115          120          125
Arg Val Val His Lys Val Thr Ile Val Pro Arg Gly Arg Ala Gly Gly
      130          135          140
Tyr Xaa Ile Ala Leu Pro Lys Glu Asp Gln Met Leu Leu Ser Lys Glu
      145          150          155          160
Asp Met Lys Glu Gln Leu Ala Gly Leu Met Gly Gly Arg Val Ala Glu
      165          170          175
Lys Ile Ile Ser Asn Val Gln Thr Thr Arg Ser Phe Lys Arg Leu
      180          185          190

```

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

Met Lys Gln Val Phe Leu Ser Thr Thr Thr Glu Phe Lys Glu Ile Asp
 1             5             10             15
Thr Leu Glu Pro Gly Thr Trp Ile Asn Leu Val Asn Pro Thr Gln Asn
             20             25             30
Glu Ser Leu Glu Ile Ala Asn Thr Phe Asp Ile Asp Ile Ala Asp Leu
             35             40             45
Arg Ala Pro Leu Asp Ala Glu Glu Met Cys Arg Ile Thr Ile Glu Asp
             50             55             60
Glu Tyr Thr Leu Ile Ile Val Asp Val Pro Val Thr Glu Glu Arg Asn
65             70             75             80
Asn Arg Thr Tyr

```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Met Ala Gln Glu Ala Leu Gln Lys Val Ala Ala Glu Met Gly Val Gly
 1             5             10             15
Ile Lys Val Glu Thr Asn Gly Ala Ser Gly Val Gly Asn Gln Leu Thr
             20             25             30
Ala Glu Asp Ile Arg Lys Ala Lys Ala Ile Ile Ile Ala Ala Asp Lys
             35             40             45
Ala Val Glu Met Asp Arg Phe Asp Gly Lys Pro Leu Ile Asn Arg Pro
             50             55             60
Val Ala Asp Gly Ile Arg Lys Thr Glu Glu Leu Ile Asn Leu Ala Ile
65             70             75             80
Ser Gly Asp Ala Glu Val Tyr Arg Ala Ala Asn Gly Ala Lys Val Ala
             85             90             95
Thr Ala Ser Asn Glu Lys Gln Ser Leu Gly Gly Ala Phe Tyr Lys His
             100            105            110
Leu Met Ser Gly Val Ser Gln Met Leu Pro Phe Val Ile Gly Gly Gly
             115            120            125

```

Ile Met Ile Ala Leu Ala Phe Leu Ile Asp Gly Ala Leu Ser Val Pro
 130 135 140
 Asn Glu Asn Leu Gly Asn Leu Gly Ser Tyr His Glu Phe Ser Phe Tyr
 145 150 155 160
 Val Pro

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Asp Ile Trp Glu Lys Met Tyr Glu Glu Ala Gln Lys Leu Tyr Asn
 1 5 10 15
 Pro His Glu Val Ser Asp Phe Val Tyr Ala Asn His Val Val Ala Ala
 20 25 30
 Val Glu Ala Gly Asp Gly Gln Ile Phe Thr Gly Phe Cys Met Glu Gly
 35 40 45
 Thr Cys Gly Val Phe His Leu Cys Ala Glu Arg Ala Ala Leu Phe Asn
 50 55 60
 Met Tyr Gln Phe Ser Gly Gln Thr Lys Val Xaa Glu Val Leu Ala Phe
 65 70 75 80
 Arg Asp Lys Pro Pro Tyr Gly Gly Ser Ser Ala Met Pro Leu Arg Cys
 85 90 95
 Leu

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Leu Tyr Leu Val Ala Thr Pro Ile Gly Asn Leu Asp Asp Met Thr Phe
 1             5             10             15
Arg Ala Ile Gln Thr Leu Lys Glu Val Asp Trp Ile Ala Ala Glu Asp
      20             25             30
Thr Arg Asn Thr Gly Leu Leu Leu Lys His Phe Asp Ile Ser Thr Lys
      35             40             45
Gln Ile Ser Phe His Glu His Asn Ala Lys Glu Lys Thr Pro Asp Leu
      50             55             60
Ile Gly Phe Leu Lys Ala Gly Gln Ser Ile Ala Gln Val Ser Asp Ala
      65             70             75             80
Gly Leu Pro Ser Ile Ser Asp Pro Gly His Gly Phe Gly Leu Arg Gln
      85             90             95
Leu Leu Glu Gly Arg Asn Cys Ser Cys Tyr Ser Ser Arg Cys Leu Cys
      100            105            110
Arg Asn Phe Cys Leu Asp Cys Gln Trp Phe Ser Ala Thr Ala Thr Tyr
      115            120            125
Leu Leu Arg Phe Phe Thr Glu Lys Ile Arg Ser Thr Glu Ala Ile Phe
      130            135            140
Trp Leu
145

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Met Pro Asp Asn Leu Ala Leu Arg Met Arg Pro Lys Thr Ile Asp Gln
 1             5             10             15
Val Ile Gly Gln Glu Xaa Leu Val Gly Pro Gly Lys Ile Ile Arg Arg
      20             25             30
Met Val Glu Ala Asn Arg Leu Ser Met Ile Leu Tyr Gly Pro Pro
      35             40             45

```

Gly Ile Gly Lys Thr Ser Ile Ala Ser Ala Ile Ala Gly Thr Thr Lys
 50 55 60
 Tyr Ala Leu Arg Asp Pro Gln Arg Asp Ser
 65 70

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met Gln Asp Glu Val Glu Val Gly Asp Val Phe Lys Asp Val Tyr Asn
 1 5 10 15
 Ala Leu Asn Glu Glu Gly Val Phe Ile Phe Asp Val His Ser Thr Tyr
 20 25 30
 Gln Thr Asp Glu Val Leu Pro Trp Leu Phe Leu Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Leu Ser Leu Ile Asp Asn Asp Pro Phe Lys Asp Asp Glu Asp Phe Val
 1 5 10 15
 Ser Thr Tyr Asp Leu Asp Lys Ser Phe Ile Ser Met Val Ser Val Asp
 20 25 30
 Val Ser Glu Tyr Leu Gly Ser Gln Glu Pro Ile Lys Lys Thr Leu Thr
 35 40 45

Ile Pro Lys Trp Ala Asp Lys Leu Gly Arg Glu Met Gly Leu Asn Phe
 50 55 60
 Ser Gln Thr Leu Thr Asp Ala Ile Ala Asp Lys Lys Val Gln Ala
 65 70 75

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:.

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Leu Thr Lys Ser Met Thr Pro Asp Arg Glu Val Ile Thr Phe Ile Pro
 1 5 10 15
 Glu Lys Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro Arg Gly
 20 25 30
 Met Met Gly Val Arg Leu Glu Met Arg Gly Leu Leu Tyr Thr Gly Pro
 35 40 45
 Arg Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala Gly Val
 50 55 60
 Gln Val Glu Asn Val Ile Ile Ser Pro Leu Ala Met Val Gln Ser Val
 65 70 75 80
 Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp Met Gly
 85 90 95
 Ala Gly Gln Thr Thr Val Ala Thr Ile Arg Asn Gln Glu Leu Gln Phe
 100 105 110
 Thr His Ile Leu Gln Glu Gly Gly Asp Tyr Val Thr Lys Asp Ile Ser
 115 120 125
 Lys Val Leu Lys Thr Ser Arg Lys Leu Ala Glu Gly Leu Lys Leu Asn
 130 135 140
 Tyr Gly Glu Ala Tyr Pro Pro Leu Ala Ser Lys Glu Thr Phe Gln Val
 145 150 155 160
 Lys Val Ile Gly Glu Val Glu Pro Val Lys Val Thr Glu Ala Tyr Leu
 165 170 175
 Ser Glu Ile Ile Ser Ala Arg Ile Lys His Ile Leu Glu Gln Ile Lys
 180 185 190
 Gln Glu Leu Asp Arg Arg Arg Leu Val Gly Pro Pro Trp Trp Tyr Cys
 195 200 205

Leu Asn Arg Trp Glu Cys His Phe Thr Arg Tyr Gly
 210 215 220

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Met Pro Glu Trp Arg Leu Asp Leu Ile Lys Glu Tyr Tyr Val Pro
 1 5 10 15
 Tyr Met Ser Asn Asp Asn Asn Tyr Pro Arg Val Phe Met Thr Gln Glu
 20 25 30
 Asp Leu Asp Lys Ile Ala His Ile Glu Ala Asp Met Asn Asp Tyr Ile
 35 40 45
 Tyr Arg Lys Arg Ala Glu Trp Ile Val Asn Gly Asn Ile Asp Thr Glu
 50 55 60
 Trp Asp Asp Tyr Lys Lys Glu Leu Glu Lys Tyr Gly Leu Ser Asp Tyr
 65 70 75 80
 Leu Ala Ile Lys Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala Asn Lys Asn
 85 90 95

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Arg Ile Ala Ile Gly Cys Asp His Phe Val Thr Asp Glu Lys Met
 1 5 10 15

Ala Val Ser Glu Phe Leu Lys Ser Lys Gly Tyr Glu Val Ile Asp Phe
 20 25 30
 Gly Thr Tyr Asp His Thr Arg Thr His Tyr Pro Ile Phe Gly Lys Lys
 35 40 45
 Val Arg Glu Ala Val Thr Ile Gly Gln Pro Asp Leu Gly Val Cys Thr
 50 55 60
 Cys Gly Thr Gly Val Gly Ile Asn Asn Pro Val Asn Lys Val Pro Arg
 65 70 75 80
 Val Arg Ser Ala Leu Val Arg Asp Met Thr Thr Ala Leu Tyr Ala Lys
 85 90 95
 Glu Gln Leu Asn Ala Asn Val Ile Gly Phe Gly Gly Lys Ile Thr Gly
 100 105 110
 Glu Leu Leu Met Cys Asp Ile Ile Glu Ala Phe Ile His Ala Glu Tyr
 115 120 125
 Lys Pro Ser Glu Glu Asn Lys Lys Leu Ile Ala Lys Ile Glu His Val
 130 135 140
 Glu Thr His Asn Ala Gln Gln Thr Asp Ala Asn Phe Phe Thr Glu Xaa
 145 150 155 160
 Pro

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Leu Lys Lys Gln Val Leu Thr Met Xaa Ile Asp Arg Arg Pro Phe Gly
 1 5 10 15
 Gly Ala Asp Ile Asp Ala Ala Gly Pro Pro Leu Pro Asp Glu Thr Leu
 20 25 30
 Lys Ala Ser Arg Glu Ala Asp Ala Ile Leu Leu Val Ala Ile Gly Ser
 35 40 45
 Pro Gln Tyr Asp Gly Val Ala Val Arg Pro Glu Gln Gly Leu Met Ala
 50 55 60
 Leu Arg Lys Asn Ser Ile Phe Thr Leu Ile Phe Val Leu
 65 70 75

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Met Ala Phe Ile Glu Lys Gly Gln Glu Ile Asp Met Glu Val Ile Lys
 1             5             10             15
Ala Glu Thr Gln Leu Ser Ala Glu Ala Leu Arg Leu Lys Glu Ser Arg
          20             25             30
Asp Arg Glu Leu Ala Asp Ile Ile Ser Gly Glu Asp Asp Arg Ile Leu
          35             40             45
Leu Val Ile Gly Pro Cys Ser Ser Asp Asn Asp
          50             55

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Met Val Met Arg Val Tyr Thr Ala Lys Pro Arg Thr Asn Gly Asp Gly
 1             5             10             15
Tyr Lys Gly Leu Val His Gln Pro Asp Thr Ser Lys Ala Pro Thr Leu
          20             25             30
Ile Asn Gly Leu Gln Ala Val Arg His Leu His Tyr Arg Phe Asp Tyr
          35             40             45
Arg Tyr Trp Phe Asp Asn Gly Arg
          50             55

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Asn Lys Arg Val Lys Ile Val Ala Thr Leu Gly Pro Ala Val Glu
 1             5             10             15
Ile Arg Gly Gly Lys Lys Phe Gly Glu Asp Gly Tyr Trp Gly Glu Lys
          20             25             30
Leu Asp Val Glu Ala Ser Ala Lys Asn Ile Ala Lys Leu Ile Glu Ala
          35             40             45
Gly Ala Asn Thr Phe Arg Phe Asn Phe Ser His Gly Asp His Gln
          50             55             60

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Met Gly Asp Lys Pro Ile Ser Phe Arg Asp Ala Asp Gly Asn Phe Val
 1             5             10             15
Ser Ala Ala Asp Val Trp Asn Glu Lys Lys Leu Glu Glu Leu Phe Asn
          20             25             30
Arg Leu Asn Pro Asn Arg Ala Leu Arg Leu Ala Arg Thr Lys Lys Glu
          35             40             45
Asn Pro Ser Gln
          50

```

(2) INFORMATION FOR SEQ ID NO:290:

MISSING UPON TIME OF PUBLICATION

MISSING UPON TIME OF PUBLICATION

MISSING UPON TIME OF PUBLICATION

MISSING UPON TIME OF PUBLICATION

MISSING UPON TIME OF PUBLICATION

MISSING UPON TIME OF PUBLICATION

MISSING UPON TIME OF PUBLICATION

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MISSING UPON TIME OF PUBLICATION

MISSING UPON TIME OF PUBLICATION

Ile Ile Val Ile Thr Pro Gln Ser Thr Gly Pro Gln Ser Ile Leu Phe
 500 505 510
 Trp Ile Asp Ala Val Gln Asn Tyr Val Leu Phe Asn Gln Leu Ser Asp
 515 520 525
 Ala Gln Glu Leu Ile Gln Arg Gln Gly Ile Glu Asn Trp Val Ser Glu
 530 535 540
 Met Gln Thr Gly Tyr His Asn Tyr Ile Thr Leu Leu Asp Asn Ile Gln
 545 550 555 560
 Arg Glu Arg Trp Val Met Leu Ala Gly Ala Val Leu Gly Ile Ala Thr
 565 570 575
 Ser Ile Leu Leu Phe Asn Thr Met Asn Arg Leu Tyr Phe Glu Glu Phe
 580 585 590
 Arg Arg Ala Ile Phe Ile Lys Arg Ile Ala Gly Leu Arg Phe Leu Glu
 595 600 605
 Ile His Arg Thr Tyr Leu Phe Ala Gln Leu Gly Val Phe Leu Leu Gly
 610 615 620
 Phe Val Ala Ser Val Phe Leu Gln Val Glu Ile Gly Val Ala Phe Leu
 625 630 635 640
 Val Leu Leu Leu Phe Thr Gly Leu Ser Leu Leu Gln Leu His Val Gln
 645 650 655
 Met Gln Lys Glu Asn Lys Met Ser Ile Leu Val Leu Lys Gly Gly
 660 665 670

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met Lys Glu Lys Glu Ile Phe Asp Ser Ile Val Thr Ile Ile Gln Glu
 1 5 10 15
 Arg Gln Gly Glu Asp Phe Val Val Thr Glu Ser Leu Ser Leu Lys Asp
 20 25 30
 Asp Leu Asp Ala Asp Ser Val Asp Leu Met Glu Phe Ile Leu Thr Leu
 35 40 45
 Glu Asp Glu Phe Ser Ile Glu Ile Ser Asp Glu Glu Ile Asp Gln Leu
 50 55 60

Gln Ser Val Gly Asp Val Val Lys Ile Ile Gln Gly Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Arg Ser Asp Phe Leu Arg Asn Lys Ile Trp Tyr Ser Ser Ser Met
 1 5 10 15
 Asn Asp Glu Ala Ser Lys Gln Leu Thr Asp Ala Arg Phe Lys Arg Leu
 20 25 30
 Val Gly Val Gln Arg Thr Thr Phe Glu Glu Met Leu Ala Val Leu Lys
 35 40 45
 Thr Ala Tyr Gln Leu Lys His Ala Lys Gly Gly Arg Lys Pro Lys Leu
 50 55 60
 Ser Leu Glu Asp Leu Leu Met Ala Thr Leu Gln Tyr Val Arg Glu Tyr
 65 70 75 80
 Arg Thr Tyr Glu Glu Ile Ala Ala Asp Phe Gly Ile His Glu Ser Thr
 85 90 95

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Lys Leu Phe Lys Met Ser Cys Arg Asn Ile Gly Gln Ala Gly Lys
 1 5 10 15

Ile Leu Ala Asp Ser Asp Tyr Gln Gly Leu Met Lys Ile Tyr Pro Gln
 20 25 30
 Ala Gln Thr Pro Arg Lys Ser Ser Lys Leu Lys Pro Leu Thr Ala Glu
 35 40 45
 Asp Lys Ala Tyr Asn His Ala Leu Ser Lys Glu Arg Ser Lys Val Glu
 50 55 60
 Asn Ile Phe Ala Lys Val Lys Thr Phe Lys Met Phe Ser Thr Thr Tyr
 65 70 75 80
 Arg Asn His Arg Lys Arg Phe Gly Leu Arg Met Asn Leu Ile Ala Gly
 85 90 95
 Ile Ile Asn His Glu Leu Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Leu Arg Lys Val Val Val Val Arg Leu Glu Lys Pro Val Thr Phe His
 1 5 10 15
 Asn Met Ile Ala Pro Asp Lys Glu Val Glu Val Ser Leu Leu Phe Phe
 20 25 30
 Ile Ile Asn Asn Ser Ser Ser Ser Gln Thr Asn Ile Leu Ala Gln Leu
 35 40 45
 Met Asp Phe Phe Thr Gly Asn Gly His Leu Glu Asp Leu Ser Lys Ile
 50 55 60
 Ser Glu Pro Glu Lys Leu Tyr Ala Tyr Ile Ala Glu Ala Thr Ala
 65 70 75

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```

Met Ile Lys Ile Leu Ala Ala Cys Gly Ala Gly Val Asn Ser Ser His
 1             5             10             15
Gln Ile Lys Ser Ala Leu Glu Glu Glu Leu Ser Asn Arg Gly Tyr Asp
      20             25             30
Val His Cys Asp Ala Val Met Val Lys Asp Val Asn Glu Asp Leu Met
      35             40             45
Lys Gly Tyr Asp Ile Phe Thr Pro Ile Ala Ala Thr Asp Leu Gly Phe
      50             55             60
Glu Pro Gly Ile Pro Val Ile Glu Ala Gly Pro Ile Leu Phe Arg Ile
      65             70             75             80
Pro Ala Met Ser Ala Pro Val Phe Asp Asn Ile Arg Leu Pro Ala Lys
      85             90             95
Gln Asn Met Val
      100

```

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

```

Met Val Val Ser Phe Ile Leu Leu Met Ala Thr Ile Val Val Glu Pro
 1             5             10             15
Leu Glu Gly Ile Phe His Val Thr Lys Leu Asp Leu Ser Gln Trp Gly
      20             25             30
Ile Val Met Ala Gly Ser Phe Ser Met Ile Ile Ile Val Glu Ile Ala
      35             40             45
Lys Phe Ile Gln Arg Lys Leu Gly Phe Asp Lys Asn Ala Ile
      50             55             60

```

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

```

Met Asn His Lys Pro Arg Gly Arg Lys Ala Ser Phe Phe Ser Gly Gly
 1             5             10             15
Val Leu Ser Ser Ile Ile Tyr Gln Gly Val Leu Gln Ala Ala Leu Val
      20             25             30
Met Ser Val Tyr Gly Leu Ala Ile Ala Tyr Pro Val His Val Gly Asp
      35             40             45
Asn His Ala Ile His Ala Asp Ala Leu Thr Met Ala Phe Ala Thr Leu
      50             55             60
Gly Leu Ile Gln Leu Phe His Ala Tyr Asn Val Lys Ser Val Tyr Gln
      65             70             75             80
Ser Ile Leu Thr Val Gly Pro Phe Lys Ser Lys Thr Phe Asn Trp Ser
      85             90             95
Ile Leu Val Ser Phe Ile Leu Leu Met Ala Thr Ile Val Val Glu Pro
      100            105            110
Leu Glu Gly Ile Phe His Val Thr Lys Leu Asp Leu Ser Gln Trp Gly
      115            120            125
Ile Val Met Ala Gly Ser Phe Ser Met Ile Ile Ile Val Glu Ile Val
      130            135            140
Lys Phe Ile Gln Arg Lys Leu Gly Phe Asp Lys Asn Ala Ile
      145            150            155

```

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Met Ala His Gln Ala Leu Arg Val Leu Ala Gly Ala Tyr Lys Ile Ile
 1             5             10             15
Asp Ser Ile Pro Glu Asn Leu Thr Ser Glu Glu Leu Glu Asn Asp Leu
      20             25             30
Ile Phe Thr Gly Leu Ile Gly Met Ile Asp Pro Glu Arg Pro Glu Ala
      35             40             45
Ala Glu Ala Val Arg Val Ala Lys Glu Ala Gly Ile Arg Pro Ile Met
      50             55             60
Ile Thr Gly Asp His Gln Asp Thr Ala Glu Ala Ile Ala Lys Arg Leu
65             70             75             80
Gly Ile Ile Asp Ala Asn Asp Thr Glu Gly His Val Leu Thr Gly Ala
      85             90             95
Glu Leu Asn Glu Leu Ser Asp Glu Glu Phe Glu Lys Val Val Gly Gln
      100            105            110
Tyr Ser Val Tyr Ala Arg Val Ser Pro Glu His Lys Val Arg Ile Val
      115            120            125
Lys Ala Trp Gln Lys Gln Gly Lys Val Val Ala Met Thr Gly Asp Gly
      130            135            140
Val Asn Asp Ala Pro Ala Leu Lys Thr Ala Asp Ile Gly Ile Gly Met
145            150            155            160
Gly Ile Thr Gly Thr Glu Val Ser Lys Gly Ala Ser Asp Met Ile Leu
      165            170            175
Ala Asp Asp Asn Phe Ala Thr Ile Ile Val Ala Val Glu Glu Gly Arg
      180            185            190
Lys Val Phe Ser Asn Ile Gln Lys Thr Ile Gln Tyr Leu Leu Ser Ala
      195            200            205
Asn Thr Ala Glu Val Leu Thr Ile Phe Leu Ser Thr Leu Phe Gly Trp
      210            215            220
Asp Val Leu Gln Pro Val His Leu Leu Trp Ile Asn Leu Val Thr Asp
225            230            235            240
Thr Phe Pro Ala Ile Val Leu Trp Cys
      245

```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

Met Lys Gln Ser Lys Met Pro Ile Pro Thr Leu Arg Glu Met Pro Ser
 1             5             10             15
Asp Ala Gln Val Ile Ser His Ala Leu Met Leu Arg Ala Gly Tyr Val
          20             25             30
Arg Gln Val Ser Ala Gly Val Tyr Ser Tyr Leu Pro Leu Ala Asn Arg
      35             40             45
Val Ile Glu Lys Ala Lys Asn Ile Met Arg Gln Glu Phe Glu Lys Ile
      50             55             60
Gly Ala Val Glu Met Leu Ala Pro Ala Leu Leu Ser Ala Glu Leu Trp
      65             70             75             80
Arg Glu Ser Gly Arg Tyr Glu Thr Tyr Gly Glu Asp Leu Tyr Lys Leu
          85             90             95
Lys Asn Arg Glu Lys Ser Asp Phe Ile Leu Gly Pro Thr His Glu Glu
      100             105             110
Thr Phe Thr Ala Ile Val Arg Asp Ser Val Lys Ser Tyr Lys Gln Leu
      115             120             125
Pro Leu Asn Leu Tyr Gln Ile Gln Pro Lys Tyr Arg Asp Glu Lys Arg
      130             135             140
Pro Arg Asn Gly Leu Leu Arg Thr Arg Glu Phe Ile Met Lys Asp Ala
      145             150             155             160
Tyr Ser Phe His Ala Asn Tyr Asp Ser Leu Asp Ser Val Tyr Asp Glu
          165             170             175
Tyr Lys Ala Ala Tyr Glu Arg Ile Phe Thr Arg Ser Gly Leu Asp Phe
          180             185             190
Lys Ala Ile Ile Gly Asp Gly Gly Ala Met Gly Gly Lys Asp Ser Gln
          195             200             205
Glu Phe Met Ala Ile Thr Ser Ala Arg Thr Asp Leu Asp Arg Trp Val
          210             215             220
Val Leu Asp Lys Ser Val Ala Ser Phe Asp Glu Ile Pro Ala Glu Val
          225             230             235             240
Gln Glu Glu Ile Lys Ala Glu Leu Leu Lys Trp Ile Val Ser Gly Glu
          245             250             255
Asp Thr Ile Ala Tyr Ser Ser Glu Ser Ser Tyr Ala Ala Asn Leu Glu
          260             265             270
Met Ala Thr Asn Glu Tyr Lys Pro Ser Asn Arg Val Val Ala Glu Glu
          275             280             285
Glu Val Thr Arg Val Glu Thr Pro Asp Val Lys Ser Ile Asp Glu Val
          290             295             300
Ala Ala Phe Leu Asn Val Pro Glu Glu Gln Thr Ile Lys Thr Leu Phe
          305             310             315             320

```

Tyr	Ile	Ala	Asp	Gly	Glu	Leu	Val	Ala	Ala	Leu	Leu	Val	Gly	Asn	Asp				
							325							330				335	
Gln	Leu	Asn	Glu	Val	Lys	Leu	Lys	Asn	His	Leu	Gly	Ala	Asn	Phe	Phe				
							340							345				350	
Asp	Val	Ala	Ser	Glu	Glu	Glu	Val	Ala	Asn	Val	Val	Gln	Ala	Gly	Phe				
							355							360				365	
Gly	Ser	Leu	Gly	Pro	Val	Gly	Leu	Pro	Glu	Asn	Ile	Lys	Ile	Ile	Ala				
							370							375				380	
Asp	Arg	Lys	Val	Gln	Asp	Val	Arg	Asn	Ala	Val	Val	Gly	Ala	Asn	Glu				
385								390							395				400
Asp	Gly	Tyr	His	Leu	Thr	Gly	Val	Asn	Pro	Gly	Arg	Asp	Phe	Thr	Ala				
							405							410				415	
Glu	Tyr	Val	Asp	Ile	Arg	Glu	Val	Arg	Glu	Gly	Glu	Ile	Ser	Pro	Asp				
							420							425				430	
Gly	Gln	Gly	Val	Leu	Asn	Phe	Ala	Arg	Gly	Ile	Glu	Ile	Gly	His	Ile				
							435							440				445	
Phe	Lys	Leu	Gly	Thr	Arg	Tyr	Ser	Ala	Ser	Met	Gly	Ala	Asp	Val	Leu				
							450							455				460	
Asp	Glu	Asn	Gly	Arg	Ala	Val	Pro	Ile	Ile	Met	Gly	Cys	Tyr	Gly	Ile				
465								470							475				480
Gly	Val	Ser	Arg	Leu	Leu	Ser	Ala	Val	Met	Glu	Gln	His	Ala	Arg	Leu				
							485							490				495	
Phe	Val																		

(2) INFORMATION FOR SEQ ID NO:311:..

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Gly Ile Ile Arg Ile Gly Ala Glu Val Lys Glu Gly Asp Ile Leu
1 5 10 15
Val Gly Lys Val Thr Pro Lys Gly Glu Lys Asp Leu Ser Ala Gly Arg
20 25 30
Thr Ser Leu Ala Arg Tyr Leu Trp Arg Gln Val Ser
35 40

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

Met Arg Val Leu Asp Glu Asp Asp Gln Glu Val Glu Leu Arg Asp Leu
 1             5             10             15
Asp Glu Gly Met Asp Glu Asp Val Ile His Val Asp Asp Leu Glu Lys
          20             25             30
Ala Arg Glu Lys Ala Ala Gln Glu Ala Lys Ala Ala Phe Glu Ala Glu
          35             40             45
Glu Ala Glu Lys Ala Thr Lys Ala Glu Ala Thr Glu Glu Ala Ala Glu
          50             55             60
Gln Glu
65

```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

Met Leu Val Asn Val Val Pro Leu Pro Ser Gln Pro Thr Trp Arg Val
 1             5             10             15
Val Val Pro Thr Ser Ser Leu Val Lys Val Phe Val Asn Leu Glu Asp
          20             25             30
Phe Val Leu Leu Val Pro Glu Arg His Glu Ser Arg Arg Ile Asp Asn
          35             40             45

```


Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Glu Ser Gln
 50 55 60
 Phe Tyr Leu Ser Leu Glu Asp Asp Leu Met Lys Arg Phe Gly Ser Glu
 65 70 75 80
 Arg Leu Lys Gly Ile Phe Glu Arg Leu Asn Met Ser Glu Glu Ala Ile
 85 90 95
 Glu Ser Arg Met Leu Thr Arg Gln Val Glu Ala Ala Gln Lys Arg Val
 100 105 110
 Glu Gly Asn Asn Tyr Asp Thr Arg Lys Gln Val Leu Gln Tyr Asp Asp
 115 120 125
 Val Met Arg Glu Gln Arg Glu Ile Ile Tyr Ala Gln Arg Tyr Asp Val
 130 135 140
 Ile Thr Ala Asp Arg Asp Leu Ala Pro Glu Ile Gln Ser Met Ile Lys
 145 150 155 160
 Arg Thr Ile Glu Arg Val Val Asp Gly His Ala Arg Ala Lys Gln Asp
 165 170 175
 Glu Lys Leu Glu Ala Ile Leu Asn Phe Ala Lys Tyr Asn Leu Leu Pro
 180 185 190
 Glu Asp Ser Ile Thr Met Glu Asp Leu Ser Gly Leu Ser Asp Lys Ala
 195 200 205
 Ile Lys Glu Glu Leu Phe Gln Arg Ala Leu Lys Val Tyr Asp Ser Gln
 210 215 220
 Val Ser Lys Leu Arg Asp Glu Glu Ala Val Lys Glu Phe Gln Lys Val
 225 230 235 240
 Leu Ile Leu Arg Val Val Asp Asn Lys Trp Thr Asp His Ile Asp Ala
 245 250 255
 Leu Asp Gln Leu Arg Asn Ala Val Gly Leu Arg Gly Tyr Ala Gln Asn
 260 265 270
 Asn Pro Val Val Glu Tyr Gln Ala Glu Gly Phe Arg Met Phe Asn Asp
 275 280 285
 Met Ile Gly Ser Ile Glu Phe Asp Val Thr Arg Leu Met Met Lys Ala
 290 295 300
 Gln Ile His Glu Gln Glu Arg Pro Gln Ala Glu Arg His Ile Ser Thr
 305 310 315 320
 Thr Ala Thr Arg Asn Ile Ala Ala His Gln Ala Ser Met Leu Glu Asp
 325 330 335
 Leu Asp Leu Ser Gln Ile Gly Arg Asn Glu Leu Cys Pro Cys Gly Ser
 340 345 350
 Gly Lys Lys Phe Lys Asn Cys His Gly Lys Arg Gln
 355 360

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

Met Ala Arg Gln Tyr Lys Val Asp Gly Ile Pro Ala Gly Ile Val Ser
 1             5             10             15
Leu Ser Ser Phe Ile Thr Val Thr Pro Phe Ile Thr Gly Glu Ala Gly
      20             25             30
Ala Gly Met Pro Thr Ala Phe Met Ala Ser Lys Gly Leu Phe Val Ala
      35             40             45
Met Ile Leu Gly Leu Ile Asn Gly Tyr Ile Tyr Gln Trp Phe Ile Asn
      50             55             60
His Asn Ile Gln Ile Lys Met Pro Asp Gly Val Pro Pro Ala Val Ser
      65             70             75             80
Lys Ser Phe Ser Ala Ile Ile Pro Gly Ala Val Thr Ile Val Gly Trp
      85             90             95
Leu Ile Val Tyr Ala Thr Leu Asp Lys Leu Ser Leu Pro Asn Leu His
      100            105            110
Glu Ile Ala Gln Val Ser Phe Gly Arg Ser Thr Trp Thr Phe Arg Lys
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

Met Leu Glu Leu Arg Asn Ile Asn Lys Val Phe Gly Asp Lys Gln Ile
 1             5             10             15
Leu Ser Asp Phe Ser Leu Ser Ile Pro Glu Lys Gln Ile Leu Ala Ile
      20             25             30
                        301

```

Val Gly Pro Ser Gly Gly Ser Lys Thr Thr Leu Leu Arg Met Leu Ala
 35 40 45
 Gly Leu Glu Thr Ile Asp Ser Gly Gln Ile Phe Tyr Asn Gly Gln Pro
 50 55 60
 Leu Glu Leu Asp Glu Leu Gln Lys Arg Asn Leu Leu Gly Phe Val Phe
 65 70 75 80
 Gln Asp Phe Gln Leu Phe Pro His Leu Ser Val Leu Glu Asn Leu Thr
 85 90 95
 Leu Ser Pro Val Lys Thr Met Gly Met Lys Gln Glu Glu Ala Glu Lys
 100 105 110
 Lys Ala Ser Gly Leu Leu Glu Gln Leu Gly Leu Gly Gly His Ala Glu
 115 120 125
 Ser Tyr Pro Phe Ser Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Leu
 130 135 140
 Ala Arg Ala Met Met Ile Asp Pro Glu Ile Ile Gly Tyr Asp Glu Pro
 145 150 155 160
 Thr Ser Ala Leu Asp Pro Glu Leu Arg Leu Glu Val Glu Lys Leu Ile
 165 170 175
 Leu Gln Asn Arg Glu Leu Gly Met Thr Gln Ile Val Val Thr His Asp
 180 185 190
 Leu Gln Phe Ala Glu Asn Ile Ala Met Tyr Tyr
 195 200

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Thr Ala Leu Phe Leu Val Ala Cys Gly Lys Asn Ser Ser Glu Thr
 1 5 10 15
 Ser Gly Asp Asn Trp Ser Lys Tyr Gln Ser Asn Lys Ser Ile Thr Ile
 20 25 30
 Gly Phe Asp Ser Thr Phe Ser Ser Gln Trp Asp Leu Leu Arg Lys Met
 35 40 45
 Val Leu Met Gln Asp Leu Ile Leu Ile
 50 55

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```

Met Thr Gln Ala Ile Leu Glu Ile Lys His Leu Lys Lys Ser Tyr Gly
 1             5             10             15
Gln Asn Glu Val Leu Lys Asp Ile Ser Leu Thr Val His Lys Gly Glu
      20             25             30
Val Ile Ser Ile Ile Gly Ser Ser Gly Ser Gly Lys Ser Thr Phe Leu
      35             40             45
Arg Ser Ile Asn Leu Leu Glu Thr Pro Thr Asp Gly Gln Ile Leu Tyr
      50             55             60
His Gly Gln Asn Val Leu Glu Lys Gly Tyr Asp Leu Thr Gln Tyr Arg
      65             70             75             80
Glu Lys Leu Gly Met Val Phe Gln Ser Phe Asn Leu Phe Glu Asn Leu
      85             90             95
Asn Val Leu Glu Asn Thr Ile Val Ala Gln Thr Thr Val Leu Lys Arg
      100            105            110
Glu Arg Thr Glu Ala Glu Glu Ile Ala Lys Glu Asn Leu Glu Lys Val
      115            120            125
Gly Met Gly Glu Arg Tyr Trp Gln Leu Pro Asn Gln Ile Ala Thr Ile
      130            135            140
Arg Trp Ser Lys Thr Thr Cys Gly His Arg Ser Cys Pro Ile Asn Glu
      145            150            155            160
Ser Arg His Leu Cys Ser Leu Met Asn Gln Leu Leu Pro Leu Thr Leu
      165            170            175
Arg Trp Leu Glu Lys
      180

```

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```

Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Gly
 1             5             10             15
Glu Val Ile Asn Val Met Lys Glu Leu Ala Glu Gln Gly Met Thr Met
      20             25             30
Ile Ile Val Thr His Glu Met Gly Phe Ala Arg Gln Val Ala Asn Arg
      35             40             45
Val Ile Phe Thr Ala Asp Gly Glu Phe Leu Glu Asp Gly Thr Pro Asp
      50             55             60
Gln Ile Phe Asp Asn Pro Gln His Pro Arg Leu Lys Glu Phe Leu Asp
      65             70             75             80
Lys Val Leu Asn Val
              85

```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

Met Ala Lys Asp Ile Leu Val Gln Ala Met Gln Arg Ile Ala Gly Glu
 1             5             10             15
Tyr Val Ala Glu Ser Thr Asn Ser Thr Val His Leu Pro Asp Asp Thr
      20             25             30
Met Lys Gly Arg Ile Ile Gly Arg Glu Gly Arg Asn Ile Arg Thr Phe
      35             40             45
Glu Ser Leu Thr Gly Val Asp Val Ile Ile Asp Asp Thr Pro Glu Val
      50             55             60
Val Thr Leu Ser Gly Phe Asp Pro Ile Arg Arg Glu Ile Ala Arg Met
      65             70             75             80

```

```

Thr Met Glu Met Leu Leu Lys Asp Gly Arg Ile His Pro Ala Arg Ile
      85                      90                      95
Glu Glu Leu Val Glu Lys Asn Arg Gln Glu Ile Asp Asn Lys Ile Arg
      100                     105                     110
Glu Tyr Gly Glu Ala Ala Ala Tyr Glu Ile Gly Ala Pro Asn Leu His
      115                     120                     125
Pro Asp Leu Met Lys Ile Met Gly Arg Leu Gln Phe Arg Thr Ser Tyr
      130                     135                     140
Gly Gln Asn Val Leu Arg His Ser Ile Glu Val Ala Lys Leu Ala Gly
      145                     150                     155                     160
Ile Met Ala Ser Glu Leu Gly Glu Asn Ala Ala Leu Ala Arg Arg Ala
      165                     170                     175
Gly Phe Leu His Asp Ile Gly Lys Ala Ile Asp His Glu Val Glu Gly
      180                     185                     190
Ser His Val Glu Ile Gly Met Glu Leu Ala Arg Lys Tyr Lys Glu Pro
      195                     200                     205
Pro Val Val Val Asn Thr Ile Ala Ser His His Gly Asp Val Glu Ala
      210                     215                     220
Glu Ser Val Ile Ala Val Ile Val Ala Ala Ala Asp Ala Leu Ser Ala
      225                     230                     235                     240
Ala Arg Pro Gly Ala Arg Ser Glu Ser Leu Glu Ser Tyr Ile Lys Arg
      245                     250                     255
Leu His Asp Leu Glu Glu Ile Ala Asn Gly Phe Glu Gly Val Gln Thr
      260                     265                     270
Ser Phe Ala Leu Gln Ala Gly Arg Glu Ile Arg Ile Met Val Asn Pro
      275                     280                     285
Gly Lys Ile Lys Asp Asp Lys Val Thr Ile Leu Ala His Lys Val Arg
      290                     295                     300
Lys Lys Ile Glu Asn Asn Leu Asp Tyr Pro Gly Asn Ile Lys Val Thr
      305                     310                     315                     320
Val Ile Arg Glu Leu Arg Ala Val Asp Tyr Ala Lys
      325                     330

```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```

Met Lys Ser Ser Gln Glu Ala Ala Glu Leu Met Leu Leu Asn Ala Glu
 1             5             10             15
Gln Glu Ala Thr Asn Leu Arg Gly Gln Ala Glu Arg Glu Ala Asp Leu
      20             25             30
Leu Val Asn Glu Ala Lys Arg Glu Ser Lys Ser Leu Lys Lys Glu Ala
      35             40             45
Leu Leu Glu Ala Lys Glu Glu Ala Arg Lys Tyr Arg Glu Glu Val Asp
      50             55             60
Ala Glu Phe Lys Ser Glu Arg Gln Glu Leu Lys Gln Ile Glu Ser Arg
      65             70             75             80
Leu Thr Glu Arg Ala Thr Ser Leu Asp Arg Lys Asp Asp Asn Leu Thr
      85             90             95
Ser Lys Glu Gln Thr Leu Glu Gln Lys Arg Thr Lys Tyr Phe Leu Ile
      100            105            110
Glu Arg Lys Thr Leu Met Arg Val Lys Ser Asn
      115            120

```

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

Met Tyr Asp Phe Lys Gly Lys Lys Phe Leu Gln Ile Leu Ile Ile Ile
 1             5             10             15
Ala Ser Met Ser Thr Pro Phe Val Gly Ala Tyr Ser Trp Ile Leu Leu
      20             25             30
Leu Gly Arg Asn Glu Val Ile Thr Lys Phe Leu Thr Asn Ala Leu Tyr
      35             40             45
Leu Pro Ala Ile Asp Ile Tyr Gly Phe Lys Gly Ile Ile Leu Val Phe
      50             55             60
Thr Leu Gln Leu Phe Pro Leu Val Phe Leu Tyr Val Ala Gly Thr Met
      65             70             75             80
Asn Ser Ile Asp Asn Ser Leu Leu Glu Ala Ala Glu Ser Met Gly Ser
      85             90             95

```

Phe Gly Phe Lys Pro Ile Val Thr Val Val Leu Pro Leu Leu Val Pro
 100 105 110
 Thr Leu Leu Ala Ala Pro Cys Leu Tyr Leu
 115 120

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Arg Ala Phe Ser Asp Phe Gly Thr Pro Met Leu Ile Gly Glu Gly
 1 5 10 15
 Tyr Arg Thr Phe Pro Val Leu Ile Tyr Thr Gln Phe Ile Ser Glu Val
 20 25 30
 Gly Gly Asn Ser Ala Phe Ala Ile Met Ala Ile Ile Ala Leu Ala
 35 40 45
 Ile Phe Leu Ile Gln Lys His Ile Ala Asn Arg Tyr Ser Phe Ser Met
 50 55 60
 Asn Leu Leu His Pro Ile Glu Pro Lys Lys Thr Thr Lys Gly Lys Met
 65 70 75 80
 Ala Ala Ile Tyr Ala Thr Val Tyr Gly Ile Ile Phe Ile Ser Val Leu
 85 90 95
 Pro Gln Ile Tyr Leu Ile Tyr Thr Ser Phe Leu Lys Thr Ser Gly Met
 100 105 110
 Val Phe Val Lys Gly Tyr Ser Pro Asn Ser Tyr Lys Val Ala Phe Asn
 115 120 125
 Arg Met Gly Ser Ala Ile Phe Asn Thr Ile Arg Ile Pro Leu Ile Ala
 130 135 140
 Leu Val Leu Val Val Pro Ile Tyr Asp Ile Tyr Leu Leu Pro Ser Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

Met Glu Ser Asn Ser Ser Leu Thr Leu Leu Lys His Gly Ser Glu Val
 1             5             10             15
Asn Leu Glu Arg Ala Leu Ser Val Asn Gly Arg Leu Gly Gly His Val
          20             25             30
Val Thr Gly His Ile Asp Gly Thr Gly Lys Ile Ser Ser Ile Lys Lys
          35             40             45
Asp Asp Asn Ala Val Trp Tyr Gln Ile Asn Thr Gln Lys Glu Ile Leu
          50             55             60
Asp Leu Ile Val Glu Lys Gly Ser Ile Thr Ile Asp Gly Ile Ser Leu
65             70             75             80
Thr Val Ala Lys Val Ser Lys Val Asn Phe Ser Val Ser Val Ile Pro
          85             90             95
His Thr Leu Lys Gln Thr Ile Leu Lys Ser Lys Gln Val Gly Ser Thr
          100            105            110
Val Asn Leu Glu Asn Asp Ile Leu Gly Lys Tyr Val Gln Lys Leu Met
          115            120            125
Asp Asn Ser Pro Lys Ser Glu Ile Ser Lys Glu Leu Leu Tyr Gln Asn
          130            135            140
Gly Phe
145

```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

Met Ser Arg Gln Thr Pro Ser Leu Ser Phe Glu Val Phe Pro Pro Asn
 1             5             10             15

```

```

Pro Ala Val Gly Asn Asp Asn Ile Ile Ser Ala Leu Gln Asp Met Gln
      20                      25                      30
Glu Leu Ala Pro His Phe Ile Ser Val Thr Ala Ser Asn Asn Lys Phe
      35                      40                      45
Asn Ile Lys Glu Thr Thr Val Arg Leu Ala Asp Phe Ile Gln Asn Asp
      50                      55                      60
Leu Ala Ile Pro Thr Ile Ala His Leu Pro Ala Ile Tyr Leu Thr Lys
      65                      70                      75                      80
Asp Lys Val Ala Glu Thr Ile Ala Asp Leu Asp Lys Val Gly Val Gln
      85                      90                      95
Lys Ile Leu Ala Leu Arg Gly Asp Ile Ile Pro Asp Val Glu Pro Gln
      100                     105                     110
Lys Asp Phe Arg Tyr Ala Thr Asp Leu Ile Glu Phe Ile Lys Glu Gln
      115                     120                     125
Thr Pro His Phe Asp Ile Ile Gly Ala Cys Tyr Pro Glu Gly His Pro
      130                     135                     140
Asp Ser Pro Asn Gln Ile Ser Asp Ile Gln Asn Leu Lys Lys Lys Val
      145                     150                     155                     160
Asp Ala Gly Cys Ser Ser Leu Val Thr Gln Leu Phe Phe Asp Asn Glu
      165                     170                     175
Arg Phe Tyr Asp Phe Gln Asp Lys Cys Ile Leu Ala Gly Ile Asp Val
      180                     185                     190
Pro Ile His Ala Gly Ile Met Pro Ile Leu Asn Arg Asn Gln Ala Leu
      195                     200                     205
Arg Leu Leu Lys Thr Cys Glu Asn Ile His Leu Pro Arg Lys Phe Lys
      210                     215                     220
Ala Ile Leu Asp Lys Tyr Glu His Asp Pro Glu Ser Leu Arg Ala Ala
      225                     230                     235                     240
Gly Leu Ala Tyr Ala Val Asp Gln Ile Val Asp Leu Val Thr Gln Asp
      245                     250                     255
Val Ala Gly Val His Leu Tyr Thr Met Asn Asn Ala Asp Thr Ala Lys
      260                     265                     270
Tyr Ile His Gln Ala Thr His Ala Leu Phe Asn His Gln Ser Leu Gly
      275                     280                     285

```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

Leu Glu Glu Leu Ala Leu Trp Phe Glu Lys Leu His Asp Phe Pro Gln
 1             5             10             15
Leu Gln Gly Asn Leu Gln Ala Phe Asn Asp Ala Gly Phe Ile Glu Asn
 20             25             30
Phe Ala Ser Glu Glu Leu Ala Arg Ile Arg Arg Lys Ile His Asp Ser
 35             40             45
Glu Ser Gln Val Arg Asp Val Leu Gln Asp Leu Leu Lys Gln Lys Ala
 50             55             60
Gln Met Leu Thr Glu Gly Ile Val Ala Ser Arg Asn Gly Arg Gln Val
 65             70             75             80
Leu Pro Val Lys Asn Thr Tyr Arg Asn Lys Ile Ala Gly Val Val His
 85             90             95
Asp Ile Ser Ala Ser Gly Asn Thr Val Tyr Ile Glu Pro Arg Glu Val
100            105            110
Val Lys Leu Ser Glu Glu Ile Ala Ser Leu Arg Ala Asp Glu Arg Tyr
115            120            125
Glu Met Leu Arg Ile Leu Gln Glu Ile Ser Glu Arg Val Arg Pro His
130            135            140
Ala Ala Glu Ile Ala Asn Asp Ala Trp Ile Ile Gly His Leu Asp Leu
145            150            155            160
Ile Arg Ala Lys Val Arg Phe Ile Gln Glu Arg Gln Ala Val Val Pro
165            170            175
Gln Leu Ser Glu Asn Gln Glu Ile Gln Leu Leu His Val Cys His Pro
180            185            190
Leu Val Lys Asn Ala Val Ala Asn Asp Val Tyr Phe Gly Gln Asp Leu
195            200            205
Thr Gly Tyr Cys His Tyr Arg Ser Gln Tyr Arg Trp Glu Asp His His
210            215            220
Ala Gln Asn Ser Gly Leu Asp Thr Gly His Gly Pro Val Arg Ile Ala
225            230            235            240
Asp Phe Ser Arg Gln Gly Lys Ser Cys Trp Tyr Phe
245            250

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Gly Ala Tyr Tyr Leu Val Met Gln Ser Leu Ser Tyr Leu Glu Tyr
 1             5             10             15
Glu Gln Gly Ile Gln Ser Thr Thr Val Arg His Leu Ile Leu Val Phe
      20             25             30
Tyr Leu Leu Phe Phe Met Gly Gly Ile Lys Lys Leu Asp Thr Tyr Leu
      35             40             45
Lys Glu Lys Leu Gln Glu Glu Leu Asn Gln Glu Gln Thr Leu Arg Tyr
      50             55             60
Arg Asp Met Glu Arg Tyr Ser Arg His Ile Glu Glu Leu Tyr Lys Glu
65             70             75             80
Ile Arg Ser Phe Arg His Asp Tyr Thr Asn Leu Leu Thr Ser Tyr Val
      85             90             95
Trp Ala Leu Lys Arg Arg Ile Trp Ser Arg
      100             105

```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

Met Ser Leu Leu Asp Phe Leu Thr Ile Val Ser Ile Leu Cys Asp Asn
 1             5             10             15
Ala Ile Lys Ala Ser Ala Glu Ala Ser Gln Pro His Val Ser Ile Ala
      20             25             30
Phe Leu Lys Asn Gly Ala Gln Glu Thr Phe Ile Ile Glu Asn Ser Ile
      35             40             45
Lys Glu Glu Gly Ile Asp Ile Ser Glu Ile Phe Ser Phe Gly Ala Ser
      50             55             60
Ser Lys Gly Glu Glu Arg Gly Val Gly Leu Tyr Thr Val Met Lys Ile
65             70             75             80

```

Val Glu Ser His Pro Asn Thr Asn Leu Asn Thr Thr Cys Gln Asn Gln
 85 90 95
 Val Phe Arg Gln Val Leu Thr Val Ile His Ala Glu
 100 105

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Leu Ile Ser Leu Gly Asn Leu Lys Met Asn His Ser Ser His Glu Val
 1 5 10 15
 Gln Ile Gly Glu Lys Met Leu Asp Leu Thr Val Lys Ser Phe Glu Leu
 20 25 30
 Leu Trp Ile Leu Ala Ser Asn Pro Glu Arg Val Phe Ser Lys Thr Asp
 35 40 45
 Leu Tyr Glu Lys Ile Trp Lys Glu Asp Tyr Val Asp Asp Thr Asn Thr
 50 55 60
 Leu Asn Val His Ile His Ala Leu Arg Gln Glu Leu Ala Lys Tyr Ser
 65 70 75 80
 Ser Asp Gln Thr Pro Thr Ile Lys Thr Val Trp Gly Leu Gly Tyr Lys
 85 90 95
 Ile Glu Lys Pro Arg Gly Gln Thr
 100

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met Ala Gln Thr Ser Lys Thr Thr Val Ser Phe Tyr Leu Asn Gly Lys
1 5 10 15
Tyr Glu Lys Met Ser Gln Glu Thr Arg Glu Lys Ile Glu Lys Val Ile
20 25 30
His Glu Thr Asn Tyr Lys Pro Ser Ile Val Ala Arg Ser Leu Lys Leu
35 40 45
Gln Thr Asn Lys Ile Asn Arg Cys Phe Asp Arg
50 55

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met	His	Tyr	Ile	Glu	Gly	Ala	Tyr	Trp	Ser	Ala	Glu	Pro	Asp	Leu	Pro
1					5				10					15	
Tyr	Leu	His	Lys	Arg	Lys	Ile	Leu	Met	Leu	Val	Glu	Asp	Val	Trp	Leu
			20					25					30		
Leu	Val	Asp	Asp	Ile	Arg	Cys	Gln	Gly	Gln	His	Glu	Ala	Leu	Thr	Gln
		35					40					45			
Phe	Ile	Leu	Asp	Lys	Asp	Val	Thr	Tyr	Gln	Asp	Gly	Lys	Ile	Asn	Gln
50						55					60				
Leu	Arg	Leu	Trp	Ser	Glu	Val	Asp	Phe	Asp	Leu	Glu	Asp	Thr	Ile	Ile
65					70					75				80	
Ser	Pro	Lys	Tyr	Asn	Glu	Leu	Glu	Arg	Ser	Ser	Lys	Leu	Thr	Lys	Arg
				85					90					95	
Gln	Phe	Phe	Glu	Asn	Gln	Met	Leu	Asp	Tyr	Thr	Ile	Ile	Ala	His	Glu
			100					105					110		
Ser	Phe	Glu	Ile	Ile	Arg	His	Ser	Val	Tyr	Gln	Thr	Asp	Asp	Arg	Glu
		115					120					125			
Val	Glu	Asn	Ala	Leu	Ala	Phe	Glu	Val	Lys	Asn	Asp	Glu	Thr	Asp	Lys
		130				135					140				
Leu	Ile	Leu	Leu	Leu	Ser	Glu	Asp	Ile	Gly	Val	Gly	Glu	Lys	Leu	Cys
145					150					155					160

Leu Val Asp Gly Thr Lys Met Arg Gly Lys Cys Leu Val Tyr Asp Lys
 165 170 175
 Ile Asn Glu Arg Met Ile Arg Leu Gln Cys
 180 185

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Met Asn Cys Glu Ala Val Ala Leu Gly Ser Phe Cys Glu Leu Lys Ser
 1 5 10 15
 Arg Arg Gly Lys Lys Gln Lys Gly Glu Ile Leu Met Ala Val Ile Ser
 20 25 30
 Met Lys Gln Leu Leu Glu Ala Gly Val His Phe Gly His Gln Thr Arg
 35 40 45
 Arg Trp Asn Pro Lys Met Ala Lys Tyr Ile Phe Thr Glu Arg Asn Gly
 50 55 60
 Ile His Val Ile Asp Leu Gln Gln Thr Val Lys Tyr Ala Asp Gln Ala
 65 70 75 80
 Tyr Xaa Phe Met Arg Asp Ala Ala Ala Asn Asp Ala Val Val Leu Phe
 85 90 95
 Val Gly Thr Lys Lys Gln Ala Ala Asp Ala Val Ala Glu Glu Ala Val
 100 105 110
 Arg Ser Gly Gln Tyr Phe Ile Asn His Arg Trp Leu Gly Gly Thr Leu
 115 120 125
 Thr Asn Trp Gly Thr Ile Gln Lys Arg Ile Ala Arg Leu Lys Glu Ile
 130 135 140
 Lys Arg Met Glu Glu Asp Gly Thr Phe Glu Val Leu Pro Lys Lys Glu
 145 150 155 160
 Val Ala Leu Leu Asn Lys Gln Arg Ala Arg Leu Glu Lys Phe Leu Gly
 165 170 175
 Gly Ile Glu Asp Met Pro Arg Ile Pro Asp Val Met Tyr Val Val Asp
 180 185 190
 Pro His Lys Glu Gln Ile Ala Val Lys Glu Ala Lys Lys Leu Gly Ile
 195 200 205

Pro Val Val Ala Met Val Asp Thr Asn Thr Asp Pro Asp Asp Ile Asp
 210 215 220
 Val Ile Ile Pro Ala Asn Asp Asp Ala Ile Arg Ala Val Lys Leu Ile
 225 230 235 240
 Thr Ala Lys Leu Ala Asp Ala Ile Ile Glu Gly Arg Gln Gly Glu Asp
 245 250 255
 Ala Val Ala Val Glu Ala Glu Phe Ala Ala Pro Glu Thr Gln Ala Asp
 260 265 270
 Ser Ile Glu Ile Val Glu Val Val Glu Gly Asp Asn Ala
 275 280 285

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Lys Gln Leu Ile Ser Leu Lys Asn Ile Phe Arg Ser Tyr Arg Asn
 1 5 10 15
 Gly Asp Gln Glu Leu Gln Val Leu Lys Asn Ile Asn Leu Glu Val Asn
 20 25 30
 Glu Gly Glu Phe Val Ala Ile Met Gly Pro Ser Gly Ser Gly Lys Ser
 35 40 45
 Thr Leu Met Asn Thr Ile Gly Met Leu Asp Thr Pro Thr Ser Gly Glu
 50 55 60
 Tyr Tyr Leu Glu Gly Gln Glu Val Ala Gly Leu Gly Glu Lys Gln Leu
 65 70 75 80
 Ala Lys Val Arg Asn Gln Gln Ile Gly Phe Val Phe Gln Gln Phe Phe
 85 90 95
 Leu Leu Ser Lys Leu Asn Ala Leu Gln Asn Val Lys Leu Pro Leu Ile
 100 105 110
 Tyr Ala Gly Val Ser Ser Ser Lys Arg Arg Lys Leu Ala Glu Glu Tyr
 115 120 125
 Leu Asp Lys Val Glu Leu Ile Glu Arg Ser His His Leu Pro Ser Glu
 130 135 140
 Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Val
 145 150 155 160

Asn Asn Pro Ser Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
 165 170 175
 Thr Lys Thr Gly Asn Gln Ile Met Gln Leu Leu Val Asp Leu Asn Lys
 180 185 190
 Glu Arg Lys Asn His Tyr His Gly Asn Ala
 195 200

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Thr Ser Val Ile Lys Trp Thr Leu Arg Lys Leu Phe Gln Ser Gln
 1 5 10 15
 Pro Phe Arg Gly Asn Asn Val Ser Arg Leu Val Asp Ile Leu Ser Glu
 20 25 30
 Asn Leu Asp Glu Gly Phe Gln Tyr Phe Pro Ser Asp Gln Ile Thr Asp
 35 40 45
 His Pro Glu Arg Phe Leu Val Ser Glu Met Val Arg Glu Lys Val Leu
 50 55 60
 His Leu Thr Arg Glu Glu Ile Pro His Ser Val Ala Val Val Val Asp
 65 70 75 80
 Ser Met Lys Arg Asp Glu Glu Thr Asp Lys Val His Ile Arg Ala Thr
 85 90 95
 Ile Met Val Glu Arg Asp Ser Gln Lys Gly Ile Ile Ile Gly Lys Gly
 100 105 110
 Gly Ala Met Leu Lys Lys Ile Gly Ser Met Ala Arg Arg Asp Ile Glu
 115 120 125
 Leu Met Leu Gly Asp Lys Val Phe Leu Glu Thr Trp Val Lys Val Lys
 130 135 140
 Lys Asn Trp Arg Asp Lys Lys Leu Asp Leu Ala Asp Leu Gly Tyr Asn
 145 150 155 160
 Glu Arg Glu Tyr

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```

Met Thr Phe Lys Ser Gly Phe Val Ala Ile Leu Gly Arg Pro Asn Val
 1             5             10             15
Gly Lys Ser Thr Phe Leu Asn His Val Met Gly Gln Lys Ile Ala Ile
      20             25             30
Met Ser Asp Lys Ala Gln Thr Thr Arg Asn Lys Ile Met Gly Ile Tyr
      35             40             45
Thr Thr Asp Lys Glu Gln Ile Val Phe Ile Asp Thr Pro Gly Ile His
      50             55             60
Lys Pro Lys Thr Ala Leu Gly Asp Phe Met Val Glu Ser Ala Tyr Ser
      65             70             75             80
Thr Leu Arg Glu Val Asp Thr Val Leu Phe Met Val Pro Ala Asp Glu
      85             90             95
Ser Arg Gly Lys Gly Asp Asp Met Ile Ile Glu Arg Leu Lys Ala Ala
      100            105            110
Lys Val Pro Val Ile Leu Val Val Asn Lys Ile Asp Lys Val His Pro
      115            120            125
Asp Gln Leu Leu Ser Gln Ile Asp Asp Phe Arg Asn Gln Met Asp Phe
      130            135            140
Lys Glu Ile Val Pro Ile Ser Ala Leu Gln Gly Lys
      145            150            155

```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```

Met Thr Glu Ile Arg Leu Glu His Val Ser Tyr Ala Tyr Gly Gln Glu
 1           5           10           15
Arg Ile Leu Glu Asp Ile Asn Leu Gln Val Thr Ser Gly Glu Val Val
      20           25           30
Ser Ile Leu Gly Pro Ser Gly Val Gly Lys Thr Thr Leu Phe Asn Leu
      35           40           45
Ile Ala Gly Ile Leu Glu Val Gln Ser Gly Arg Ile Val Leu Asp Gly
      50           55           60
Glu Glu Asn Pro Lys Gly His Val Ser Tyr Met Leu Gln Lys Asp Leu
      65           70           75           80
Leu Leu Glu His Lys Thr Val Leu Gly Asn Ile Ile Leu Pro Leu Leu
      85           90           95
Ile Gln Lys Val Asp Lys Ala Glu Ala Ile Ser Arg Ala Asp Lys Ile
      100           105           110
Leu Ala Thr Phe Gln Leu Thr Ala Val Arg Asp Lys Tyr Pro His Glu
      115           120           125
Leu Ser Gly Gly Met Arg Gln Arg Val Ala Leu Leu Arg Thr Tyr Leu
      130           135           140
Phe Gly His Lys Asn Arg Asn Pro
145           150

```

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```

Met Thr Lys Met Glu Leu His Ala Trp Tyr Leu Glu Ile His Lys Gln
 1           5           10           15
Leu Gln Leu Thr Thr Leu Ile Xaa Thr His Ser Ile Glu Glu Ala Leu
      20           25           30
Xaa Leu Ser Asp Arg Ile Tyr Ile Leu Xaa Asn Xaa Pro Gly Gln Ile
      35           40           45
Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Xaa Glu Val
      50           55           60

```

Xaa Lys Ile Ala Xaa Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu Asp
 65 70 75 80
 Lys

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met Arg Cys Lys Met Leu Asp Pro Ile Ala Ile Gln Leu Gly Pro Leu
 1 5 10 15
 Ala Ile Arg Trp Tyr Ala Leu Cys Ile Val Thr Gly Leu Ile Leu Ala
 20 25 30
 Val Tyr Leu Thr Met Lys Glu Ala Pro Arg Lys Lys Ile Ile Pro Asp
 35 40 45
 Asp Ile Leu Asp Phe Ile Leu Val Ala Phe Pro Leu Ala Ile Leu Gly
 50 55 60
 Ala Arg Leu Tyr Tyr Val Ile Phe Arg Phe Asp Tyr Tyr Ser Gln Asn
 65 70 75 80
 Leu Gly Glu Ile Phe Ala Ile Trp Asn Gly Gly Leu Ala Ile Tyr Gly
 85 90 95
 Gly Leu Ile Thr Gly Ala Leu Val Leu Tyr Ile Phe Ala Asp Arg Lys
 100 105 110
 Leu Ile Asn Thr Trp Asp Phe Leu Asp Ile Ala Ala Pro Ser Val Met
 115 120 125
 Ile Ala Gln Ser Leu Gly Arg Trp Gly Asn Phe Phe Asn Gln Glu Ala
 130 135 140
 Tyr Gly Ala Thr Val Asp Asn Leu Asp Tyr Leu Pro Gly Phe Ile Arg
 145 150 155 160
 Asp Gln Met Tyr Ile Glu Gly Ser Tyr Arg Gln Pro Thr Phe Leu Tyr
 165 170 175
 Glu Ser Leu Trp Asn Leu Leu Gly Phe Ala Leu Ile Leu Ile Phe Arg
 180 185 190
 Arg Lys Trp Lys Ser Leu Arg Arg Gly His Ile Thr Ala Phe Tyr Leu
 195 200 205
 319

```

Ile Trp Tyr Gly Phe Gly Arg Met Val Ile Glu Gly Met Arg Thr Asp
 210                      215                      220
Ser Leu Met Phe Phe Gly Leu Arg Val Ser Gln Trp Leu Ser Val Val
 225                      230                      235                      240
Phe Ile Gly Leu Gly Ile Met Ile Val Ile Tyr Gln Asn Arg Lys Lys
                      245                      250                      255
Ala Pro Tyr Tyr Ile Thr Glu Glu Glu Asn
                      260                      265

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Met Ser Lys Ile Ile Asp Arg Tyr Arg Pro Ala Gly Glu Gly Phe Val
 1                      5                      10                      15
Arg Ile Asp Thr Gln Asn Asn Met Pro Thr Ala Ala Gly Leu Ser Ser
                      20                      25                      30
Ser Ser Ser Gly Leu Ser Ala Leu Val Lys Ala Cys Asn Ala Tyr Phe
                      35                      40                      45
Lys Leu Gly Leu Asp Arg Ser Gln Leu Ala Gln Glu Ala Lys Phe Ala
                      50                      55                      60
Ser Gly Ser Ser Ser Arg Ser Phe Tyr Gly Pro Leu Gly Ala Trp Asp
 65                      70                      75                      80
Lys Asp Ser Gly Glu Ile Tyr Pro Val Glu Thr Asp Leu Lys Leu Ala
                      85                      90                      95
Met Ile Met Leu Val Leu Glu Asp Lys Lys Lys Pro Ile Ser Ser Arg
                      100                      105                      110
Asp Gly Met Lys Leu Cys Val Glu Thr Ser Thr Thr Phe Asp Asp Trp
                      115                      120                      125
Val Arg Gln Ser Glu Lys Asp Tyr Gln Asp Met Leu Ile Tyr Leu Lys
                      130                      135                      140
Glu Asn Asp Phe Ala Lys Ile Gly Glu Leu Thr Glu Lys Asn Ala Leu
 145                      150                      155                      160
Ala Met His Ala Thr Thr Lys Thr Ala Ser Pro Ala Phe Ser Tyr Leu
                      165                      170                      175

```

320

Thr Asp Ala Ser Tyr Glu Ala Met Ala Phe Val Arg Gln Leu Arg Glu
 180 185 190
 Lys Gly Glu Ala Cys Tyr Phe Thr Met Asp Ala Gly Pro Asn Val Lys
 195 200 205
 Val Phe Cys Gln Glu Lys Asp Leu Glu His Leu Ser Glu Ile Phe Gly
 210 215 220
 Gln Arg Tyr Arg Leu Ile Val Ser Lys Thr Lys Asp Leu Ser Gln Asp
 225 230 235 240
 Asp Cys Cys

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Met His Asn Gly Phe Val Asn Ile Asp Asn Val Lys Met Ser Lys Ser
 1 5 10 15
 Leu Gly Asn Phe Ile Thr Val His Asp Ala Leu Lys Thr Leu Asp Gly
 20 25 30
 Gln Val Leu Arg Phe Phe Phe Ala Thr Gln His Tyr Arg Lys Pro Ile
 35 40 45
 Asn Phe Thr Glu Lys Ala Val Arg Asp Ala Glu Thr Asn Leu Lys Tyr
 50 55 60
 Leu Lys Asn Thr Tyr Glu Gln Pro Phe Thr Gly Asn Val Asp Ala Gln
 65 70 75 80
 Glu Leu Gln Asn Phe Lys Asp Lys Phe Val Ala Ala Met Asp Glu Asp
 85 90 95
 Phe Asn Ala Ala Asn Gly Ile Thr Val Val Phe Glu Met Ala Lys Trp
 100 105 110
 Ile Asn Ser Gly Asn Tyr Asp Ala Ser Val Lys Gln Ala Leu Ala Asp
 115 120 125
 Met Leu Glu Ile Phe Gly Ile Val Phe Val Glu Glu Val Leu Asp Ala
 130 135 140
 Glu Ile Glu Asp Leu Ile Gln Lys Arg Gln Glu Ala Arg Ala Asn Arg
 145 150 155 160

Asp Phe Glu Thr Ala Asp Gln Ile Arg Asp Gln Leu Val Thr Gln Gly
 165 170 175
 Ile Lys Leu Leu Asp Thr Lys Asp Gly Val Arg Trp Thr Arg Asp
 180 185 190

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Met Lys Arg Thr Gly Leu Phe Thr Lys Ile Phe Ile Tyr Thr Phe Ser
 1 5 10 15
 Ile Phe Ser Val Leu Val Ile Cys Leu His Leu Ala Ile Tyr Phe Leu
 20 25 30
 Phe Pro Ser Thr Tyr Leu Ser His Arg Gln Glu Thr Ile Gly Gln Lys
 35 40 45
 Ala Thr Ala Ile Ala Gln Ser Leu Glu Gly Lys Asp Arg Gln Ser Ile
 50 55 60
 Glu Gln Val Leu Asp Leu Tyr Ser Gln Thr Ser Asp Ile Lys Gly Thr
 65 70 75 80
 Val Lys Gly Glu Met Thr Glu Asp Lys Leu Glu Val Lys Asp Ser Leu
 85 90 95
 Pro Leu Asp Thr Asp Arg Gln Thr Thr Ser Leu Phe Ile Glu Glu Arg
 100 105 110
 Glu Val Lys Thr Gln Asp Gly Gly Thr Met Ile Leu Gln Phe Leu Ala
 115 120 125
 Ser Met Asp Leu Gln Lys Glu Ala Glu Gln Ile Ser Leu Gln Phe Leu
 130 135 140
 Pro Tyr Thr Leu Leu Ala Ser Phe Leu Ile Ser Leu Leu Val Ala Tyr
 145 150 155 160
 Ile Tyr Ala Arg Thr Ile Val Ala Pro Ile Leu Glu Ile Lys Arg Val
 165 170 175
 Thr Arg Arg Met Met Asp Leu Asp Ser Gln Val Arg Leu Arg Val Asp
 180 185 190
 Ser Lys Asp Glu Ile Gly Asn Leu Lys Glu Gln Ile Asn Ser Leu Tyr
 195 200 205

Gln His Leu Leu Thr Val Ile Ala Asp Leu His Glu Lys Asn Glu Ala
 210 215 220
 Ile Leu Gln Leu Glu Lys Met Lys Val Glu Phe Leu Gln Gly Ala Ser
 225 230 235 240
 His Glu Leu Lys His Thr Ala Gly
 245

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Leu Leu Glu Ser Tyr Ser Arg Glu Gln Val Asn Phe Phe Val Asp Gln
 1 5 10 15
 Gly Ala Val Thr Ile Val Gln Lys Glu Val Arg Arg Ser Ala Ala Tyr
 20 25 30
 Phe Glu Gly Ile Glu Ala Ser Arg Pro Leu Glu Leu Asn Pro Glu Gln
 35 40 45
 Arg Gln Ala Arg Asp Ala Val Ser Ser Ile Gly Ser Ser Gln Pro
 50 55 60
 Pro Phe Leu Leu Gln Gly Ile Thr Gly Ser Gly Lys Thr Glu Val Tyr
 65 70 75 80
 Leu Gln Ile Ile Gln Gly Ala Leu Asp Lys Gly Lys Thr Ala Ile Leu
 85 90 95
 Leu Val Pro Glu Ile Ser Leu Thr Pro Gln Met Thr Glu Arg Phe Ile
 100 105 110
 Ala Arg Phe Gly Asp Lys Val Ala Ile Leu His Ser Gly Leu Ser Asn
 115 120 125
 Gly Glu Lys Tyr Asp Glu Trp Arg Lys Val Glu Arg Gly Asp Ala Gln
 130 135 140
 Val Val Val Gly Ala Arg Ser Ala Ile Phe Ala Pro Leu Lys Asn Leu
 145 150 155 160
 Gly Val Met Ile Ile Asp Glu Glu His Glu Ala Ala Tyr Lys Gln Asp
 165 170 175
 Ser Asn Pro Arg Tyr His Ala Arg Glu Val Ala Ile Leu Arg Ala Arg
 180 185 190
 323

Tyr Asn Gln Ala Thr Leu Val Leu Gly Ser Ala Thr Pro Ser Leu Glu
 195 200 205
 Ser Arg Ala Arg Ala Gly Lys Gly Val Tyr Gln His Leu Arg Leu Thr
 210 215 220
 Gln Arg Ala Asn Pro Leu Ala Thr Ile Pro Glu Val Ser Ser Asp
 225 230 235

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Cys Met Val Met Gln Leu Leu Gly His Gln Leu Val Leu Ile Gly
 1 5 10 15
 Phe Lys Gly Ser Arg Lys Cys Thr Pro Phe Ala Ala Gln Met Ala Ser
 20 25 30
 Glu Ala Ala Ala Lys Ser Ala Gln Glu His Gly Leu Lys Ser Val Glu
 35 40 45
 Val Thr Val Lys Gly Pro Gly Ser Gly Arg Glu Ser Ala Ile Arg Ala
 50 55 60
 Leu Ala Ala Ala Gly Leu Glu Val Thr Ala Ile Arg Asp Val Thr Pro
 65 70 75 80
 Val Pro His Asn Gly Ala Arg Pro Pro Lys Arg Arg Arg Val
 85 90

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

Met Ile Ser Leu Pro Glu Asn Leu Phe Ala Asn Ala Lys Gln Ser Lys
  1                      5                      10                      15
Thr Ile Phe Ile Leu Gln Lys Lys Ser Glu Ile Ala Val Glu Pro Phe
      20                      25                      30
Val Tyr Pro Leu Ala Ser Leu Gln Asp Ala Ser Val Leu Met Lys Phe
      35                      40                      45
Lys Glu Asn Phe Gln Lys Trp Thr Gln Gly Thr Glu Ile
      50                      55                      60

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met	Gly	Lys	Phe	Arg	Gln	Ser	Gln	Pro	Ser	Val	Ser	Asn	Asn	Gly	Leu
1				5					10					15	
Ala	Thr	Val	Val	Pro	Ser	Val	Arg	Glu	Gly	Glu	Pro	Val	Arg	Val	Ile
			20					25					30		
Ala	Lys	Ala	Glu	Asn	Gly	Asp	Ile	Leu	Gly	Glu	Tyr	Arg	Leu	His	Phe
		35					40					45			
Thr	Lys	Asp	Lys	Asn	Leu	Leu	Ser	His	Lys	Pro	Val	Ala	Ala	Val	Lys
	50					55					60				
Gln	Ala	Arg	Leu	Leu	Gln	Val	Gly	Gln	Ala	Leu	Glu	Leu	Pro	Thr	Lys
65					70					75				80	
Val	Pro	Val	Tyr	Phe	Thr	Gly	Lys	Asp	Gly	Tyr	Glu	Thr	Lys	Asp	Leu
				85					90					95	
Ser	Val	Glu	Trp	Glu	Glu	Val	Pro	Ala	Glu	Asn	Leu	Thr	Lys	Ala	Gly
		100						105					110		
Gln	Phe	Thr	Val	Arg	Gly	His	Val	Leu	Gly	Ser	Asp	Leu	Val	Ala	Glu
		115					120					125			
Val	Thr	Val	Arg	Val	Thr	Asp	Lys	Leu	Gly	Glu	Ala	Leu	Ser	Asp	Asn
	130						135				140				
Pro	Asn	Tyr	Asp	Glu	Asn	Ser	Asn	Gln	Ala	Phe	Ala	Ser	Ala	Thr	Asn
145					150					155					160

```

Asp Ile Asp Lys Asn Ser His Asp Arg Val Asp Tyr Leu Asn Asp Gly
      165                      170                      175
Asp His Ser Glu Asn Arg Arg Trp Thr Asn Trp Ser Pro Thr Pro Ser
      180                      185                      190
Ser Asn Pro Glu Val Ser Ala Gly Val Ile Phe Arg Glu Asn Gly Lys
      195                      200                      205
Ile Val Glu Arg Thr Val Ala Gln Ala Lys Leu His Phe Phe Ala Asp
      210                      215                      220
Ser Gly Thr Asp Ala Pro Thr Lys Leu Val Leu Glu Arg Tyr Val Gly
      225                      230                      235                      240
Pro Glu Phe Glu Val Pro Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp
      245                      250                      255
Ala Asp His Pro Phe Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr
      260                      265                      270
Arg Ala Asp Lys Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe
      275                      280                      285
Lys Ala Val Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala
      290                      295                      300
Asp Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser
      305                      310                      315                      320
Glu Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys
      325                      330                      335
Glu Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr
      340                      345                      350
Lys Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala
      355                      360                      365
Ser Thr Val Val Asp Ser Gly Glu Asp Cys Leu Pro Val Leu Val Arg
      370                      375                      380
Leu Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Tyr Pro Val
      385                      390                      395                      400
Asp

```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

Met Asn Ile Gln Glu Glu Ile Lys Lys Arg Arg Thr Phe Ala Ile Ile
 1           5           10           15
Ser His Pro Asp Ala Gly Lys Thr Thr Ile Thr Glu Gln Leu Tyr
          20           25           30
Phe Gly Gly Glu Ile Arg Glu Ala Gly Thr Val Lys Gly Lys Lys Thr
          35           40           45
Gly Thr Phe Ala Lys Ser Asp Trp Met Asp Ile Glu Lys Gln Arg Gly
          50           55           60
Ile Ser Val Thr Ser Ser Val Met Gln Phe Asp Tyr Asp Gly Lys Arg
          65           70           75           80
Val Asn Ile Leu Asp Thr Pro Gly His Glu Asp Phe Ser Glu Asp Thr
          85           90           95
Tyr Arg Thr Leu Met Ala Val Asp Ala Ala Val Met Val Val Asp Ser
          100          105          110
Ala Lys Gly Ile Glu Ala Gln Thr Lys Lys Leu Phe Glu Val Val Lys
          115          120          125
His Arg Gly Ile Pro Val Phe Thr Phe Met Asn Lys Leu Asp Arg Asp
          130          135          140
Gly Arg Glu Pro Leu Asp Leu Leu Gln Glu Leu Glu Glu Ile Leu Gly
          145          150          155          160
Ile Ala Ser Tyr Pro Met Asn Trp Pro Ile Gly Met Gly Lys Ala Phe
          165          170          175
Glu Gly Leu Tyr Asp Leu Tyr Asn Gln Arg Leu Glu Leu Tyr Lys Gly
          180          185          190
Asp Glu Arg Phe Ala Ser Pro Arg Arg Trp Arg Gln Thr Phe Trp
          195          200          205

```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```

Met Leu Ile Asn Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys Arg Ile
 1           5           10           15

```

Glu Glu Val Phe Ala Glu Ser Pro Glu Asn Ile His Ser Glu Leu Glu
 20 25 30
 Gln Lys Gln Val Thr Ser Gly Arg Val Leu Gln Val Gln Glu Leu Thr
 35 40 45
 Phe Thr Tyr Pro Asp Ala Ala Gln Pro Ser Leu Arg Asp Ile Ser Phe
 50 55 60
 Asp Met Thr Gln Gly Gln Ile Leu Gly Ile Ile Gly Gly Thr Gly Ser
 65 70 75 80
 Gly Lys Ser Ser Leu Val Gln Leu Leu Leu Gly Leu Tyr Pro Val Asp
 85 90 95
 Lys Gly Asn Ile Asp Leu Tyr Gln Asn Gly Arg Ser Pro Leu Asn Leu
 100 105 110
 Glu Gln Trp Arg Ser Trp Ile Ala Tyr Val Pro Gln Lys Val Lys Leu
 115 120 125
 Phe Lys Gly Thr Ile Arg Ser Asn Leu Thr Leu Gly Leu Asn Gln Glu
 130 135 140
 Val Ser Asp Gln Lys Leu Trp Gln Ala Leu Glu Ile Ala Gln Ala Lys
 145 150 155 160
 Asp Phe Val Ser Glu Lys Glu Gly Leu Leu Asp Ala Leu Ile Glu Ala
 165 170 175
 Gly Gly Arg Asn Phe Ser Gly Gly Gln Lys Gln Arg Leu Ser Ile Ala
 180 185 190
 Arg Ala Val Leu Arg Gln Ala Pro Phe Ile Ile Leu Asp Asp Ala Thr
 195 200 205
 Ser Ala Leu Asp Thr Ile Thr Glu Ser Lys Leu Leu Lys Ala Ile Arg
 210 215 220
 Glu Asn Phe Pro Asn Thr Ser Leu Ile Leu Ile Ser Gln Arg Thr Ser
 225 230 235 240
 Thr Leu Gln Met Ala Asp Gln Ile Leu Leu Leu Glu Lys Gly Glu Leu
 245 250 255
 Leu Ala Val Gly Lys His Asp Asp Leu Met Lys Ser Ser Gln Val Tyr
 260 265 270
 Arg Glu Ile Asn Ala Ser Gln His Gly Lys Glu Asp
 275 280

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```

Met Ile Asp Asp Ala Gly Val Gly Val Lys Ile Leu Thr Ser Ser Lys
 1             5             10             15
Asp Ala Asn Asp Leu Leu Glu Lys Lys Ile Asp Gly Leu Ile Glu Lys
          20             25             30
Phe Lys His Ala Tyr Ala Asn Val Lys Ile Glu Lys Leu Glu Thr Ile
          35             40             45
Asn Ser Lys Glu Ile Glu Arg Lys Trp
 50             55

```

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

```

Met Thr Gly Ala Gly Phe Gly Gly Cys Ala Ile Ala Leu Val Gln Lys
 1             5             10             15
Asp Thr Val Glu Ala Phe Lys Glu Ala Val Gly Lys Leu Tyr Lys Glu
          20             25             30
Val Val Gly Tyr Pro Xaa Ser Leu Leu Tyr Arg
          35             40

```

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Met Ala Gln His Leu Thr Thr Glu Ala Leu Arg Lys Asp Phe Leu Ala
 1 5 10 15
 Val Phe Gly Gln Glu Ala Asp Gln Thr Phe Phe Ser Pro Gly Arg Ile
 20 25 30
 Asn Leu Ile Gly Glu His Thr Asp Tyr Asn Gly Gly His Val Phe Thr
 35 40 45
 Trp Cys Tyr Phe Leu Gly Asn Leu Arg Cys Ser Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Thr Asp Arg Tyr Asn Tyr Glu Ala Val Gln Met Ala Phe Leu Pro
 1 5 10 15
 Thr Lys Gln Arg Ala Asn Met Gly Phe Gly Ile Cys Gly Phe Ala Asn
 20 25 30
 Thr Val Asp Thr Leu Ser Ala Ile Lys Tyr Ala Thr Val Lys Pro Ile
 35 40 45
 Arg Asp Glu Asp Gly Tyr Ile Tyr Asp Tyr Glu Thr Ile Gly Asp Tyr
 50 55 60
 Pro Arg Trp Gly Glu Asp Asp Pro Arg Ser Asn Glu Leu Ala Glu Trp
 65 70 75 80
 Leu Ile Glu Ala Tyr Thr Thr Arg Leu Arg Ser His Lys Leu Tyr Lys
 85 90 95
 Asp Ala Glu Ala Thr Val Ser Leu Leu Thr Ile Thr Ser Asn Val Ala
 100 105 110
 Tyr Ser Lys Gln Thr Gly Asn Ser Pro Val His Lys Gly Val Tyr Leu
 115 120 125
 Asn Glu Asp Gly Ser Val Asn Leu Ser Lys Leu Glu Phe Phe Ser Pro
 130 135 140
 Gly Ala Asn Pro Ser Asn Lys Ala Lys Gly Gly Trp Leu Gln Asn Leu
 145 150 155 160

Asn Ser Leu Ser Ser Leu Asp Phe Ser Tyr Ala Ala Asp Gly Ile Ser
 165 170 175
 Leu Thr Thr Gln Val Ser Pro Arg Ala Leu Gly Lys Thr Arg Asp Glu
 180 185 190
 Gln Val Asp Asn Leu Val Thr Ile Leu Asp Gly Tyr Phe Glu Asn Gly
 195 200 205
 Gly Gln His Val Asn Leu Asn Val Met Asp Leu Asn Asp Val Tyr Glu
 210 215 220
 Lys Ile Met Ser Gly Glu Asp Val Ile Val Arg Ile Ser Gly Tyr Cys
 225 230 235 240
 Val Asn Thr Lys Tyr Leu Thr Pro Glu Gln Lys Thr Glu Leu Thr Gln
 245 250 255
 Arg Val Phe His Glu Val Leu Ser Met Asp Asp Ala Leu Asp Ala Leu
 260 265 270
 Ser Ser Asn Pro Ala Ala Pro Gly Ser His
 275 280

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met Met Ile Ala Leu Asp Val Val Leu Thr Pro Ile Phe Arg Ile Glu
 1 5 10 15
 Gly Met Ala Pro Met Ser Ser Val Val Asn Ile Leu Ala Gly Ile Met
 20 25 30
 Met Gly Pro Val Tyr Ala Leu Ala Met Ala Thr Val Thr Ala Phe Ile
 35 40 45
 Arg Met Thr Thr Gln Gly Tyr Ser Asp Lys Leu Leu Tyr Leu Ser Gln
 50 55 60
 Glu Arg Leu Leu Glu Pro Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```

Met Thr Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu
 1           5           10           15
Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu Trp Val Tyr Asp Ser His
          20           25           30
Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Ala Lys Asn
          35           40           45
Glu Thr Val Asp Gly Tyr Gln Leu Glu Ser Asp Gly Lys Trp Leu Gly
          50           55           60
Gly Lys Ala Thr Asn Glu Asn Ala Ala Tyr Tyr Gln Val Val Pro Val
65           70           75           80
Thr Ala Asn Val Tyr Asp Ser Asp Gly Gly Lys Ala Phe Pro Ile Tyr
          85           90           95
Arg Lys Val Val Ser Tyr Gly
          100

```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

Leu Asp His Thr Ile Phe Cys Val Gly Tyr Arg Val Met Gln Lys Asp
 1           5           10           15
Leu Glu Gly Thr Leu Asp Ala Glu Lys Leu Lys Ala Ala Gly Val Pro
          20           25           30
Phe Gly Pro Leu Phe Gly Lys Ile Lys Asn Gly Gln Asp Leu Val Leu
          35           40           45

```

Glu Asp Gly Thr Glu Ile Lys Ala Ala Asp Tyr Ile Ser Ala Pro Arg
 50 55 60
 Pro Gly Lys Ile Ile Thr Ile Leu Gly Asp Thr Arg Lys Thr Asp Ala
 65 70 75 80
 Ser Val Arg Leu Ala Val Asn Ala Asp Val Leu Val His Glu Ser Thr
 85 90 95
 Tyr Gly Lys Gly Asp Glu Lys Ile Ala Arg Asn His Gly His Ser Thr
 100 105 110
 Asn Met Gln Ala Ala Gln Val Ala Val Glu Ala Gly Ala Lys Arg Leu
 115 120 125
 Leu Leu Asn His Ile Ser Ala Arg Phe Leu Ser Lys Asp Ile Ser Lys
 130 135 140
 Leu Lys Lys Asp Ala Ala Thr Ile Phe Glu Asn Val His Val Val Lys
 145 150 155 160
 Asp Leu Glu Glu Val Glu Ile
 165

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met Pro Thr Ile Leu Ile Thr Gly Ala Ser Gly Gly Leu Ala Gln Glu
 1 5 10 15
 Met Val Lys Leu Leu Pro Asn Asp Gln Leu Ile Leu Leu Gly Arg Asn
 20 25 30
 Lys Glu Lys Leu Ala Gln Leu Tyr Gly Asn Tyr Ser His Ala Glu Leu
 35 40 45
 Ile Glu Ile Asp Ile Thr Asp Asp Ser Ala Leu Glu Ala Leu Val Thr
 50 55 60
 Asp Leu Tyr Leu Arg Tyr Gly Lys Ile Asp Val Leu Ile Asn Asn Ala
 65 70 75 80
 Gly Tyr Gly Ile Phe Glu Gly Phe Asp Gln Ile Ala Asp Lys Asp Ile
 85 90 95
 His Gln Met Phe Glu Val Asn Thr Phe Ala Leu Met Asn Leu Ser Arg
 100 105 110
 333

His Leu Ala Ala Arg Met Lys Glu Ser Ser Lys Gly His Ile Ile Asn
 115 120 125
 Ile Val Ser Met Ala Gly Leu Ile Ala Thr Gly Lys Ser Ser Leu Tyr
 130 135 140
 Ser Ala Thr Lys Phe Ala Ala Ile Gly Phe Ser Asn Ala Leu Arg Leu
 145 150 155 160
 Glu Leu Met Pro Tyr Gly Val Tyr Val Thr Thr Val Asn Pro Gly Pro
 165 170 175
 Ile Arg Thr Gly Phe Phe Asp Gln Ala Asp Pro Asp Gly Thr Tyr Leu
 180 185 190
 Lys Ser Val Asp Arg Phe Leu Leu Glu Ala Asp Ala Val Ala Lys Lys
 195 200 205
 Ile Val Lys Ile Ile Gly Lys Asn Lys Arg Glu Leu Asn Leu Pro Ile
 210 215 220
 Leu Leu Asn Leu Ala His Lys Phe Tyr Thr Leu Phe Pro Lys Leu Ala
 225 230 235 240
 Asp Lys Leu Ala Gly Glu Thr Phe Asn Tyr Lys
 245 250

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Ser Cys Leu Val Trp Asp Gln Ser Gln Gln Lys Asn Asn Ala Lys
 1 5 10 15
 Leu Gly Ile Glu Asn Leu Gln Asp Leu Leu Leu Tyr Phe Pro Phe Arg
 20 25 30
 Tyr Glu Asp Phe Lys Thr Lys Gln Val Leu Glu Leu Glu Asp Gly Glu
 35 40 45
 Lys Ala Val Leu Ser Gly Gln Val Val Thr Pro Ala Ser Val Gln Tyr
 50 55 60
 Tyr Gly Phe Lys Arg Asn Arg Leu Arg Phe Ser Leu Lys Gln Gly Glu
 65 70 75 80
 Val Val Phe Ala Val Asn Phe Phe Asn Gln Pro Tyr Leu Ala Asp Lys
 85 90 95

Ile Glu Leu Gly Ala Thr Leu Ala Val Phe Gly Lys Trp Asp Arg Ala
 100 105 110
 Lys Gly

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Met Lys Val Leu Ala Gln Val Glu Asp Asp Leu Gln Pro Val Tyr Arg
 1 5 10 15
 Leu Ala Gln Gly Ile Ser Gln Ala Ser Leu Val Lys Val Ile Lys Thr
 20 25 30
 Ala Phe Asp Gln Gly Leu Asp Leu Leu Ile Glu Glu Asn Leu Pro Gln
 35 40 45
 Ser Leu Leu Asp Lys Tyr Lys Leu Met Ser Arg Cys Gln Ala Val Arg
 50 55 60
 Ala Met His Phe Pro Lys Asp Leu Ala Glu Asn Lys Gln Ala Leu Arg
 65 70 75 80
 Arg Ile Lys Phe Glu Glu Leu Phe Tyr Phe Gln Met Gln Leu Gln Thr
 85 90 95
 Leu Lys Ser Glu Asn Arg Val Gln Gly Ser Gly Leu Val Leu Asp Trp
 100 105 110
 Ser Gln Glu Lys Val Thr Ala Val Lys Ala Ser Leu Pro Phe Ala Leu
 115 120 125
 Thr Gln Ala Gln Glu Lys Ser Leu Gln Glu Ile Leu Thr Asp Met Lys
 130 135 140
 Ser Asp His His Met Asn Arg Leu Leu Gln Gly Asp Val Gly Ser Gly
 145 150 155 160
 Lys Thr Val Val Ala Gly Leu Ala Met Phe Ala Ala Val Thr Ala Gly
 165 170 175
 Tyr Gln Ala Ala Leu Met Val Pro Thr Glu Ile Leu Ala Glu Gln His
 180 185 190
 Phe Glu Ser Leu Gln Asn Leu Phe Pro Asn Leu Lys Leu Ala Leu Leu
 195 200 205
 335

```

Thr Gly Ser Leu Lys Ala Ala Glu Lys Arg Glu Val Leu Glu Thr Ile
 210                      215                      220
Ala Lys Gly Glu Ala Asp Leu Ile Ile Gly Thr His Ala Leu Ile Gln
225                      230                      235                      240
Asp Gly Val Glu Tyr Ala Arg Leu Gly Leu Ile Ile Ile Asp Glu Gln
                      245                      250                      255
His Arg Phe Gly Val Gly Gln Arg Arg Ile Leu Arg Glu Lys Gly Asp
                      260                      265                      270
Asn Pro Asp Val Leu Met Met Thr Ala Thr Pro Ile Pro Arg Thr Leu
                      275                      280                      285
Ala Ile Thr Ala Phe Gly Asp Met Asp Val Ser Ile Ile Asp Gln Met
290                      295                      300
Pro Ala Gly Arg Lys Pro Ile Val Thr Arg Trp Ile Lys His Glu Gln
305                      310                      315                      320
Leu Pro Gln Val Leu Thr Trp Leu Glu Gly Glu Ile Gln Lys Gly Ser
                      325                      330                      335
Gln Val Tyr Val Ile Ser Pro Leu Ile Glu Glu Ser Gln Ala Pro Arg
                      340                      345                      350
Phe Glu Lys Met Pro Leu Pro Tyr Gln Arg Ser
355                      360

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

Met Lys Asp Leu Val Gln Lys Leu Ala Ser Lys Glu Glu Leu Ser Thr
 1                      5                      10                      15
Ala Asp Asn Glu Met Ile Glu Leu Leu Ala Arg Phe Asn Glu Arg Gln
                      20                      25                      30
Ala Ser Phe Phe Gly Gln Phe Ser Val Arg Gly Tyr Val Asn Tyr Asp
                      35                      40                      45
Lys His Val Ala Lys Tyr Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr
                      50                      55                      60
Gln Ala Ile Glu Asp Val Val Lys Ala Asp Ala Glu Lys Asn Thr Ser
65                      70                      75                      80

```

```

Asn Asn Glu Met Gly Met Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys
      85                      90                      95
Lys Asp Leu Lys Lys Leu Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu
      100                    105                    110
Lys Ser Pro Glu Tyr Asn Asp Leu Gln Leu Val Leu Thr Gln Phe Ser
      115                    120                    125
Lys Ser Lys Val Asn Pro Ile Phe Ile Ile Pro Pro Val Asn Lys Lys
      130                    135                    140
Trp Met Asp Tyr Ala Gly Leu Arg Glu Asp Met Tyr Gln Gln Thr Val
      145                    150                    155                    160
Gln Lys Ile Arg Tyr Gln Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala
      165                    170                    175
Asn Phe Ser Lys Asp Gly Gly Glu Pro Phe Phe Met Lys Asp Thr Ile
      180                    185                    190
His Leu Gly Trp Leu Gly Leu Val Gly Phe
      195                    200

```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```

Met Lys Gln Leu Ser Ser Ala Gln Val Arg Gln Met Trp Leu Asp Phe
  1              5              10              15
Trp Ala Thr Lys Gly His Ser Val Glu Pro Ser Val Ser Leu Val Pro
      20              25              30
Val Asn Asp Pro Thr Leu Leu Trp Ile Asn Ser Gly Val Ala Thr Leu
      35              40              45
Lys Lys Tyr Phe Asp Gly Thr Ile Ile Pro Glu Asn Pro Arg Ile Thr
      50              55              60
Asn Ala Gln Lys Ala Ile Arg Thr Asn Asp Ile Glu Asn Val Arg Glu
      65              70              75              80
Arg Leu Arg Val Thr Ile Pro Cys Leu Lys Cys Trp Gly Thr Ser Leu
      85              90              95
Ser Gly Ile Thr Ser Val Thr Lys Leu Ser Leu Gly Leu Met Ser Phe
      100             105             110

```

337

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```

Met Ile Ala Leu Gly Trp Ser Asn Ile Gly Ala Ala Ile Ala Pro Asp
 1             5             10             15
Ala Ala Leu Ala Ser Val Ala Ala Ala Ile Ile Met Val Leu Gly Gly
      20             25             30
Asp Phe Thr Lys Thr Gly Ile Gly Val Ala Gln Ala Val Ala Ile Pro
      35             40             45
Leu Ala Val Ala Gly Leu Phe Leu Thr Met Ile Val Arg Thr Ile Ser
      50             55             60
Val Gly Leu Val His Thr Ala Asp Ala Ala Ala Lys Lys Gly Asp Phe
      65             70             75             80
Gly Ala Val Glu Arg Ala His Phe Ile Ala Leu Leu Phe Gln Gly Leu
      85             90             95
Arg Ile Ala Leu Pro Ala Ala Leu Leu Pro Tyr Gly Thr Asn
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

Met Leu Pro Leu Lys Lys Val Thr Ser Ala Leu Trp Ser Val Arg Ile
 1             5             10             15

```

```

Ser Leu Arg Tyr Phe Ser Lys Asp Phe Val Ser Arg Phe Leu Gln Leu
      20              25              30
Phe Ser Leu Met Val Pro Thr Glu Thr Val Gln Ser Ile Leu Ser Ala
      35              40              45
Met Pro Asp Trp Leu Lys Asp Gly Met Ala Ile Gly Gly Gly Met Val
      50              55              60
Val Ala Val Gly Tyr Ala Met Val Ile Asn Met Met Ala Thr Arg Glu
      65              70              75              80
Val Trp Pro Phe Phe Ala Leu Gly Phe Val Leu Ala Ala Val Ser Asp
              85              90              95
Ile Thr Leu Ile Gly Phe Gly Ala Ile Gly Val Ala Ile Ala Leu Ile
      100              105              110
Tyr Leu His Leu Ser Lys Thr Gly Gly Asn Gly Gly Gly Gly Ala Ala
      115              120              125
Thr Ser Asn Asp Pro Ile Gly Asp Ile Leu Glu Asp Tyr
      130              135              140

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

Met Ala Lys Asn Gly Val Asp Gly Val Tyr Asn Ala Asp Pro Lys Lys
  1              5              10              15
Asp Lys Thr Ala Val Lys Phe Glu Glu Leu Thr His Arg Asp Val Ile
      20              25              30
Asn Lys Gly Leu Arg Ile Met Asp Ser Thr Ala Ser Thr Leu Ser Met
      35              40              45
Asp Asn Asp Ile Asp Leu Val Val Phe Asn Met Asn Gln Ser Gly Asn
      50              55              60
Ile Lys Arg Val Val Phe Gly Glu Asn Ile Gly Thr Thr Val Ser Asn
      65              70              75              80
Asn Ile Glu Glu Lys Glu
              85

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

Leu Ile Asn Leu Tyr Pro Asp Leu Asp Phe Ile Val Thr Thr Val Ala
 1             5             10             15
Leu Gln Glu Pro Ala Ser Val Pro Phe Val Leu Val Ser Ala Phe Leu
             20             25             30
Thr Glu Gly Asp Lys Gln Arg Leu Gln Ala Lys Ile Gln Glu Ile Asn
             35             40             45
Tyr Glu
             50

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

Met Ser Tyr Phe Lys Lys Tyr Lys Phe Asp Lys Ser Gln Phe Lys Leu
 1             5             10             15
Gly Met Arg Thr Phe Lys Thr Gly Ile Ala Val Phe Leu Val Leu Leu
             20             25             30
Ile Phe Gly Phe Phe Gly Trp Lys Gly Leu Gln Ile Gly Ala Leu Thr
             35             40             45
Ala Val Phe Ser Leu Arg Glu Ser Phe Asp Glu Ser Val His Phe Gly
             50             55             60
Thr Ser Arg Ile Leu Gly Asn Ser Ile Gly Gly Leu Tyr Ala Leu Val
65             70             75             80

```

```

Phe Phe Leu Leu Asn Thr Phe Phe His Glu Ala Phe Trp Val Thr Leu
      85                      90                      95
Val Val Val Pro Ile Cys Thr Met Leu Thr Ile Met Thr Asn Val Ala
      100                    105                    110
Met Asn Asn Lys Ala Gly Val Ile Gly Gly Val Ala Ala Met Leu Ile
      115                    120                    125
Ile Thr Leu Ser Ile Pro Ser Gly Glu Thr Ile Leu Tyr Val Phe Val
      130                    135                    140
Arg Val Leu Glu Thr Phe Met Gly Val Phe Val Ala Ile Ile Val Asn
      145                    150                    155                    160
Tyr Asn Ile Asp Arg Ile Arg Leu Phe Leu Glu Lys Lys Glu Lys
      165                    170                    175

```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

Met Ile Ala Lys Glu Phe Glu Thr Phe Leu Leu Gly Gln Glu Glu Thr
  1             5             10             15
Phe Leu Thr Pro Val Lys Asn Leu Val Val Leu Ile Asp Thr His Asn
      20             25             30
Ala Asp His Ala Thr Leu Leu Leu Ser Gln Met Thr Tyr Thr Arg Val
      35             40             45
Pro Val Val Thr Asp Glu Ile Gln Leu Arg Trp Arg Gln Asp Val Leu
      50             55             60
Tyr Gln Gln Val Leu
65

```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

Met Ala Lys Gln Thr Ile Ile Val Met Ser Asp Ser His Gly Asp Ser
 1           5           10           15
Leu Ile Val Glu Glu Val Arg Asp Arg Tyr Val Gly Lys Val Asp Ala
      20           25           30
Val Phe His Asn Gly Asp Ser Glu Leu Arg Pro Asp Ser Pro Leu Trp
      35           40           45
Glu Gly Ile Arg Val Val Lys Gly Asn Met Asp Phe Tyr Ala Gly Tyr
      50           55           60
Pro Glu Arg Leu Val Thr Glu Leu Gly Ser Thr Lys Ile Ile Gln Thr
      65           70           75           80
His Gly His Leu Phe Asp Ile Asn Phe Asn Phe Gln Lys Leu Asp Tyr
      85           90           95
Trp Ala Gln Glu Glu Glu Ala Ala Ile Cys Leu Tyr Gly His Leu His
      100          105          110
Val Pro Ser Ala Trp Leu Glu Gly Lys Ile Leu Phe Leu Asn Pro Gly
      115          120          125
Ser Ile Ser Gln Pro Arg Gly Thr Ile Arg Glu Cys Leu Tyr Ala Arg
      130          135          140
Val Glu Ile Asp Asp Ser Tyr Phe Lys Val Asp Phe Leu Thr Arg Asp
      145          150          155          160
His Glu Val Tyr Pro Gly Leu Ser Lys Glu Phe Ser Arg
      165          170

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Ser Thr Thr Ile Ile Gly Phe Pro Arg Leu Gly Glu Phe Arg Glu
 1           5           10           15

```

Leu Lys Phe Thr Thr Glu Lys Tyr Phe Arg Lys Glu Ile Ser Glu Glu
 20 25 30
 Glu Leu Leu Ala Ala Ala Lys Asp Leu Arg Gly Lys His Trp Asn Ile
 35 40 45
 Val Lys Gly Lys Gly Ile Thr Glu Ile Pro Ser Asn Asp Phe Ser His
 50 55 60
 Tyr Asp Asn Phe Leu Asp Ala Ala Phe Leu Phe Asn Val Val Pro Ala
 65 70 75 80
 Ser Val Gln Asn Leu Asp Leu Ser Asp Leu Glu Arg Tyr Phe Ala Leu
 85 90 95
 Gly Arg Gly Tyr Gln Gly Gly Lys Gly Asp Val Arg Ala Leu Pro Met
 100 105 110
 Lys Lys Trp Phe Asn Thr Asn Tyr His Tyr Ile Val Pro Lys Phe Glu
 115 120 125
 Lys Asp Thr Gln Val Lys Leu Ala Gly His Lys Ile Phe Asp Glu Phe
 130 135 140
 Gln Glu Ala Lys Glu Leu Gly Leu Asn Thr Arg Pro Val Leu Val Gly
 145 150 155 160
 Pro Phe Thr Phe Leu Gln Leu Ser Asp Phe Glu Glu Gly Val Lys Ala
 165 170 175
 Asp Asp Phe Val Asp Ser Leu Val Ala Ala Tyr Gln Glu Val Phe Ala
 180 185 190
 Lys Leu Ala Glu Leu Gly Ala Thr Arg Ile Gln Leu Asp Glu Ala Ala
 195 200 205
 Leu Val Lys Asp Leu Thr Ala Glu Glu Lys Ala Leu Phe Leu Asn Leu
 210 215 220
 Tyr Asn Lys Leu Leu Ala Asp Lys Lys Gly Leu Glu Val Leu Leu Gln
 225 230 235 240
 Thr Tyr Phe Gly Asp Val Arg Asp Val Tyr Ala Asp Leu Val Asn Leu
 245 250 255
 Pro Val Asp Ala Ile Gly Leu Asp Phe Val Glu Gly Lys Lys Thr Leu
 260 265 270
 Glu Leu Val Lys Gly Gly Phe Pro Ala Asp Lys Thr Leu Tyr Val Gly
 275 280 285
 Ile Val Asn Gly Lys Asn Ile Trp Arg Asn Asn Tyr Glu Lys Ser Leu
 290 295 300
 Ala Val Leu Glu Gln Ile Pro Ala Glu Asn Ile Val Leu Thr Ser Ser
 305 310 315 320
 Cys Ser Leu Leu His Val Pro Phe Thr Thr Ala Asn Glu Glu Phe Glu
 325 330 335
 Pro Ala Leu Leu Asn His Phe Ala Phe Ala Val Glu Lys Leu Asp Glu
 340 345 350

```

Ile Arg Asp Leu Asp Ala Ile Arg Asn Gly Gln Gly Ser Glu Ala Leu
   355                               360                               365
Ala Ala Asn Lys Glu Leu Phe Ala Thr Glu Arg Val Gly Glu Asn Ala
   370                               375                               380
Glu Leu Arg Ala Arg Ile Ala Gly Leu Thr Asp Ala Asp Tyr Thr Arg
  385                               390                               395                               400
Leu Pro Ala Phe Ala Glu Arg Glu Ala Ile Gln Gly Glu Gly Phe Lys
                   405                               410                               415
Phe Pro Ala Phe Pro Thr Thr Arg Ile Gly Ser Phe Pro Gln Thr Lys
                   420                               425                               430
Glu Val Arg Ala Lys Arg Leu Ala Tyr Arg Lys Gly Glu Leu Ser Gln
                   435                               440                               445
Lys Glu Tyr Asp Ala Phe Pro Cys
   450                               455

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

Met Leu Thr Gly Ile Leu Lys Pro Thr Ser Gly Phe Cys Arg Ile Asn
  1                               5                               10                               15
Gly Lys Ile Pro Gln Glu Asn Arg Gln Asp Tyr Val Lys Asp Ile Gly
                   20                               25                               30
Val Val Phe Gly Gln Arg Thr Gln Leu Trp Trp Asp Leu Ala Leu Gln
                   35                               40                               45
Glu Thr Tyr Ser Val Leu Lys Glu Ile Tyr Asp Val Pro Asp Ala Val
                   50                               55                               60
Phe Gln Lys Arg Met Asp Phe Leu Asn Asp Val Leu Asp Leu Lys Glu
                   65                               70                               75                               80
Phe Ile Lys Asp Pro Val Arg Thr Leu Ser Leu Gly Gln Arg Met Arg
                   85                               90                               95
Ala Asp Ile Ala Ala Ser Leu Leu His Asn Pro Lys Val Leu Phe Leu
                   100                               105                               110
Asp Glu Pro Thr Ile Gly Leu Asp Val Ser Val Lys Asp Asn Ile Arg
                   115                               120                               125

```

344

Arg Ala Ile Thr Gln Ile Asn Gln Glu Glu Glu Thr Thr Ile Leu Leu
 130 135 140
 Thr Thr His Asp Leu Ser Asp Ile Glu Gln Phe Val Ile Gly Phe Ser
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Met Lys Val Ile Asn Gln Thr Leu Leu Glu Lys Val Ile Ile Glu Arg
 1 5 10 15
 Ser Arg Ser Ser His Lys Gly Asp Tyr Gly Arg Leu Leu Leu Leu Gly
 20 25 30
 Gly Thr Tyr Pro Tyr Gly Gly Ala Ile Ile Met Ala Ala Leu Ala Ala
 35 40 45
 Val Lys Ser Gly Ala Gly Leu Val Thr Val Gly Thr Asp Arg Glu Lys
 50 55 60
 Tyr Pro Gly Ser Ala Gln Pro Phe Thr
 65 70

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met Xaa Val Ile Asn Gln Ser Leu Leu Xaa Xaa Val Ile Ile Asp Arg
 1 5 10 15

Pro Arg Ser Ser Leu Lys Gly Asp Tyr Gly Arg Leu Pro Xaa Leu Gly
 20 25 30
 Gly Xaa Tyr Gly Gly Gly Gly Xaa Thr Ser Xaa Ala Ala Xaa Xaa Gly
 35 40 45
 Xaa Xaa Xaa Xaa Ala
 50

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met Ile Asn Arg Tyr Ser Arg Pro Glu Met Ala Asn Ile Trp Ser Glu
 1 5 10 15
 Glu Asn Lys Tyr Arg Ala Trp Leu Glu Val Glu Ile Leu Ser Asp Glu
 20 25 30
 Ala Trp Ala Glu Leu Gly Glu Ile Pro Lys Glu Asp Val Ala Leu Ile
 35 40 45
 Arg Lys Lys Ala Asp Phe Asp Ile Asp Arg Ile Leu Glu Ile Glu Gln
 50 55 60
 Glu Thr Arg His Asp Val Val Ala Phe Thr Arg Ala Val Ser Glu Thr
 65 70 75 80
 Leu Gly Glu Glu Arg Lys Trp Val His Tyr Gly Leu Thr Ser Thr Asp
 85 90 95
 Val Val Asp Thr Ala Tyr Gly Tyr Leu Tyr Lys Gln Ala Asn Asp Ile
 100 105 110
 Ile Arg Arg Asp Leu Glu Asn Phe Thr Asn Ile Ile Ala Asp Lys Ala
 115 120 125
 Lys Glu His Lys Phe Thr Ile Met Met Gly Arg Thr His Gly Val His
 130 135 140
 Ala Glu Pro Thr Thr Phe Gly Leu Lys Leu Ala Thr Trp Tyr Ser Glu
 145 150 155 160
 Met Lys Arg Asn Ile Gly Ala Leu Arg Ala Cys Gly Cys Trp Cys Arg
 165 170 175
 Ser Trp

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

Met Lys Thr Asn Asp Ile Val Tyr Gly Val His Ala Val Thr Glu Ala
 1             5             10             15
Leu Leu Ala Asn Thr Gly Asn Lys Leu Tyr Leu Gln Glu Asp Leu Arg
             20             25             30
Gly Lys Asn Val Glu Lys Val Lys Glu Leu Ala Val Thr Phe
             35             40             45

```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

Met Leu Leu Ser Ala Phe His Lys Tyr Glu Asn Gln Leu Asp Lys Val
 1             5             10             15
Arg Phe Ile Gly Leu His Thr Gly His Leu Gly Phe Tyr Thr Asp Tyr
             20             25             30
Arg Asp Phe Glu Leu Asp Lys Leu Val Thr Asn Leu Gln Leu Asp Thr
             35             40             45
Gly Ala Arg Val Ser Tyr Pro Val Leu Asn Val Lys Val Phe Leu Glu
             50             55             60
Asn Gly Glu Val Lys Ile Phe Arg Ala Leu Asn Glu Ala Ser Ile Arg
             65             70             75             80

```


Arg Ser Asp Arg Thr Met Val Ala Asp Ile Val Ile Asn Gly Val Pro
 85 90 95
 Phe Glu Arg Phe Arg Gly Asp Gly Leu Thr Val Ser Thr Pro Thr Gly
 100 105 110
 Ser Thr Ala Tyr Asn Lys Ser Leu Gly Gly Ala Val Leu His Pro Thr
 115 120 125
 Ile Glu Ala Leu Gln Leu Thr Glu Ile Ala Ser Leu Asn Asn Arg Val
 130 135 140
 Tyr Arg Thr Leu Gly Ser Ser Ile Ile Val Pro Lys Lys Asp Lys Ile
 145 150 155 160
 Glu Leu Ile Pro Thr Arg Asn Asp Tyr His Thr Ile Ser Val Asp Asn
 165 170 175
 Ser Val Tyr Ser Phe Arg Asn Ile Glu Arg Ile Glu Tyr Gln Ile Asp
 180 185 190
 His His Lys Ile His Phe Val Ala Thr Pro Ser His Thr Ser Phe Trp
 195 200 205
 Asn Arg Val Lys Asp Ala Phe Ile Gly Glu Val Asp Glu
 210 215 220

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Met Leu Val Pro Lys Arg Val Lys His Arg Arg Glu Phe Arg Gly Lys
 1 5 10 15
 Met Arg Gly Glu Ala Lys Gly Gly Lys Glu Val Ala Phe Gly Glu Tyr
 20 25 30
 Gly Leu Gln Ala Thr Thr Ser His Trp Ile Thr Asn Arg Gln Ile Glu
 35 40 45
 Ala Ala Arg Ile Ala Met Thr Arg Tyr Met Lys Arg Gly Gly Lys Val
 50 55 60
 Trp Ile Lys Ile Phe Pro His Lys Ser Tyr Thr Ala Lys Ala Ile Gly
 65 70 75 80
 Val Arg Met Gly Ser Gly Lys Gly Ala Pro Glu Gly Trp Val Ala Pro
 85 90 95

Val Lys Arg Gly Lys Val Met Phe Glu Ile Ala Gly Val Ser Glu Glu
 100 105 110
 Ile Ala Arg Glu Ala Leu Arg Leu Ala Ser His Lys Leu Pro Val Lys
 115 120 125
 Cys Lys Phe Val Lys Arg Glu Ala Glu
 130 135

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Tyr Thr Val Ser Gly Ile Ala Tyr Arg Trp Phe Ser Thr Ile Leu
 1 5 10 15
 Ala Leu Val Ser Ala Thr Ser Val Phe Val Leu Thr Thr Ile Ser Leu
 20 25 30
 Ile Gly Val Glu Thr Phe Ser Lys Ile Pro Val Phe Gly Tyr Val Ala
 35 40 45
 Lys Arg Phe Ser Ala Phe Phe Asn Pro Phe Ala Asp Arg Ala Asp Ala
 50 55 60
 Gly His Gln Leu Ala Asn Ser Tyr Phe Ala Met Val Asn Gly Gly Trp
 65 70 75 80
 Phe Gly Leu Gly Leu Gly Asn Ser Ile Glu Lys Arg Gly Tyr Leu Pro
 85 90 95
 Glu Ala His Thr Asp Phe Val Phe Ser Ile Val Ile Glu Glu Phe Gly
 100 105 110
 Phe Val Gly Ala Ser Leu Ile Leu Ala Leu Leu Phe Phe Met Ile Leu
 115 120 125
 Arg Ile Ile Leu Val Gly Ile Arg Ala Glu Asn Pro Phe Asn Ala Met
 130 135 140
 Val Ala Leu Gly Val Gly Gly Met Met Leu Val Gln Val Phe Val Asn
 145 150 155 160
 Ile Gly Gly Ile Ser Gly Leu Ile Pro Ser Thr Gly Val Thr Phe Pro
 165 170 175
 Phe Leu Ser Gln Gly Gly Asn Ser Leu Leu Val Leu Ser Val Ala Val
 180 185 190
 349

Ala Phe Val Leu Asn Ile Asp Ala Ser Glu Lys Arg Ala Lys Leu Tyr
 195 200 205
 Arg Glu Leu Glu Asn Gln Pro Met Asn Leu Leu Leu Lys
 210 215 220

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Leu Leu Ile Val Ile Ile Ile Gly Thr Phe Tyr Phe Phe Asn Arg
 1 5 10 15
 Ala Arg Tyr Leu Gly Val Thr Tyr Tyr Ser Arg Phe His Phe Thr Ile
 20 25 30
 Leu Gly Cys Phe Phe Leu Thr Leu Ala Ile Thr Ala Leu Leu Met Leu
 35 40 45
 Gln Asn Tyr Gln Phe Asn Ile Glu Ile Tyr Gln His Asn Pro Leu Asn
 50 55 60
 Phe Lys Tyr Leu Ser Ala Trp Val Ile Thr Tyr Val Ile Tyr Leu Pro
 65 70 75 80
 Trp Val Phe Ile Gly Asn Leu Gly Leu Lys Ser Tyr Gly Glu Trp Ala
 85 90 95
 Gln Lys Lys Phe Glu Gln Asp Met Asp Glu Leu Glu Ser Gly Glu
 100 105 110

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

350

```

Met Leu Asp Val Glu Ala Ile Arg Lys Asp Phe Pro Ile Leu Asp Gln
 1           5           10           15
Ile Val Asn Asp Glu Pro Leu Val Tyr Leu Asp Asn Ala Ala Thr Thr
           20           25           30
Gln Lys Pro Leu Val Val Leu Lys Ala Ile Asn Ser Tyr Tyr Glu Gln
           35           40           45
Asp Asn Ala Asn Val His Arg Gly Val His Thr Leu Ala Glu Arg Ala
           50           55           60
Thr Ala Ser Leu
65

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

Met Gly Phe Asn Gln Pro Leu Ser Trp Leu Ile Leu His Ala Lys Gly
 1           5           10           15
Leu Thr Glu Ser Phe Ile Lys Ala Ser Ala Gln Thr Gly Ala Asp Arg
           20           25           30
Ile Thr Tyr Ile Ser Cys Asn Val Arg Asn His Gly Ala Val Asp Ile
           35           40           45
Lys Leu Tyr Gln Glu Leu Gly Tyr Glu Leu Lys Lys Val Gln Pro Val
           50           55           60
Asp Leu Phe Xaa Gln Thr His His Val Glu Thr Val Ala Leu Leu Ser
65           70           75           80
Lys Leu Asp Val Asp Lys His Ile Ser Val Glu Ile Glu Leu Asp Glu
           85           90           95
Met Asp Leu Thr Ser Ala Glu Ser Lys Ala Thr Tyr Ala Gln Ile Lys
           100          105          110
Glu Tyr Val Trp Asn Lys Phe Glu Leu Lys Val Ser Thr Leu Tyr Ile
           115          120          125
Ala Gln Ile Lys Lys Lys Cys Gly Ile Glu Leu Arg Glu His Tyr Asn
           130          135          140

```

Lys Xaa Lys Lys Asp Lys Gln Ile Ile Pro Gln Cys Thr Pro Glu Lys
145 150 155 160
Glu Glu Ala Ile Met Asp Ala Leu Arg Xaa Phe Lys Met Ile
 165 170

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

[illegible]

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

Met Gln Glu Ile Ile Ala Glu Asp Ile Gln Lys Phe Gly Ile Ile Pro
 1             5             10             15
Glu Leu Ile Gly Arg Leu Pro Val Phe Ala Ala Leu Glu Gln Leu Thr
      20             25             30
Val Asp Asp Leu Val Arg Ile Leu Lys Glu Pro Arg Asn Ala Leu Val
      35             40             45
Lys Gln Tyr Gln Thr Leu Leu Ser Tyr Asp Asp Val Glu Leu Glu Phe
      50             55             60
Asp Asp Glu Ala Leu Gln Glu Ile Ala Asn Lys Ala Ile Glu Arg Lys
      65             70             75             80
Thr Gly Ala Arg Gly Leu Arg Ser Ile Ile Glu Glu Thr Met Leu Asp
      85             90             95
Val Met Phe Glu Val Pro Ser Gln Glu Asn Val Lys Leu Val Arg Ile
      100            105            110
Thr Lys Glu Thr Val Asp Gly Thr Asp Lys Pro Ile Leu Glu Thr Ala
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

Met Glu Gly Gln Ser Ala Met Gln Ser Gln Glu Gln Asp Ser Asn Gly
 1             5             10             15
Ala Val Lys Ser Ile Val Ser Lys Ser Pro Gly Ala Ile Ser Tyr Leu
      20             25             30
Ser Leu Thr Tyr Ile Asp Asp Ser Val Lys Ser Met Lys Leu Asn Gly
      35             40             45
Tyr Asp Leu Ser Pro Glu Asn Ile Ser Ser Asn Asn Trp Pro Leu Trp
      50             55             60
Ser Tyr Glu His Met Tyr Thr Leu Gly Gln Pro Asn Glu Leu Ala Ala
      65             70             75             80
Glu Phe Leu Asn Phe Val Leu Ser Asp Glu Thr Gln Glu Gly Ile Val
      85             90             95

```

Lys Gly Leu Lys Tyr Ile Pro Ile Lys Glu Met Lys Val Glu Lys Asp
 100 105 110
 Ala Ala Gly Thr Val Thr Val Leu Glu Gly Arg Gln
 115 120

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Met Glu Ile Lys Ile Glu Thr Gly Gly Leu Arg Leu Asp Lys Ala Leu
 1 5 10 15
 Ser Asp Leu Ser Glu Leu Ser Arg Ser Leu Ala Asn Glu Gln Ile Lys
 20 25 30
 Ser Gly Gln Val Leu Val Asn Gly Gln Val Lys Lys Ala Lys Tyr Thr
 35 40 45
 Val Gln Glu Gly Asp Val Val Thr Tyr His Val Pro Glu Pro Glu Val
 50 55 60
 Leu Glu Tyr Val Ala Glu Asp Leu Pro Leu Glu Ile Val Tyr Gln Asp
 65 70 75 80
 Glu Asp Val Ala Val Val Asn Lys Pro Gln Gly Met Val Val His Pro
 85 90 95
 Ser Ala Gly His Thr Ser Gly Thr Leu Val Asn Ala Leu Met Tyr His
 100 105 110
 Ile Lys Asp Leu Ser Gly Ile Asn Gly Val Leu Arg Pro Gly Ile Val
 115 120 125
 His Arg Ile Asp Lys Asp Thr Ser Gly Leu Leu Met Ile Ala Lys Asn
 130 135 140
 Asp Asp Ala His Leu Ala Leu Ala Gln Glu Leu Lys Asp Lys Lys Ser
 145 150 155 160
 Leu Pro Gln Ile Leu Gly Asp Cys Ser Met Glu Ile Cys Leu Met Ile
 165 170 175
 Val Val Leu Ile Glu Thr Pro Glu Leu Ala Asn Glu Lys Glu Pro
 180 185 190

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

Met Lys Ile Leu Val Thr Gly Phe Asn Pro Phe Gly Gly Glu Lys Ile
 1           5           10           15
Asn Pro Ala Leu Glu Ala Val Lys Leu Leu Pro Ser Glu Ile Asn Gly
          20           25           30
Ala Glu Val Arg Trp Val Glu Ile Pro Thr Val Phe Tyr Lys Ser Ser
          35           40           45
Glu Val Leu Glu Ala Glu Ile Leu Arg Tyr Gln Pro Asp Ala Val Leu
          50           55           60
Cys Ile Gly Gln Ala Gly Gly Arg Thr Gly Leu Thr Pro Glu Arg Val
          65           70           75           80
Ala Ile Asn Gln Asp Asp Ala Arg Ile Pro Asp Asn Glu Gly Asn Gln
          85           90           95
Pro Ile Asp Thr Pro Ile Arg Ile Asp Gly Ala Ser Ala Tyr Phe Ser
          100          105          110
Ser Leu Pro Ile Lys Ala Met Val Gln Ala Ile Lys Lys Gln Gly Leu
          115          120          125
Pro Ala Val Val Ser Asn Ser Ala Gly Thr Phe Val Cys Asn His Leu
          130          135          140
Met Tyr Gln Ala Leu Tyr Leu Val Asp Lys Glu Ile Pro
          145          150          155

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

355


```

Met Leu Arg Ala Gly Phe His Ala Tyr Ser Ile Tyr Asp Gly Thr Ser
 1             5             10             15
Ser Glu Gln Lys Pro Asn Thr Pro Asp Tyr Glu Phe Tyr Val Asp Ile
             20             25             30
Arg Arg Lys Gly Ile Glu Ala Ala Ile Gly Ala Met Ile Glu His Gly
             35             40             45
Asp Gln Glu Leu Lys Leu Val Gly Gly Glu Ile His
50             55             60

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

Met Lys Phe Arg Lys Leu Ala Cys Thr Val Leu Ala Gly Ala Ala Val
 1             5             10             15
Leu Gly Leu Ala Ala Cys Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala
             20             25             30
Lys Ser Gly Gly Asp Gly Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe
             35             40             45
Pro Val Phe Thr Gln Glu Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu
             50             55             60
Lys Ser Ile Ile Glu Ala Phe
65             70

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```

Met Ala Leu Gly Thr Thr Leu Thr Val Gln Ala Ile Cys Leu Gln Thr
 1             5             10             15
Ala Gly Gly Ser Thr Gln Thr Ala Thr Gly Thr Gly Ser Thr Thr Pro
          20             25             30
Gly Glu Met Ala Thr Gly Trp Lys Ser Pro Thr Leu Leu Phe Phe Asn
          35             40             45
Thr Ser Tyr Phe Asp Leu Thr Gly Trp Ser
 50             55

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

Met Glu Ala Glu Leu Lys Lys Leu Glu Val Asn Leu Val Asn Leu Ala
 1             5             10             15
Gly Gln Leu Ala Ser Ala Arg His Asn Leu Ala Gln Gln Leu Glu Ala
          20             25             30
Glu Ile Lys Gln Glu Leu Gln Asp Leu Tyr Met Glu Lys Ala Gln Phe
          35             40             45
Gln Val Arg Phe Ser Lys Gly Lys Phe Ser Arg Glu Gly Asn Lys Met
          50             55             60
Val Glu Phe Tyr Ile Ser Thr Asn Pro Gly Glu Asp Phe Lys Pro Leu
          65             70             75             80
Val Lys Val Ala Ser Gly Gly Glu Leu Ser Arg Leu Met Leu Ala Ile
          85             90             95
Lys Ser Ala Phe Ser Arg Lys Glu Gly Lys Thr Ser Ile Val Phe Asp
          100            105            110
Glu Val Glu Thr Gly Val Ser Gly Arg Val Ala Gln Ala Ile Ala Gln
          115            120            125
Lys Ile His Lys Ile Gly Gln His Gly Gln Val Leu Ala Ile Ser His
          130            135            140
Leu Pro Gln Val Ile Ala Ile Ala Asp Tyr Gln Phe Phe Ile Glu Lys
          145            150            155            160

```

Ile Ser Asn Asp His Ser Thr Val Ser Thr Val Arg Leu Leu Thr Val
 165 170 175
 Glu Glu Arg Val Glu Glu Val Ala Lys Met Leu Ala Gly Asp Asp Val
 180 185 190
 Thr Glu Ala Ala Leu Thr Gln Ala Arg Glu Leu Leu Arg Asn Arg Glu
 195 200 205
 Lys

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met Met Gly Glu Asn Leu Phe Arg Ser Ile Lys Ile Arg Gly Glu Phe
 1 5 10 15
 Leu His Met His Val Arg Met Ile Pro Lys Ser Thr Pro Asp Thr Lys
 20 25 30
 Phe Ala Asp Val Ala Thr His Gln Pro Glu Tyr Ser Arg Asp Asn Val
 35 40 45
 Ala Gly Thr Ile Val Gly Phe Trp Thr Pro Glu Ile Phe His Gly Val
 50 55 60
 Ser Val Ala Gly Tyr His Leu His Phe Ile Ser Asp Asp Leu Thr Phe
 65 70 75 80
 Gly Gly His Val Met Asp Phe Val Ile Lys Glu Gly Ile Ile Glu Val
 85 90 95
 Gly Ala Val Asp Gln Leu Asp Gln Arg Phe Pro Val Gln Asp Arg Gln
 100 105 110
 Tyr Leu Phe Ala Lys Phe Asn Val Asp Glu Met Lys Lys Asp Ile Glu
 115 120 125
 Lys Ala Glu
 130

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

358

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```

Met Ala Gly Ser Ser Arg Asp His Ala Ala Trp Ala Leu Ala Asp Tyr
 1             5             10             15
Gly Phe Lys Val Val Ile Ala Gly Ser Phe Gly Asp Ile His Tyr Asn
      20             25             30
Asn Glu Leu Asn Asn Gly Met Leu Pro Ile Val Gln Pro Arg Glu Val
      35             40             45
Arg Glu Lys Leu Ala Gln Leu Lys Pro Thr Asp Gln Val Thr Val Asp
      50             55             60
Leu Glu Gln Gln Lys Ile Ile Ser Pro Val Glu Glu Phe Thr Phe Glu
65             70             75             80
Ile Asp Ser Lys Trp Lys His Lys Leu Leu Asn Ser Leu Asp Asp Ile
      85             90             95
Gly Ile Thr Leu Gln Tyr Glu Glu Leu Ile Ala Ala Tyr Glu Lys Gln
      100            105            110
Arg Pro Ala Tyr Trp Gln Asp
      115

```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```

Met Asn Ile Tyr Asp Gln Leu Gln Ala Val Glu Asp Arg Tyr Glu Glu
 1             5             10             15
Leu Gly Glu Leu Leu Ser Asp Pro Asp Val Val Ser Asp Thr Lys Arg
      20             25             30

```

Phe Met Glu Leu Ser Lys Glu Glu Ala Ser Asn Arg Asp Thr Val Ile
 35 40 45
 Ala Tyr Arg Glu Tyr Lys Gln Val Leu Gln Asn Ile Val Asp Ala Glu
 50 55 60
 Glu Met Ile Lys Glu Ser Gly Gly Asp Ala Asp Leu Glu Glu Leu Ala
 65 70 75 80
 Lys Gln Glu Leu Lys Asp Ala Lys Ala Glu Lys Glu Glu Tyr Glu Glu
 85 90 95
 Lys Leu Lys Ile Leu Leu Leu Pro Lys Asp Pro Asn Asp Asp Lys Asn
 100 105 110
 Ile Ile Leu Glu Ile Arg Gly Ala Ala Gly Gly Asp Glu Ala Ala Leu
 115 120 125
 Phe Ala Gly Asp Leu Leu Thr Met Tyr Gln Lys Tyr Ala Glu Ala Gln
 130 135 140
 Gly Trp Arg Phe Glu Val Met Glu Ala Ser Met Asn Gly Val Gly Gly
 145 150 155 160
 Phe Lys Glu Val Val Ala Met Val Ser Gly Gln Ser Val Tyr Ser Lys
 165 170 175
 Leu Lys Tyr Glu Ser Gly Ala His Arg Val Gln Arg Val Pro Val Thr
 180 185 190
 Glu Ser Gln Gly Arg Val His Thr Ser Thr Ala Thr Val Leu Val Met
 195 200 205
 Pro Glu Val Glu Glu Val Glu Tyr Asp Ile Asp Pro Lys Asp Leu Arg
 210 215 220
 Val Asp Ile Tyr His Ala Ser Gly Ala Gly Gly Gln Asn Val Asn Lys
 225 230 235 240
 Val Ala Thr Ala Val Arg Ile Val His Leu Pro Thr Asn Ile Lys Val
 245 250 255
 Glu Met Gln Glu Glu Arg Thr Gln Gln Lys Asn Arg Glu Lys Ala Met
 260 265 270
 Lys Ile Ile Arg Ala Arg Val Ala Asp His Phe Ala Gln Ile Ala Gln
 275 280 285
 Asp Glu Gln Asp Ala Glu Arg Lys Ser Thr Ile Gly Thr Gly Asp Arg
 290 295 300
 Ser Glu Arg Ile Arg Thr Tyr Asn Phe Pro Gln Asn Arg Val Thr Asp
 305 310 315 320
 His Arg Ile Gly Leu Thr Leu Gln Lys Leu Asp Thr Ile Leu Ser Gly
 325 330 335
 Lys Leu Asp Glu Val Val Asp Ala Leu Val Leu Tyr Asp Gln Thr Gln
 340 345 350
 Lys Leu Glu Glu Leu Asn Lys
 355

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

Met Asn Asn Asn Phe Asn Asn Phe Asn Asn Met Asp Asp Leu Phe Asn
 1             5             10             15
Gln Leu Met Gly Gly Met Arg Gly Tyr Ser Ser Glu Asn Arg Arg Tyr
      20             25             30
Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe Ala His Tyr Arg
      35             40             45
Thr Thr Gly Gln Leu Pro Gly Asn Ala Glu Thr Asp Val Gln Met Pro
      50             55             60
Gln Gln Ala Ser Gly Met Lys Gln Asp Gly Val Leu Ala Lys Leu Gly
      65             70             75             80
Arg Asn Leu Thr Ala Glu Ala Arg Glu Gly Lys Leu Asp Pro Val Ile
      85             90             95
Gly Arg Asn Lys Glu Ile Gln Glu Thr Ser Glu Ile Leu Ser Arg Arg
      100            105            110
Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys Thr
      115            120            125
Ala Val Val Glu Gly Leu Ala Gln Ala Ile Val Asn Gly Asp Val Pro
      130            135            140
Ala Ala Ile Lys Asn Lys Glu Ile Ile Ser Ile Asp Ile Ser Gly Leu
      145            150            155            160
Glu Ala Gly Thr Gln Tyr Arg Gly Ser Phe Glu Glu Asn Val Gln Asn
      165            170            175
Leu Val Asn Glu Val Lys Glu Ala Gly Asn Ile Ile Leu Phe Phe Asp
      180            185            190
Glu Ile His Asn Ser Trp Cys Trp
      195            200

```

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
 361

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

Met Gln Gly Gln Ile Ile Lys Ala Leu Ala Gly Phe Tyr Tyr Val Glu
 1             5             10             15
Ser Asp Gly Gln Val Tyr Gln Thr Arg Ala Arg Gly Asn Phe Arg Lys
          20             25             30
Lys Gly His Thr Pro Tyr Val Gly Asp Trp Val His Phe Ser Ala Glu
          35             40             45
Glu Asn Ser Glu Gly Tyr Ile Leu Lys Ile His Glu Arg Lys Asn Ser
          50             55             60
Leu Val Arg Pro Pro Ile Val Asn Ile Asp Gln Pro Val Val Ile Met
65             70             75             80
Ser Val Lys Glu Pro Asp Phe Asn Ser Asn Leu Leu Asp Arg Phe Leu
          85             90             95
Val Leu Leu Glu His Lys Gly Ile His Pro Ile Val Tyr Ile Ser Lys
          100            105            110
Met Asp Leu Leu Glu Asp Arg Gly Glu Leu Asp Phe Tyr Arg Gln Thr
          115            120            125
Tyr Gly Asp Ile Gly Tyr Asp Phe Val Thr Ser Lys Glu Glu Leu Leu
          130            135            140
Ser Leu Leu Thr Gly Lys Val Thr Val Phe Met Gly Gln Thr Gly Val
          145            150            155            160
Gly Lys Ser Thr Leu Leu Asn Lys Leu Val Pro Asp Leu Asn Leu Glu
          165            170            175
Thr Gly Glu Ile Ser Asp Ser Leu Gly Arg Gly Arg His Thr Thr Arg
          180            185            190
Ala Val Ser Phe Tyr Asn Leu Asn Gly Gly Lys Ile Ala Asp Thr Pro
          195            200            205
Gly Phe Ser Ser Leu Asp Tyr Glu Val Ser Arg Ala Glu Asp Leu Asn
          210            215            220
Gln Ala Phe Pro Glu Ile Ala Thr Val Ser Arg Asp Cys Lys Phe Arg
          225            230            235            240
Thr Cys Thr His Thr His Glu Pro Ser Cys Ala Val Lys Pro Ala Val
          245            250            255
Glu Glu Gly Val Ile Ala Thr Phe Arg Phe Asp Asn Tyr Leu Gln Phe
          260            265            270

```

Leu Ser Glu Ile Glu Asn Arg Arg Glu Thr Tyr Lys Lys Val Ser Lys
 275 280 285
 Lys Ile Pro Lys
 290

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Met Ile Ile Thr Ile Pro Ile Lys Asn Gln Lys Asp Ile Gly Thr Pro
 1 5 10 15
 Ser Asp Ser Val Val Val Leu Gly Tyr Phe Asp Gly Ile His Lys Gly
 20 25 30
 His Gln Glu Leu Phe Arg Val Ala Asn Lys Ala Ala Arg Lys Asp Leu
 35 40 45
 Leu Pro Ile Val Val Met Thr Phe Asn Glu Ser Pro Lys Ile Ala Leu
 50 55 60
 Glu Pro Tyr His Pro Asp Leu Phe Leu His Ile Leu Asn Pro Ala Glu
 65 70 75 80
 Arg Glu Arg Lys Leu Lys Arg Glu Gly Val Glu Glu Leu Tyr Leu Leu
 85 90 95
 Asp Phe Ser Ser Gln Phe Ala Ser Leu Thr Ala Gln Glu Phe Phe Ala
 100 105 110
 Thr Tyr Ile Lys Ala Met Asn Ala Lys Ile Ile Val Ala Gly Phe Asp
 115 120 125
 Tyr Thr Phe Gly Ser Asp Lys Lys Thr Ala Glu Asp Leu Lys Asp Tyr
 130 135 140
 Phe Asp Gly Glu Val Ile Ile Val Pro Pro Val Glu Asp Glu Lys Gly
 145 150 155 160
 Lys Ile Ser Ser Thr Arg Ile Arg Gln Ala Ile Leu Asp Gly Asn Val
 165 170 175
 Lys Glu Ala Gly Lys Leu Leu Gly Ala Pro Leu Pro Ser Arg Gly Met
 180 185 190
 Val Val His Gly Asn Ala Arg Gly Arg Thr Ile Gly Tyr Pro Thr Ala
 195 200 205
 363


```

Asn Leu Val Leu Leu Asp Arg Thr Tyr Met Pro Ala Asp Gly Val Tyr
 210                      215                      220
Val Val Asp Val Glu Ile Gln Arg Gln Lys Tyr Arg Ala Met Ala Ser
 225                      230                      235                      240
Val Gly Lys Asn Val Thr Phe Asp Gly Glu Glu Ala Arg Phe Glu Val
                      245                      250                      255
Asn Ile Phe Asp Phe Asn Gln Asp Ile Tyr Gly Glu Thr Val Met Val
                      260                      265                      270
Tyr Trp Leu Asp Arg Ile Arg Asp Met Thr Lys Phe Asp Ser Val Asp
                      275                      280                      285
Gln Leu Val Asp Arg Leu Lys Ala Asp Glu Glu Val Thr Arg Asn Trp
 290                      295                      300
Ser
305

```

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

```

Met Ala Thr Thr Glu Leu Ile Glu Leu Ala Ile Glu Thr Ser Lys His
 1              5              10              15
Ala Tyr Val Pro Tyr Ser His Phe Pro Ile Gly Ala Val Leu Val Ala
      20              25              30
Lys Asp Gly Asn Val Tyr Thr Gly Val Asn Ile Glu Asn Ala Ser Tyr
      35              40              45
Pro Leu Thr Asn Cys Gly Glu Arg Thr Ala Ile Phe Lys Ala Ile Ser
      50              55              60
Glu Gly Gln Arg Glu Phe Ser Glu Leu Ile Val Tyr Gly Gln Thr Glu
      65              70              75              80
Lys Pro Ile Ser Pro Cys Gly Ala Cys Arg Gln Val Met Val Glu Phe
              85              90              95
Phe Glu Gln Asp Leu Lys Val Thr Leu Val Ala Lys Asp Lys Ser Thr
      100              105              110

```

Val Glu Met Thr Val Gly Glu Leu Leu Pro Tyr Ser Phe Thr Asp Leu
 115 120 125
 Asn

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Met Asp Leu Met Arg Thr Phe Asp Lys Val Asp Ala Leu Leu Asp Gln
 1 5 10 15
 Leu Ser Ala Asn Ser Lys Asp Lys Thr Ala Leu Leu Glu Ser Thr Lys
 20 25 30
 Ala Ile Leu Val Leu Asn His Gln Ile Gln Ser Lys Ala Ser Ala Ser
 35 40 45
 Glu Glu Thr Ser Pro Ala Arg Asn Ala Glu Ala Asn Gly Asp Asn Thr
 50 55 60
 Ser Ala Glu Asn Gln Pro Asn Ala Thr Ala Glu Ser Asn Ile Glu Thr
 65 70 75 80
 Ala Ser Asp Glu Asn Lys Pro Ser Asn Thr Arg Asp Ser Lys Pro Ala
 85 90 95
 Glu Ser Thr Ser Glu Asn Lys Thr Thr Glu Ser Ser Thr Thr Thr Gly
 100 105 110
 Asn Gln Glu Lys Pro Val Glu
 115

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

```

Met Val Arg Tyr Val Ile Glu Lys Ser Gly His Thr Asp Trp Asp Gly
 1             5             10             15
Arg Lys Ile Tyr Gln Glu Ala Ala Ala Gly Asn Ala Leu Cys Gln Glu
      20             25             30
Ala Ile Glu Arg Met Asn Arg Asn Leu Ala Gln Gly Leu Leu Asn Ile
      35             40             45
Gln Tyr Leu Ile Asp Pro Asp Val Ile Ser Leu Gly Gly Ser Ile Ser
      50             55             60
Gln Asn Pro Asp Phe Ile Gln Asp Val Lys Lys Ala Val Asp Asn Phe
65             70             75             80
Val Asp Thr Tyr Glu Glu Tyr Thr Val Ala Pro Val Ile Gln Ala Cys
      85             90             95
Thr Tyr His Ala Asp Ala Asn Leu Tyr Gly Ala Leu Val Asn Trp Leu
      100            105            110
Gln Glu Glu Lys Gln Trp
      115

```

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```

Met Gln Gly Asp Phe Gln Ser Asn Ile Tyr Glu Gln Val Glu Gly His
 1             5             10             15
Phe Asp His Val Ile Ser Asn Pro Pro Ile Arg Ala Gly Lys Gln Val
      20             25             30
Val His Glu Ile Ile Glu Lys Ser Lys Asp Phe Leu Glu Thr Gly Gly
      35             40             45
Asp Leu Thr Ile Val Ile Gln Lys Lys Gln Gly Ala Pro Ser Ala Lys
      50             55             60
Ser Lys Met Glu Asp Val Phe Gly Asn Cys Glu Ile Leu Lys Lys Asp
65             70             75             80

```

367

Leu Phe Ser Ile Ile Leu Ser Val Ala Leu Ile Ser Leu Val Ser Leu
 1 5 10 15
 Val Thr Gly Pro Ile Leu Pro Phe Leu Ser Lys Pro Ala Ser Gln Asp
 20 25 30
 Cys Asp Ile Phe Ile Ala Leu Thr Glu His Asp Glu Val Asn Met Ile
 35 40 45
 Ala Ala Val Leu Ala Lys Lys Met Gly Ala Lys Glu Thr Ile Val Arg
 50 55 60
 Val Arg Asn Pro Glu Tyr Ser Asn Ser Tyr Phe Lys Glu Lys Asn Ile
 65 70 75 80
 Leu Gly Phe Ser Leu Ile Val Asn Pro Glu Leu Leu Ala Ala Arg Ala
 85 90 95
 Ile Ala Asn Ile Ile Asp Phe Pro Asn Ala Leu Ser Val Glu Arg Phe
 100 105 110
 Ala Gly Gly Arg Val Ser Leu Met Glu Phe Val Val Lys Ser Thr Ser
 115 120 125
 Gly Leu Cys Gln Met Pro Ile Ser Asp Phe Arg Lys Lys Phe Gly Asn
 130 135 140
 Val Ile Val Cys Ala Ile Glu Arg Asp His Gln Ile Ile Ile Pro Ser
 145 150 155 160
 Gly Asp Met Thr Val Gln Asp Lys Asp Arg Ile Phe Val Thr Gly Asn
 165 170 175
 Arg Val Asp Met Ile Leu Phe His Asn Tyr Phe Lys Ser Arg Ala Val
 180 185 190
 Lys Ser Leu Leu Ile Val Gly Ala Gly Arg Ile Thr Tyr Tyr Leu Leu
 195 200 205
 Gly Ile Leu Lys Asp Ser Arg Ile Asp Thr Lys Val Ile Glu Ile Asn
 210 215 220
 Pro Glu Ile Ala Ser Phe Phe Ser Glu Lys Phe Pro Asn Leu Tyr Ile
 225 230 235 240
 Val Gln Gly Asp Gly Thr Ala Lys Asp Ile Leu Leu Glu Glu Ser Ala
 245 250 255
 Gln His Tyr Asp Ala Val Ala Thr Leu Thr Gly Val Asp Glu Glu Asn
 260 265 270
 Leu Ile Thr Ser Met Phe Leu Asp Arg Val Gly Val Gln Lys Asn Ile
 275 280 285
 Thr Lys Val Asn Arg Thr Ser Leu Leu Glu Ile Ile Asn Ala Pro Asp
 290 295 300
 Phe Ser Ser Ile Ile Thr Pro Lys Ser Ile Ala Val Asp Thr Ile Met
 305 310 315 320
 His Phe Ile Arg Gly Arg Val Asn Ala Gln Tyr Ser Arg Pro Ser Ser
 325 330 335
 368

(2) INFORMATION FOR SEQ ID NO:399:

(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Met	Leu	Phe	Thr	Ala	Leu	Gln	Met	Asn	Thr	Asp	Ile	Leu	Ala	Ile	Ser
1					5				10					15	
Gln	Glu	Val	Gly	Asp	Trp	Arg	Ile	Asp	Leu	Ala	Ser	Ser	Gln	Thr	Glu
			20					25					30		
Met	Gln	Leu	Ala	Thr	Ser	Phe	Ile	Ser	Pro	Ser	Gln	Ala	Leu	Leu	Asn
		35					40					45			
Leu	Pro	Gln	Glu	Asp	Phe	Asp	Ser	Cys	Lys	Ser	Ser	Ala	Gln	Ala	Asp
	50					55				60					
Trp	Glu	Asn	Leu	Leu	His	Arg	Phe	Asp	Ile	Ile	Glu	Ile	Gly	Glu	Ala
65					70					75				80	
Asp	Arg	Thr	Phe	Phe	Asp	His	Cys	Leu	Tyr	Arg	Leu	Phe	Leu	Phe	Pro
			85						90				95		
Gln	Thr	Phe	Tyr	Glu	Ile	Asn	Glu	Ser	Gly	Gln	Ala	Ile	His	Met	Asp
		100					105				110				
Leu	Ala	Thr	Gly	Thr	Val	Lys	Pro	Gly	Val	Leu	Phe	Ser	Asn	Asn	Gly
	115					120				125					
Phe	Trp	Asp	Thr	Phe	Arg	Thr	Thr	Phe	Pro	Leu	Phe	Ala	Leu	Ile	Ile
	130				135					140					
Pro	Glu	His	Tyr	Gln	Arg	Phe	Leu	Glu	Gly	Phe	Leu	Asn	Ser	Tyr	Arg
145				150					155					160	
Asp	Thr	Gly	Phe	Leu	Pro	Lys	Trp	Leu	Ala	Pro	Asp	Glu	Arg	Gly	Met
			165					170				175			
Met	Pro	Gly	Thr	Leu	Leu	Asp	Gly	Ile	Ile	Ala	Asp	Ser	Ala	Cys	Lys
		180				185				190					
Asp	Met	Ala	Pro	Asp	Leu	Glu	Gly	Glu	Leu	Phe	Gln	Ala	Met	Leu	Arg
	195					200				205					

Asn Ser Gln Gln Ser Arg Pro Ser Arg Asn Gln Trp Pro Pro Arg Thr
 210 215 220
 Ser Pro Ile Pro Arg Thr Arg Leu Pro Leu Tyr Arg Pro Pro Arg Lys
 225 230 235 240
 Cys

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Met Met Val Ser His Ala Cys Ala Val Lys Leu Tyr Lys Glu Lys Gly
 1 5 10 15
 Tyr Lys Gly Glu Ile Gly Val Val His Ala Leu Pro Thr Lys Tyr Pro
 20 25 30
 Leu Asp Pro Glu Asn Pro Ala Asp Val Arg Ala Ala Glu Leu Glu Asp
 35 40 45
 Ile Ile His Asn Lys Phe Ile Leu Asp Ala Thr Tyr Leu Gly Arg Tyr
 50 55 60
 Ser Ala Glu Thr Met Glu Gly Val Asn His Ile Leu Ser Val Asn Gly
 65 70 75 80
 Gly Ser Leu Asp Leu Arg Glu Glu Asp Phe Thr Ala Leu Glu Ala Ala
 85 90 95
 Lys Asp Leu Asn Asp Phe Leu Gly Ile Asn Tyr Tyr Met Ser Asp Trp
 100 105 110
 Met Glu Ala Phe Asp Gly Glu Thr Glu Ile Ile His Asn Gly Lys Gly
 115 120 125
 Glu Lys Gly Ser Ser Lys Tyr Gln Ile Lys Gly Ile Gly Arg Leu Val
 130 135 140
 Ala Pro
 145

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

370

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

Met Asn Thr Ser Leu Lys Leu Ser Lys Gln Leu Ser Phe Gly Glu Glu
 1           5           10           15
Ile Ala Asn Ser Val Thr His Ala Val Gly Ala Val Ile Met Leu Ile
          20           25           30
Leu Leu Pro Ile Ser Ser Ile Tyr Ser Tyr Glu Ala His Gly Phe Leu
        35           40           45
Ser Ser Ile Gly Val Ser Ile Phe Val Ile Ser Leu Phe Leu Met Phe
      50           55           60
Leu Ser Ser Thr Ile Tyr His Ser Met Ala Tyr Gly Ser Thr His Lys
     65           70           75           80
Tyr Val Leu Arg Ile Ile Asp His Ser Met Ile Tyr Val Ala Ile Ala
          85           90           95
Gly Ser Tyr Thr Pro Val Val Leu Thr Leu Met Asn Asn Trp Phe Gly
        100           105           110
Tyr Leu Ile Ile Val Ile Gln Trp Gly Thr Thr Ile Phe Gly Ile Leu
        115           120           125
Tyr Lys Ile Phe Ala Lys Lys Val Asn Glu Lys Phe Ser Leu Ala Leu
       130           135           140
Tyr Leu Ile Met Gly Trp Leu Val Leu Ala Ile Ile Pro Ala Ile Ile
      145           150           155           160
Ser Gln Xaa Thr Pro Val Phe Trp Ile Leu Met Val Thr Gly Gly Leu
          165           170           175
Cys Tyr Thr Val Gly Ala Asp
          180

```

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

```

Met Leu Glu Asn Leu Cys Glu Leu Pro Phe Arg Pro Glu Ala Gln Arg
 1             5             10             15
Val Val Thr Lys Gly Tyr Leu Asn Leu Gln Asn Arg Asn Asp Leu Leu
      20             25             30
Leu Val Glu Asp Ile Thr Ala Asp Glu Trp Met Asp Val Gln Phe Glu
      35             40             45
Leu Gln Pro Thr Ile Tyr Lys Leu Lys Glu Gly Asp Thr Leu Arg Leu
      50             55             60
Val Leu Tyr Thr Thr Asp Phe Glu Ile Thr Ile Arg Asp Asn Thr Asp
      65             70             75             80
Tyr His Leu Thr Val Asp Leu Ala Gln Ser Met Leu Thr Leu Pro Cys
      85             90             95

```

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```

Met Asn Lys Ser Glu His Arg His Gln Leu Ile Arg Ala Leu Ile Thr
 1             5             10             15
Lys Asn Lys Ile His Thr Gln Ala Glu Leu Gln Ala Leu Leu Ala Glu
      20             25             30
Asn Asp Ile Gln Val Thr Gln Ala Thr Leu Ser Arg Asp Ile Lys Asn
      35             40             45
Met Asn Leu Ser Lys Val Arg Glu Glu Asp Ser Ala Tyr Tyr Val Leu
      50             55             60
Asn Asn Gly Ser Ile Ser Lys Trp Glu Lys Arg Leu Glu Leu Tyr Met
      65             70             75             80
Glu Asp Ala Leu Val Trp Met Arg Pro Val Gln His Gln Val Leu Leu
      85             90             95
Lys Thr Leu Pro Gly Leu Ala Gln Ser Phe Gly Ser Ile Ile Asp Asp
      100            105            110

```

Phe Glu Leu Pro
115

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Met	Gly	Lys	Leu	Ser	Ser	Ile	Leu	Leu	Gly	Thr	Val	Ser	Gly	Ala	Ala
1				5					10					15	
Leu	Ala	Leu	Phe	Leu	Thr	Ser	Asp	Lys	Gly	Lys	Gln	Val	Cys	Ser	Gln
			20					25					30		
Ala	Gln	Asp	Phe	Leu	Asp	Asp	Leu	Arg	Glu	Asp	Pro	Glu	Tyr	Ala	Lys
		35					40					45			
Glu	Gln	Val	Cys	Glu	Lys	Gln	Thr	Glu	Val	Lys	Glu	Gln	Ala	Thr	Asp
	50					55					60				
Phe	Val	Leu	Asn	Asn	Lys	Arg	Thr	Gly							
65						70									

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met	Tyr	Leu	Gly	Asp	Leu	Met	Glu	Lys	Ala	Glu	Cys	Gly	Gln	Phe	Ser
1				5					10					15	
Ile	Leu	Ser	Phe	Leu	Leu	Gln	Glu	Ser	Gln	Thr	Thr	Val	Lys	Ala	Val
			20					25					30		

Met Glu Glu Thr Gly Phe Ser Lys Ala Thr Leu Thr Lys Tyr Val Thr
 35 40 45
 Leu Leu Asn Asp Lys Ala Leu Asp Ser Gly Leu Glu Leu Thr Ile His
 50 55 60
 Ser Glu Asp Glu Asn Leu Arg Leu Ser Ile Gly Ala Ala Thr Lys Gly
 65 70 75 80
 Arg Asp Ile Arg Ser Leu Phe Phe Gly
 85

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Arg Phe Tyr Phe Met Glu Asn Val Val Val His Ile Ile Ser His
 1 5 10 15
 Ser His Trp Asp Arg Glu Trp Tyr Leu Pro Phe Glu Ser His Arg Met
 20 25 30
 Gln Leu Val Glu Leu Phe Asp Asn Leu Phe Asp Leu Phe Glu Asn Asp
 35 40 45
 Pro Glu Phe Lys Ser Phe His Leu Asp Gly Gln Thr Ile Val Leu Asp
 50 55 60
 Asp Tyr Leu Gln Ile Arg Pro Glu Asn Arg Asp Lys Val Gln Arg Tyr
 65 70 75 80
 Ile Asp Glu Gly Lys Leu Lys Ile Gly Pro Phe Tyr Ile Leu Gln Asp
 85 90 95
 Asp Tyr Leu Ile Ser Ser Glu Ala Asn Val Arg Asn Thr Leu Ile Gly
 100 105 110
 Gln Gln Glu Ala Ala Lys Trp Gly Lys Ser Thr Gln Ile Gly Tyr Phe
 115 120 125
 Pro Asp Thr Phe Gly Asn Met Gly Gln Ala Pro Gln Ile Leu Gln Lys
 130 135 140
 Ser Gly Ile His Val Ala Ala Phe Gly Arg Gly Val Lys Pro Ile Gly
 145 150 155 160
 Phe Asp Asn Gln Val Leu Glu Asp Glu Gln Phe Thr Ser Gln Phe Ser
 165 170 175

Glu Met Tyr Trp Gln Gly Val Asp Gly Ser Arg Val Leu Gly Ile Leu
 180 185 190
 Phe Ala Asn Trp Tyr Ser Asn Gly Asn Glu Ile Pro Val Asp Lys Asp
 195 200 205
 Glu Ala Leu Thr Phe Trp Lys Gln Lys Leu Ser Asp Val Arg Cys Leu
 210 215 220
 Arg Phe Asp Gln Pro Met Val Asp Asp Glu Thr Ala Val Thr Thr Ser
 225 230 235 240
 Leu Ser Gln Glu Lys Ser Glu Arg Ser His Ser Val Leu Gln Met Asn
 245 250 255
 Ser Ser Arg Met
 260

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Leu Thr Ala Ser Pro Leu Lys Lys Ser Ile Lys Lys Lys Asn Arg Lys
 1 5 10 15
 Leu Thr Asn Lys Xaa Glu Lys His Met Ser Lys Ile Ile Gly Ile Asp
 20 25 30
 Leu Gly Thr Thr Asn Ser Ala Val Ala Val Leu Glu Gly Thr Glu Ser
 35 40 45
 Lys Ile Ile Ala Asn Pro Glu Gly Asn Arg Thr Thr Pro Ser Val Val
 50 55 60
 Ser Phe Lys Asn Gly Glu Ile Ile Val Gly Asp Ala Ala Lys Arg Gln
 65 70 75 80
 Ala Val Thr Asn Pro Asp Thr Val Ile Ser Ile Lys Ser Lys Met Gly
 85 90 95
 Thr Ser Glu Lys Val Ser Ala Asn Gly Lys Glu Tyr Thr Pro Thr Arg
 100 105 110
 Asn Leu Ser Tyr Asp Pro Ser Ile Leu Glu Arg Leu Arg
 115 120 125

(2) INFORMATION FOR SEQ ID NO:408:

375

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

```

Met Asp Ser Thr Pro Val Ile Xaa Gly Ala Met Leu Ile Ser Pro Leu
 1             5             10             15
Met Thr Pro Ile Leu Gly Val Gly Leu Ser Leu Ala Ile Phe Asp Phe
 20             25             30
Lys Leu Leu Arg Lys Ser Phe Lys Ile Leu Ala Ile Gln Ile Leu Ala
 35             40             45
Ser Leu Ile Ala Ser Thr Leu Tyr Phe Tyr Leu Ser Pro Ile Ser Tyr
 50             55             60
Ala Ser Ser Glu Ile Val Ala Arg Thr Ser Pro Thr Ile Trp Asp Val
 65             70             75             80
Leu Ile Ala Phe Val Gly Gly Ile Ala Gly Ile Ile Gly Ala Arg Lys
 85             90             95
Lys Glu Thr Asn Asn Ile Val Pro Gly Val Ala Ile Ala Thr Ala Leu
100            105            110
Met Pro Pro Leu Cys Thr Val Gly Tyr Ala Ile Ala Ser Ala Asn Leu
115            120            125
Lys Phe Ile Ile Gly Ser Ser Tyr Leu Phe Leu Ile Asn Cys Ser Phe
130            135            140
Ile Val Ile Ala Thr Tyr Ile Gly Val Arg Leu Met Met Val Lys Lys
145            150            155            160
His Tyr Phe Lys Asp Asn Glu Glu Asp Ser Lys Met Arg Arg Ile Leu
165            170            175
Leu Leu Val Ala Val Leu Leu Met Ile Pro Ser Phe Ile Ser Ala Thr
180            185            190
Thr Leu Val Arg Glu Thr Leu Lys Lys Glu Ser Leu Lys Lys Phe Ile
195            200            205
Ser Glu Gln Phe Gln Gly His Asn Ile Leu Lys Lys Thr Tyr Ser Lys
210            215            220
Lys Thr His Thr Leu Lys Leu Thr Ile Ser Gly Asn Tyr Leu Thr Glu
225            230            235            240
Glu Glu Leu Asp Met Ile Ser Ser Lys Arg Gly Asp Tyr Gly Leu Ser
245            250            255

```

Asp Val Ser Val Gln Val Ser Gln Leu Ser Asp Ser Glu Gln Leu Ser
 260 265 270
 Lys Glu Glu Leu Val Glu Tyr Phe Phe Gln Tyr Ile Lys Asp Lys Glu
 275 280 285
 Ala Lys Glu Lys Glu Lys Ala Asn Lys Phe Tyr Thr Glu Ser Glu Glu
 290 295 300
 Gln
 305

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Ile Ala Arg Ser Tyr Gln Glu Met Asp Asp Leu Asp Thr Ala Tyr
 1 5 10 15
 Glu His Tyr Gln Glu Leu Thr Gly Asp Leu Lys Asp Asn Pro Glu Phe
 20 25 30
 Leu Glu His Tyr Ile Tyr Leu Leu Arg Glu Leu Gly His Phe Glu Glu
 35 40 45
 Ala Lys Val His Ala His Thr Tyr Leu Lys Leu Val Pro Asp Asp Val
 50 55 60
 Gln Met Gln Glu Leu Phe Glu Arg Leu
 65 70

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```

Met Leu Glu Glu Thr Gln Glu Ile Val Ala Gly Arg Val Ala Ser Val
 1           5           10           15
Glu Thr Leu Lys Arg Ile Glu Glu Leu Gly Phe Asp Phe Val Cys Leu
 20           25           30
Thr Gly Asn Pro Gly Thr Gly Val Ser Asn Arg Glu Ile Ile Lys Ala
 35           40           45
Val Gln Thr Ala Lys Glu Asn Phe Ser Gly Leu Ile Ile Ala Gly Lys
 50           55           60
Met His Gly Ala Gly Val Asn Glu Pro Val Ala Glu Leu Ser Val Ala
 65           70           75           80
Glu Gln Leu Leu Glu Ala Gly Ala Asp Val Ile Leu Val Pro Ala Val
 85           90           95
Gly Thr Val Pro Ala Phe His Asp Gln Glu Leu Arg Glu Val Val Asp
100           105           110
Leu Val His Ser Lys Gly Gly Leu Val Leu Ser Ala Ile Gly Thr Ser
115           120           125
Gln Glu Thr Ser Asp Thr Asp Thr Ile Lys Glu Ile Ala Leu Arg Asn
130           135           140
Lys Ile Cys Gly Val Asp Ile Gln His Ile Gly Asp Ala Gly Tyr Gly
145           150           155           160
Gly Leu Ala Thr Val Asp Asn Ile Tyr Ala Leu Ser Lys Ala Ile Arg
165           170           175
Gly Val Arg His Thr Val Ser Arg Leu Ala Arg Ser Val Asn Arg
180           185           190

```

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```

Met Ala Lys Val Thr Ile Met Leu Ala Cys Ala Ala Gly Met Ser Thr
 1           5           10           15
Ser Leu Leu Val Thr Lys Met Gln Lys Ala Ala Glu Asp Lys Gly Leu
 20           25           30

```

```

Asp Ala Glu Ile Phe Ala Val Pro Ala Pro Glu Ala Glu Glu Ile Val
      35              40              45
Ala Thr Lys Glu Val Asn Val Leu Leu Leu Gly Pro Gln Val Arg Tyr
      50              55              60
Leu Leu Gly Asp Phe Gln Glu Lys Leu Lys Asp Arg Gln Ile Pro Val
      65              70              75              80
Ala Val Ile Pro Met Thr Asp Tyr Gly Met Met Asn Gly Ser Lys Val
              85              90              95
Leu Asp Leu Ala Glu Ser Leu Leu Asp
      100              105

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

Met Leu Gln Arg Gln Gln Ala Ser Ala Ile Ile Asp Ala Arg Lys Met
  1              5              10              15
Ile Val Asp Gly Ala Val Gly Met Val Glu Met Ala Leu Glu Arg Leu
      20              25              30
Asn Glu Gly Glu Leu Val Glu Leu Asp Glu Glu Arg Lys Ala Ala Met
      35              40              45
Val Ser Asn Leu Leu Val Val Leu Cys Gly Asn His Asp Ala Gln Pro
      50              55              60
Ile Val Asn Thr Gly Ser Leu Tyr
      65              70

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Met Val Ala Gly Phe Thr Gly Glu Phe Val Lys Ser Lys Asp Ala Val
 1 5 10 15
 Glu Ala Phe Lys Trp Gly Val Ala Cys Gly Thr Ala Thr Thr Phe Ser
 20 25 30
 Asp Asp Leu Ala Thr Ala Glu Phe Ile Lys Glu Thr Tyr Gly Lys Val
 35 40 45
 Glu Val Glu Lys Arg
 50

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Tyr Glu Ser Pro Val Gly Phe Arg His Gly Pro Lys Ser Leu Ile
 1 5 10 15
 Asn Asp Asn Thr Val Val Leu Val Phe Gly Thr Thr Thr Asp Tyr Thr
 20 25 30
 Arg Lys Tyr Asp Leu Asp Leu Val Arg Glu Val Ala Gly Asp Gln Ile
 35 40 45
 Ala Arg Arg Val Val Leu Leu Ser Asp Gln Ala Phe Gly Leu Glu Asn
 50 55 60
 Val Lys Glu Val Ala Leu Gly Cys Gly Gly Val Leu Asn Asp Ile Tyr
 65 70 75 80
 Arg Val Phe Pro Tyr Ile Val Tyr Ala Gln Leu Phe Ala Leu Leu Thr
 85 90 95
 Ser Leu Lys Val Glu Asn Lys Pro Asp Thr Pro Ser Pro Thr Gly Thr
 100 105 110
 Val Asn Arg Val Val Gln Gly Val Ile Ile His Glu Tyr Gln Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

Met Ser His Asp His Asn His Asp His Glu Glu Arg Glu Leu Ile Thr
 1             5             10             15
Leu Val Asp Glu Gln Gly Asn Glu Thr Leu Phe Glu Ile Leu Leu Thr
          20             25             30
Ile Asp Gly Lys Glu Glu Phe Gly Lys Asn Tyr Val Leu Leu Val Pro
      35             40             45
Val Asn Ala Glu Glu Asp Glu Asp Gly Gln Val Glu Ile Gln Ala Tyr
      50             55             60
Ser Phe Ile Glu Asn Glu Asp Gly Thr Glu Gly Glu Leu Gln Pro Ile
65             70             75             80
Pro Glu Asp Ser Glu Asp Glu Trp Asn Met Ile Glu Glu Val Phe Asn
          85             90             95
Ser Phe Met Glu Glu
          100

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```

Met Glu Met Gln Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu
 1             5             10             15
Lys Asn Pro Leu Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr
          20             25             30
Glu Glu Phe Thr Asn Pro Trp His Ala Ala Ile Ser Ser Phe Val Ala
      35             40             45

```

Phe Phe Leu Arg Ser Leu Pro Pro Met Leu Ser Val Thr Ile Phe Pro
 50 55 60
 Ser Glu Tyr Arg Ile Pro Ala Thr Val Leu Ile Val Gly Val Ala Leu
 65 70 75 80
 Leu Leu Thr Gly Tyr Thr Ser Ala Arg Leu Gly Lys Asp Pro Thr Arg
 85 90 95
 Thr Val

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Pro Trp Asn Ala Ala Tyr Val Glu Pro Ser Arg Arg Pro Ala Asp
 1 5 10 15
 Gly Arg Tyr Gly Glu Asn Pro Asn Arg Leu Tyr Gln His His Gln Phe
 20 25 30
 Gln Val Val Met Lys Pro Ser Pro Ser Asn Ile Gln Glu Leu Tyr Leu
 35 40 45
 Glu Ser Leu Glu Lys Leu Gly Ile Asn Pro Leu Glu His Asp Ile Arg
 50 55 60
 Phe Val Glu Asp Asn Trp Glu Asn Pro Ser Thr Gly Ser Ala Gly Leu
 65 70 75 80
 Gly Trp Glu Val Trp Leu Asp Gly Met Glu Ile Thr Gln Phe Thr Tyr
 85 90 95
 Phe Gln Gln Val Gly Gly Leu Ala Thr Gly Pro Val Thr Ala Glu Val
 100 105 110
 Thr Tyr Gly Leu Glu Arg Leu Ala Ser Tyr Ile Gln Glu Val Asp Ser
 115 120 125
 Val Tyr Asp Ile Glu Trp Ala Asp Gly Val Lys Tyr Gly Glu Ile Phe
 130 135 140
 Ile Gln Pro Glu Tyr Glu His Ser Lys Tyr Ser Phe Glu Ile Ser Asn
 145 150 155 160
 Gln Glu Met Leu Leu Glu Asn Phe Asp Lys Phe Glu Lys Glu Ala Gly
 165 170 175

Arg Ala Leu Glu Glu Gly Leu Val His Pro Ala Tyr Asp Tyr Val Leu
 180 185 190
 Lys Cys Ser His Thr Phe Asn Leu Leu Asp Ala Arg Gly Ala Val Ser
 195 200 205
 Val Thr Glu Pro Cys Arg Leu Tyr Arg Ser Val Ser Val Thr Trp Pro
 210 215 220
 Val Leu
 225

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met Ser Lys Glu Leu Thr Phe Gln Glu Ile Ile Leu Thr Leu Gln Gln
 1 5 10 15
 Phe Trp Asn Asp Gln Gly Cys Met Leu Met Gln Ala Tyr Asp Asn Glu
 20 25 30
 Lys Gly Ala Gly Thr Met Ser Pro Tyr Thr Phe Leu Arg Ala Tyr Arg
 35 40 45
 Thr

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Met Phe Ile Thr Met Gly Val Gly Ala Ala Ile Leu Leu Leu Ile Trp
 1 5 10 15
 Ile Phe Phe Lys Gln Leu Leu Ile Thr Ser Phe Asp Glu Leu Leu Ala
 20 25 30
 Lys Ala Met Gly Met Pro Val Asn Phe Tyr His Tyr Leu Leu Met Val
 35 40 45
 Leu Leu Thr Leu Val Ser Val Thr Ala Met Gln Ser Val Gly Thr Ile
 50 55 60
 Leu Ile Val Ala Met Leu Ile Thr Pro Ala Ala Thr Ala Tyr Leu Tyr
 65 70 75 80
 Ala Asn Ser Leu Lys Ser Met Ile Phe Leu Ser Ser Thr Phe Gly Ala
 85 90 95
 Thr Ala Ser Val Leu Gly Leu Phe Ile Gly Tyr Ser Phe Asn Val Ala
 100 105 110
 Ala Gly Ser Ser Ile Val Leu Thr Ala Ala Ser Phe Phe Leu Ile Ser
 115 120 125
 Phe Phe Ile Ala Pro Lys Gln Arg Tyr Leu Lys Leu Lys Asn Lys His
 130 135 140
 Leu Leu Lys
 145

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Met Leu Arg Asn Arg Leu Glu Thr Glu Phe Gly Lys Arg Val Glu Val
 1 5 10 15
 Val Asp Val Ile Gly Tyr Tyr Glu Leu Asn Gln Glu Lys Leu Lys Gly
 20 25 30
 Ile Asp Phe Ile Val Ser Ala Val Asp Leu Ser Asn Leu Tyr Phe Gln
 35 40 45
 Ile Pro Val Phe Lys Val Ser Val Phe Leu Lys Ser Asp Glu Met Glu
 50 55 60
 Met Ile Arg Lys Ala Met Val Gln Met Gln Val Ser Ser Tyr Val Gln
 65 70 75 80

Ser Ser Lys Ile Asn Lys Phe Glu Asn Asn Gly Phe Arg Gln Tyr Phe
 85 90 95
 Ser Lys Glu Asn Phe Leu Ile Cys Thr Glu Ser Asp Lys Val Asn Leu
 100 105 110
 Leu Glu Lys Met Val Glu Ser Leu Ser Val Gly Glu Ser Asn Glu Phe
 115 120 125
 Glu Gln Ser Leu Leu Tyr Gly Ile Lys Gln Arg Glu Glu Leu Ser Ser
 130 135 140
 Val Val Phe Ser Glu Lys Ile Ala Val Pro His Pro Ile Gln Pro Phe
 145 150 155 160
 Gly Thr Glu Glu Lys Val Ser Val Ala Ile Cys Lys Asp Ser Leu Leu
 165 170 175
 Trp Asp Asn Gln Ser Ser His Val Gln Thr Ser Tyr Phe Phe Tyr Leu
 180 185 190
 His Gln Tyr Met Gly Thr Glu Gly Leu Ala Thr Val Thr Lys Lys Ile
 195 200 205
 Val Ser Leu Thr Glu Asn Asp Glu Leu Gln Asn Gln Leu Ile Ser Cys
 210 215 220
 Asn Asn Phe Glu Asp Phe Ile Asn Ile Phe Glu Lys Ile Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Met Pro Arg Ala Ser Phe Asp Gln Val Asn Gln Val Arg Gln Glu Asn
 1 5 10 15
 Gly Glu Pro Glu Phe Ala Asn Pro Arg Asn Ala Ala Ala Gly Thr Ile
 20 25 30
 Val Ser Val Gly Tyr Ser Ser Ser Phe Gln Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

385

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

Met Arg Gln Gln Glu Leu Leu Cys Gln Leu Asp Thr Ala Val Val Ser
 1           5           10           15
Lys Arg Asn Leu Ala Thr Phe Leu Tyr Gln Glu Ala Ser Pro Ser Thr
          20           25           30
Arg Asp Ser Gln Glu Lys Gly Leu Lys Tyr Leu Glu Gln Leu Gly Ile
          35           40           45
Val Val Asn His Lys Arg Ile Phe Gly Trp Lys Ile Asp Lys Ile Trp
          50           55           60
Asn Phe Ile Gln Glu Val Gly Gln Glu Arg Glu Asn Leu Pro
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```

Met Ala Leu Thr Glu Gln Lys Arg Ala Arg Leu Glu Lys Leu Ser Asp
 1           5           10           15
Glu Asn Gly Ile Ile Ser Ala Leu Ala Phe Asp Gln Arg Gly Ala Leu
          20           25           30
Lys Arg Leu Met Ala Gln His Gln Thr Glu Glu Pro Thr Val Ala Gln
          35           40           45
Met Glu Glu Leu Lys Val Leu Val Ala Asp Glu Leu Thr Lys Tyr Ala
          50           55           60
Ser Ser Met Leu Leu Asp Pro Glu Tyr Gly Leu Pro Ala Thr Lys Ala
65           70           75           80

```

Leu Asp Glu Lys Ala Gly Leu Leu Leu Ala Tyr Glu Lys Thr Gly Tyr
 85 90 95
 Asp Thr Thr Ser Thr Lys Arg Leu Pro Asp Cys Leu Asp Val Trp Ser
 100 105 110
 Ala Lys Arg Ile Lys Glu Glu Gly Ala Asp Ala Val Lys Phe Leu Leu
 115 120 125
 Tyr Tyr Asp Val Asp Ser Ser Asp Glu Leu Asn Gln Glu Lys Gln Ala
 130 135 140
 Tyr Ile Gly Ala Tyr Arg Phe
 145 150

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Leu Asn Trp Ile Leu Leu Gln Gly Leu Ile Cys Gln Arg Asp Ala Ser
 1 5 10 15
 Tyr Asp Met Lys Gln Asp Asp Leu Asp Lys Val Ala Asp Tyr Leu Phe
 20 25 30
 Lys Thr Glu Glu Trp Thr Met Tyr Glu Leu Ile Leu Phe Gly Asn Leu
 35 40 45
 Tyr Ser Phe Tyr Asp Val Asp Tyr Val Thr Arg Ile Gly Arg Glu Val
 50 55 60
 Met Glu Arg Glu Glu Phe Tyr Gln Glu Ile Ser Arg His Lys Arg Leu
 65 70 75 80
 Val Leu Ile Leu Ala Leu Asn Cys Tyr Gln His Cys Leu Glu His Ser
 85 90 95
 Ser Phe Tyr Asn Ala Asn Tyr Phe Glu Ala Tyr Thr Glu Lys Ile Ile
 100 105 110
 Asp Lys Gly Ile Lys Leu Tyr Glu Arg Asn Val Phe His Tyr Leu Lys
 115 120 125
 Gly Phe Ala Leu Tyr Gln Lys Gly Gln Cys Lys Glu Gly Cys Lys Gln
 130 135 140
 Met Gln Glu Thr Met His Ile Phe Asp Val Leu Gly Leu Pro Glu Gln
 145 150 155 160

Val Ala Tyr Tyr Gln Glu His Tyr Glu Lys Phe Val Lys Ser
 165 170

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Tyr Pro Asp Asp Ser Leu Thr Leu His Thr Asp Leu Tyr Gln Ile
 1 5 10 15
 Asn Met Met Gln Val Tyr Phe Asp Gln Gly Ile Tyr Asn Lys Lys Ala
 20 25 30
 Val Phe Glu Val Tyr Phe Arg Gln Gln Pro Phe Lys Asn Gly Tyr Ala
 35 40 45
 Val Phe Ala Gly Leu Glu Arg Ile Val Asn Tyr Leu Glu Asp Leu Arg
 50 55 60
 Phe Ser Asp Ser Asp Ile Ala Tyr Leu Glu Ser Leu Gly Tyr His Gly
 65 70 75 80
 Ala Phe Leu Asp Tyr Leu Arg Asn Phe Lys Leu Glu Leu Thr Val Arg
 85 90 95
 Ser Ala Gln Glu Gly Asp Leu Val Phe Ala Asn Glu Pro Ile Val Gln
 100 105 110
 Val Glu Gly Pro Leu Ala Gln Cys Gln Leu Val Glu Thr Ala Leu Leu
 115 120 125
 Asn Ile Val Asn Tyr Gln Thr Leu Val Ala Thr Lys His Ser Tyr Ser
 130 135 140
 Phe Gly Tyr Arg Arg
 145

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

Met Leu Val Leu Asn Tyr Val Tyr Ala Val Pro Leu Tyr Ala Lys Phe
 1             5             10             15
Ala Asn Phe Asp Ile Gly Lys Ile Leu Gly Leu Ser Asn Tyr Leu Met
          20             25             30
Thr Met Val Leu Pro Phe Asn Leu Ile Glu Gly Val Ile Phe Ser Val
      35             40             45
Ser Phe Trp Leu Leu Tyr Val Leu Leu Lys Pro Thr Leu Lys His Tyr
      50             55             60
Glu Arg
65

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

Met Glu Glu Ser Lys Glu Leu Asn Ala Val Ile Asp Val Ile Met Leu
 1             5             10             15
Ala Gly Thr Ile Leu Leu Lys Ser Gly Ser Glu Ile His Arg Val Glu
          20             25             30
Asp Thr Met Ile Arg Ile Ala His Ser Gln Gly Ile Val Asp Cys Asn
      35             40             45
Val Leu Ala Met Pro Ala Ala Ile Phe Phe Ser Ile Glu Asn Thr Asn
      50             55             60
Ile Ser Arg Met Asn Ala
65             70

```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids

389

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```

Leu Phe Glu Lys Lys Gly Leu Thr Val Asp Ala Asn Gly Asn Ala Thr
 1             5             10             15
Val Asp Leu Thr Phe Lys Glu Asp Ser Glu Lys Gly Lys Ser Arg Phe
             20             25             30
Gly Val Ser Leu Lys Phe Lys Asp Thr Asn Asn Asn Val Phe Val Gly
             35             40             45
Tyr Asp Lys Asp Gly Trp Phe Trp Glu Tyr Lys Ser Pro Thr Thr Ser
             50             55             60
Thr Trp Tyr Arg Gly Ser Arg Val Ala Ala Pro Glu Thr Gly Ser Thr
             65             70             75             80
Asn Arg Leu Ser Ile Ser Leu Gln Val Arg Arg Ser Gly Lys Cys Gln
             85             90             95
Ala Asn Lys Asp Val Asn Leu Leu
             100
  
```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

Met Val Glu Asn Pro Glu Gly Phe His Phe Asp Asp Leu Gln Leu Gln
 1             5             10             15
Thr His Ala Asp Asn Asp Ile Glu Ala Leu Val Ser Leu Ala Asn Met
             20             25             30
Asp Gly Glu Lys Val Glu Phe Asn Ala Thr Gly Gln Gly Ser Val Glu
             35             40             45
Ala Ile Phe Asn Ala Ile Asp Lys Phe Phe Asn Gln Ser Val Arg Leu
             50             55             60
  
```

390

```

Val Ser Tyr Thr Ile Asn Ala Val Thr Asp Gly Ile Asp Ala Gln Asp
65              70              75              80
Arg Val Leu Val Thr Val Glu Asn Arg Asp Thr Glu Thr Ile Phe Asn
85              90              95
Ala Ala Gly Leu Asp Phe Asp Val Leu Lys Ala Ser Ala Ile Ala Tyr
100            105            110
Ile Asn Ala Asn Thr Phe Val Gln Lys Glu Asn Ala Gly Glu Met Gly
115            120            125
Arg Ser Val Ser Tyr His Asp Met Pro Ser Val
130            135

```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

Met Ala Lys Lys Lys Ile Lys Lys Glu Lys Ile Asp Asn Val Gly Ile
1              5              10              15
His Ser Phe Ser Lys Lys Ala Asp Ile Phe Phe Ser Ile Ile Ser Gly
20            25            30
Leu Ile Ala Leu Ser Cys Ile Leu Pro Phe Val Phe Val Ile Ile Ile
35            40            45
Ser Val Thr Asp Glu Lys Ser Leu Leu Gln Tyr Gly Tyr Ser Phe Phe
50            55            60
Pro Ser Gln Phe Gly Leu Asp Gly Phe Glu Phe Leu Ala Gln Phe Lys
65            70            75            80
Asp Lys Ile Leu Gln Ala Leu Phe Ile Ser Val Phe Val Thr Val Val
85            90            95
Gly Thr Leu Thr Asn Val Phe Ile Thr Thr Thr Tyr Ala Tyr Ala Ile
100           105           110
Ser Arg Thr Thr Phe Lys Tyr Arg Arg Phe Phe Thr Ile Phe Val Leu
115           120           125
Leu Ser Met Leu Phe Asn Ala Gly Leu Val Pro Gly Tyr Ile Met Val
130           135           140
Thr Arg Val Leu Gln Leu Gly Asp Thr Val Trp Ala Phe Asp Cys Ser
145           150           155           160

```

(2) INFORMATION FOR SEQ ID NO:431:

(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

(2) INFORMATION FOR SEQ ID NO:432:

(A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

Met Ile Arg Lys Val Glu Met Ala Asp Val Glu Val Leu Ala Lys Ile
 1             5             10             15
Ala Lys Gln Thr Phe Arg Glu Thr Phe Ala Tyr Asp Asn Thr Glu Glu
          20             25             30
Gln Leu Gln Glu Tyr Phe Glu Glu Ala Tyr Ser Leu Lys Thr Leu Ser
          35             40             45
Thr Glu Leu Gly Asn Pro Asp Ser Glu Thr Tyr Phe Ile Met Gln Glu
          50             55             60
Glu Glu Ile Ala Ala Phe Leu Lys Val Asn Trp Gly Ser Ala Gln Thr
          65             70             75             80
Glu Arg Glu Leu Glu Asp Ala Phe Glu Ile Gln Arg Leu Tyr Val Leu
          85             90             95
Gln Lys Phe Gln Gly Phe Gly Leu Gly Lys Gln Leu Phe Glu Phe Ala
          100             105             110
Leu Glu Leu Ala Thr Lys Asn Ser Phe Ser Trp Ala Trp Leu Gly Val
          115             120             125
Trp Glu His Asn Thr Lys Ala Gln Ala Phe Tyr Asn Arg Tyr Gly Phe
          130             135             140
Glu Lys Phe Ser Gln His His Phe Met Val Gly Gln Lys Val Asp Thr
          145             150             155             160
Asp Trp Leu Leu Arg Lys Lys Leu Arg
          165

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

Met Lys Ser Ile Ile Asp Val Lys Asn Leu Ser Phe Arg Tyr Lys Glu
 1             5             10             15
Asn Gln Asn Tyr Tyr Asp Val Lys Asp Ile Thr Phe His Val Lys Arg
          20             25             30

```

Gly Glu Trp Leu Ser Ile Val Gly His Asn Gly Ser Gly Lys Ser Thr
 35 40 45
 Thr Val Arg Leu Ile Asp Gly Leu Leu Glu Ala Glu Ser Gly Glu Ile
 50 55 60
 Val Ile Asp Gly Gln Arg Leu Thr Glu Glu Asn Val Trp Asn Ile Arg
 65 70 75 80
 Arg Gln Ile Gly Met Val Phe Gln Asn Pro Asp Asn Gln Phe Val Gly
 85 90 95
 Ala Thr Val Glu Asp Asp Val Ala Phe Gly Leu Glu Asn Gln Gly Leu
 100 105 110
 Ser Arg Gln Glu Met Lys Lys Arg Val Glu Glu Ala Leu Ala Leu Val
 115 120 125
 Gly Met Leu Asp Phe Lys Lys Arg Glu Pro Ala Arg Pro Ile Arg Cys
 130 135 140
 Gln Lys His Val Trp Pro Leu Gln Val Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Gln Val Ala Phe Thr Gly Glu Thr Ser Pro Gln Val Leu Lys Glu
 1 5 10 15
 Ile Gly Thr Asp Tyr Val Val Ile Gly His Ser Glu Arg Arg Asp Tyr
 20 25 30
 Phe His Asp Thr Asp Glu Asp Val Asn Lys Lys Ala Lys Ala Ile Phe
 35 40 45
 Ala Asn Gly Met Leu Pro Ile Ile Cys Cys Gly Glu Ser Leu Glu Thr
 50 55 60
 Tyr Glu Ala Gly Lys Ala Ala Glu Phe Val Gly Ala Gln Val Ser Ala
 65 70 75 80
 Ala Leu Ala Gly Leu Thr Ala Glu Gln Val Ala Ala Ser Val Ile Ala
 85 90 95
 Tyr Glu Pro Ile Trp Ala Ile Gly Thr Gly Lys Ser Ala Ser Gln Asp
 100 105 110
 394

Asp Ala Gln Lys Met Cys Lys Val Val Arg Asp Val Val Ala Ala Asp
 115 120 125
 Phe Gly Gln Glu Val Ala Asp Lys Val Arg Val Gln Tyr Gly Gly Ser
 130 135 140
 Val Lys Pro Glu Asn Val Ala Ser Tyr Met Ala Cys Pro Asp Val Asp
 145 150 155 160
 Gly Ala Leu Val Gly Gly Ala Ser Leu Glu Ala Glu Ser Phe Leu Ala
 165 170 175
 Leu Leu Asp Phe Val Lys
 180

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Gly Lys Lys Arg Trp Ala Arg Asn Gly Phe Glu Ser Asn Asp Ala
 1 5 10 15
 Ser Tyr Ala Gln Val Val Ser Leu Tyr Asp Asp Thr Ser Ile Ser Val
 20 25 30
 Ser Asn Asn Glu Thr Asp Lys Val Leu Ala Gly Ser Leu Tyr Thr Asp
 35 40 45
 Thr Asn Glu Gln Gly Leu Thr Ile Pro Ser Ser Leu Leu Lys Asn Trp
 50 55 60
 Asn Glu Gln Thr Gly Lys Asn Leu Thr Ala Asn Asp Leu Ile Gly Lys
 65 70 75 80
 Ser Val Ser Val Ser Ile Val Glu Ser Ala Ala Glu Thr Ser Lys Ile
 85 90 95
 Ala Gln Phe Gln Thr Lys Ile Val Arg Val Ile Asn Asp Glu Asp Asp
 100 105 110
 Met Glu Asp Ser Asn Ser Phe Met Leu Ser His Gln Met Glu Thr Ile
 115 120 125
 Leu Lys Glu Ala Gly Phe Thr Lys Ala Val Ser Tyr Phe Ile Leu Glu
 130 135 140
 Leu Lys Asp Pro Ser Gln Thr Lys Val Val Thr Glu Glu Leu Gln Lys
 145 150 155 160

Asn Lys Lys Tyr Thr Val Leu Ser
165

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met	Met	His	Thr	Tyr	Leu	Gln	Lys	Lys	Ile	Glu	Asn	Ile	Lys	Thr	Thr
1					5				10					15	
Leu	Gly	Glu	Met	Ser	Gly	Gly	Tyr	Arg	Arg	Met	Val	Ala	Ala	Met	Ala
				20				25					30		
Asp	Leu	Gly	Phe	Ser	Gly	Thr	Met	Lys	Ala	Ile	Trp	Asp	Asp	Leu	Phe
		35					40					45			
Ala	His	Arg	Ser	Phe	Ala	Gln	Trp	Ile	Tyr	Leu	Leu	Val	Ser	Gly	Ser
	50					55					60				
Phe	Pro	Leu	Trp	Leu	Glu	Leu	Val	Tyr	Glu	His	Arg	Ile	Val	Asp	Trp
65				70					75					80	
Ile	Gly	Met	Ile	Cys	Ser	Leu	Thr	Gly	Ile	Ile	Cys	Val	Ile	Phe	Val
			85						90				95		
Ser	Glu	Gly	Arg	Ala	Ser	Asn	Tyr	Leu	Phe	Gly	Leu	Ile	Asn	Ser	Val
			100				105						110		
Ile	Tyr	Leu	Ile	Leu	Ala	Leu	Gln	Lys	Gly	Phe	Tyr	Gly	Glu	Val	Leu
		115					120					125			
Thr	Thr	Leu	Tyr	Phe	Thr	Val	Met	Gln	Pro	Ile	Gly	Leu			
	130						135					140			

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

Met Met Arg His Lys Phe His Gly Ser Gly Leu Val Gln Lys Lys Thr
 1             5             10             15
Gly Ser Ile Pro Leu Glu Ile Glu Leu Thr Gln Lys Gly Ile Val Thr
             20             25             30
Lys Val Asn His Leu Lys Gln Ala Arg Leu Ser Gly Tyr Val Gly His
             35             40             45
Val Gln Val Val Ser Leu Ala Pro Glu Asp Leu Gln Ile Ile Lys Gly
             50             55             60
Ala Pro Trp Ile Arg Arg
65             70

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

Met Arg Gly Ile His Phe Val Gln Ile Pro Thr Ser Leu Thr Ala Gln
 1             5             10             15
Val Asp Ser Ser Ile Gly Gly Lys Thr Gly Val Asn Thr Pro Phe Ala
             20             25             30
Lys Asn Met Val Gly Thr Phe Ala Gln Pro Asp Gly Val Leu Ile Asp
             35             40             45
Pro Leu Val Leu Glu Thr Leu Gly Lys Arg Glu Leu Ile Glu Gly Met
             50             55             60
Gly Glu Val Ile Lys Tyr Gly Leu Ile Glu Asp Pro Glu Leu Trp Ala
65             70             75             80
Leu Leu Thr Gly Leu Asn Gly Ser Val Glu Ser Ile Leu Glu His Ala
             85             90             95
Glu Thr Leu Ile Glu His Ser Cys Gln Val Lys Arg Lys Met Val Val
             100            105            110
Glu Asp Glu Leu Asp Asn Gly Ile Arg Leu Tyr Leu Asn Phe Gly His
             115            120            125

```

Thr Ile Gly His Ala Ile Glu Ala Thr Ala Gly Tyr Gly Lys Val Met
 130 135 140
 His Gly Glu Ala Val Ala Met Gly Met Val Gln Ile Ser Lys Ile Ala
 145 150 155 160
 Glu Glu Lys Gly Leu Met Pro Ala Gly Ile Thr Gln Ser Ile Thr Glu
 165 170 175
 Met Cys Gln Lys Phe Gly Leu Pro Val Asp Tyr Glu Asn Trp Glu Val
 180 185 190
 Asp Lys Leu Tyr Gln Ala Leu Thr His Asp Lys Lys Ala Arg Gly Asn
 195 200 205
 Thr Leu Lys Leu Val Leu Val Pro Glu Leu Gly Ser Ala Thr Ile His
 210 215 220
 Pro Val Ser Leu Glu Glu Met Lys Asp Tyr Leu Val Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Gly Lys Glu Lys Val Trp Leu Pro Arg Lys Gln Gly Leu Pro Gly
 1 5 10 15
 Leu Ala Tyr Tyr Val Ile Glu Val Ala His Lys Glu Glu Leu Leu Thr
 20 25 30
 Ile Ala Gln Arg Ala Gln Glu Val Asp Val Pro Ile Lys Trp Met Thr
 35 40 45
 Ser Ser Gln Leu Glu Ile Thr Asp Ser Asp Gly Ile Val Thr Cys Ile
 50 55 60
 Arg Leu Ala Arg
 65

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

Met Cys Ile Thr Pro Val Ala Ser Leu Ala Pro Asp Val Phe Cys Val
 1             5             10             15
Ser Met Asn Gly Leu Ser Lys Ser His Arg Ile Ala Gly Phe Arg Val
          20             25             30
Gly Trp Met Val Leu Ser Gly Pro Lys Thr His Val Lys Gly Tyr Ile
          35             40             45
Glu Gly Leu Asn Met Leu Ser Asn Met Arg Leu Cys Ser Asn Val Leu
          50             55             60
Ala Gln Gln Val Val Gln Thr Ser Leu Gly Gly His Gln Ser Val Asp
65             70             75             80
Glu Leu Leu Leu Ser Trp Trp Thr Asn Leu Arg Ala Lys Lys Phe His
          85             90             95
Leu

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Met Arg Leu Glu Gln Asp Cys Pro Val Phe Leu Lys Ile Lys Glu Lys
 1             5             10             15
Asp Met Ala Ser Lys Met Leu His Thr Cys Leu Arg Val Glu Asn Leu
          20             25             30
Glu Lys Ser Ile Ala Phe Tyr Gln Asp Ala Phe Gly Phe Lys Glu Leu
          35             40             45
Arg Arg Arg Asp Phe Pro Asp His Ala Phe Thr Ile Val Tyr Leu Gly
          50             55             60

```

(2) INFORMATION FOR SEQ ID NO:442:

(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

(2) INFORMATION FOR SEQ ID NO:443:

(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

400

Val Asn Glu Val Gly Pro Tyr Ile Lys Glu Leu Gly Tyr Lys Lys Ala
 20 25 30
 Leu Leu Val Thr Asp Lys Tyr Ile Glu Gly Ser Asp Ile Leu Pro Lys
 35 40 45
 Val Leu Lys Pro Leu Asp Thr Glu Gly Ile Glu Tyr Val Ile Phe Ser
 50 55 60
 Asp Val Asp Ala Lys Pro Tyr Leu
 65 70

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Met Pro Ser Phe Asp Ala Gln His Pro Glu Ile Leu Glu Thr Ile Arg
 1 5 10 15
 Asp Thr Lys Asp Leu Pro Glu Glu Ala Val Leu Asp Ala Ala Ile Thr
 20 25 30
 Glu Phe Leu Asn Gln Ser Ser Phe Pro Ile Arg Ile Glu Val Ser Asp
 35 40 45
 Gly Ser Val Ser Lys
 50

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Ile Leu Leu Ile Asp Asn Tyr Asp Ser Phe Thr Tyr Asn Leu Ala
 1 5 10 15
 Gln Tyr Ile Gly Asn Phe Ala Glu Val Gln Val Leu Arg Asn Asp Asp
 20 25 30
 Ser Lys Leu Tyr Glu Glu Ala Glu Lys Ala Asp Gly Leu Val Phe Ser
 35 40 45
 Pro Gly Pro Gly Trp Pro Val Asp Ala Gly Lys Met Glu Asp Met Ile
 50 55 60
 Arg Asp Phe Ala Gly Lys Lys Pro Ile Leu Gly Ile Cys Leu Gly His
 65 70 75 80
 Gln Ala Ile Ala Glu Val Phe Gly Gly Lys Leu Gly Leu Ala Pro Lys
 85 90 95
 Val Met His Gly Lys Gln Ser Asn Ile Asn Phe Glu Ala Pro Ser Val
 100 105 110
 Leu Tyr Gln Gly Ile Glu Asp Gly Arg Ala Val Met Arg Tyr His Ser
 115 120 125
 Ile Leu Ile Glu Glu Met Pro Glu Asp Phe Glu Val Thr Ala Arg Ser
 130 135 140
 Thr Asp Asp Gln Ala Ile Met Gly Ile Gln His Lys Asn Leu Pro Ile
 145 150 155 160
 Tyr Gly Phe Gln Tyr His Pro Glu Ser Ile Gly Thr Pro Asp Gly Leu
 165 170 175
 Ser Ser Ile Arg Asn Phe Ile Glu Glu Val Val Lys
 180 185

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Leu Leu Ala Phe Val Ala Trp Asn Phe Val Thr Phe Phe Leu Cys Pro
 1 5 10 15
 Pro Thr Arg Asn Glu Ile Ser Tyr Gln His Ala Ala Pro Thr Phe Thr
 20 25 30
 Gly Val Thr Ala Phe Leu Met Tyr Phe Phe Tyr Pro Val Ile Ala Gly
 35 40 45

Pro Ile Phe Glu Asp Met Ile Tyr Arg Gly Leu Val Met Thr Ala Leu
 50 55 60
 Glu Lys Gly Lys Lys Trp Gly Leu Asp Val Leu Gly Ser Ala Val Leu
 65 70 75 80
 Phe Gly Val Ser His Ile Ser Asn His Gly Trp Val Leu Thr Asp Phe
 85 90 95
 Val Phe Tyr Met Gly Gly Gly Leu Ile Phe Ala Val Leu Phe Arg Met
 100 105 110
 Thr Lys Ser Ile Tyr Trp Pro Ile Gly Leu His Ile Val Tyr Asn Gly
 115 120 125
 Ile Gly Gln Leu Leu Met Leu Leu
 130 135

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Met Thr Val Asp Arg Glu Gly Phe Glu Ala Ala Met Lys Glu Gln Gln
 1 5 10 15
 Glu Arg Ala Arg Ala Ser Ala Val Lys Gly Gly Ser Met Gly Met Gln
 20 25 30
 Asn Glu Thr Leu Gln Asn Ile Thr Val Glu Ser Ala Phe Asn Tyr Asn
 35 40 45
 Ala Ser Gln Leu Ser Ser Lys Leu Val Ala Ile Val Ala Asp Asn Ala
 50 55 60
 Glu Val Glu Ala Val Ser Glu Gly Thr Ala Ser Leu Ile Phe Ala Glu
 65 70 75 80
 Thr Ser Phe Tyr Ala Glu Met Gly Gly Gln Val Ala Asp Tyr Gly Gln
 85 90 95
 Ile Leu Asp Glu Ser Gly Lys Val Val Ala Thr Val Thr Asn Val Gln
 100 105 110
 Lys Ala Pro Asn Gly Gln Ala Leu His Thr Val Glu Val Leu Ala Pro
 115 120 125
 Leu Ala Leu Asn Gln Glu Tyr Thr Leu Ala Ile Asp Ser Asn Arg Arg
 130 135 140

His Arg Val Met Lys Asn His Thr Ala Thr His Leu Leu His Ala Ala
 145 150 155 160
 Leu His Asn Ile Leu Gly Asn His Ala Thr Gln Ala Gly Ser Leu Asn
 165 170 175
 Glu Val Glu Phe Leu Arg Phe Asp Phe Thr His Phe Gln Ala Val Thr
 180 185 190
 Ala Glu Glu Leu Arg Ala Ile Glu Gln Gln Val Asn Glu Lys Ile Trp
 195 200 205
 Glu Ala Leu Glu Val Lys Thr Val Glu Thr Asp Ile Asp Thr Ala Lys
 210 215 220
 Glu Asn Gly Arg Ser Asn Ser Cys Ser Pro Gly Gly Ser Thr Asn Ser
 225 230 235 240
 Xaa Xaa Ala Ala Thr Ala Val Glu Leu His Phe Xaa Phe Pro Leu Met
 245 250 255
 Lys Val Asn Cys Xaa Leu Gly Leu Xaa Trp Pro Xaa Arg Phe Pro Phe
 260 265 270

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met Asp Ala Glu Val Ser Lys Asn Leu Arg Leu Ile Leu Glu Arg Lys
 1 5 10 15
 Gly Met Thr Ile Leu Thr Gly Thr Lys Leu Gln Glu Ile Ile Glu Glu
 20 25 30
 Asn Gly Gln Leu Arg Ile Lys Val Glu Gly Lys Asp Asn Ile Ile Ala
 35 40 45
 Ser Lys Ala Leu Leu Ser Ile Gly Arg Met Pro Asp Leu Glu Gly Ile
 50 55 60
 Gly Glu Val Glu Phe Glu Leu Asp Arg Gly Cys Ile Lys Val Asn Glu
 65 70 75 80
 Tyr Met Glu Thr Ser Val Pro Gly Ile Tyr Ala Pro Gly Asp Ile Asn
 85 90 95
 Gly Thr Lys Met Leu Ala His Ala Ala Phe Arg Met Gly Glu Val Ser
 100 105 110
 404

```

Ala Glu Asn Ala Leu Lys Gly Asn His Ala Val Ala Lys Leu Asn Leu
    115                      120                      125
Thr Pro Ala Ala Ile Tyr Thr Leu Pro Glu Val Ala Ala Val Gly Leu
    130                      135                      140
Thr Glu Glu Gln Ala Arg Glu Lys Tyr Asp Val Ala Ile Gly Lys Phe
    145                      150                      155                      160
Asn Phe Ala Ala Asn Gly Arg Ala Ile Ala Ser Asp Ala Ala Gln Gly
                      165                      170                      175
Phe Val Lys Val Ile Ala Asp Lys Lys Tyr Gly Glu Ile Leu Gly Val
                      180                      185                      190
His Ile Ile Val Pro Ala Ala Ala Glu Leu Ile Asn Glu Ala Ser Ser
                      195                      200                      205
Ile Ile Glu Met Glu Ile Thr Val Glu Glu Met Leu Lys Thr Ile His
                      210                      215                      220
Gly His Pro Thr Tyr Phe Glu Val Met Tyr Glu Ala Phe Ala Asp Val
    225                      230                      235                      240
Leu Gly Met Ala Ile His Ser Pro Lys Lys Lys
                      245                      250

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

Leu Ile Val Glu Thr Ile Leu Gly Ile Leu Gly Ser Arg Gly Ile His
  1              5              10              15
Leu Ala Val Gln Gly Cys Glu His Val Asn Arg Ala Leu Val Val Glu
      20              25              30
Arg Gln Val Ala Glu Gln Phe Asp Leu Glu Ile Val Ser Val His Pro
      35              40              45
Thr Leu His Ala Gly Gly Ser Gly Gln Leu Ala Ala Phe Lys Phe Met
      50              55              60
Gln Asp Pro Val Glu Val Glu Phe Ile Lys Ala His Ala Gly Leu Asp
      65              70              75              80
Ile Gly Asp Thr Ala Ile Gly Met His Val Lys His Val Gln Val Pro
      85              90              95

```

Ile Arg Pro Ile Leu Arg Glu Ile Gly His Ala His Val Thr Ala Leu
 100 105 110
 Ala Ser Arg Pro Lys Leu Ile Gly Gly Ala Arg Ala His Tyr Pro Gln
 115 120 125
 Asp Ala Ile Arg Lys Ser
 130

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Lys Ile Val Ser Gly Ile Tyr Gly Gly Arg Pro Leu Lys Thr Leu
 1 5 10 15
 Glu Gly Lys Thr Thr Arg Pro Thr Ser Asp Lys Val Arg Gly Ala Ile
 20 25 30
 Phe Asn Met Ile Gly Pro Tyr Phe Glu Val Gly Arg Val Leu Asp Leu
 35 40 45
 Tyr Ala Gly Ser Gly Gly Leu Ser Ile Glu Ala Val Ser Arg Gly Met
 50 55 60
 Ser Ser Ala Val Leu Val Glu Arg Asp Arg Lys Ala Gln Thr Ile Arg
 65 70 75 80
 Gly

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

Met Arg Phe Val Lys Glu Phe Gly Ala Val Phe Leu Ile Gly Ile Gly
 1           5           10           15
Gly Glu Leu Pro Asp Gly Lys Pro His Asp Gly Arg Ala Pro Asp Tyr
      20           25           30
Asp Asp Trp Thr Ser Glu Ser Glu Asn Gly Tyr Lys Gly Leu Asn Gly
      35           40           45
Asp Ile Leu Val Trp Asn Glu Ser Leu Gly Gly Ala Phe Glu Leu Ser
      50           55           60
Ser Met Gly Ile Arg Val Asp Glu Glu Thr Leu Arg Arg Gln Val Glu
65           70           75           80
Ile Thr Gly Asp Glu Asp Arg Leu Glu Leu Glu Trp His Lys Ser Leu
      85           90           95
Leu Asn Gly Leu Phe Pro Leu Thr Ile Gly Gly Gly Ile Gly Gln Ser
      100          105          110
Arg Met Ala Met Phe Leu Leu Arg Lys Arg His Ile Gly Glu Val Gln
      115          120          125
Thr Ser Val Trp Pro Gln Val Ser Pro Arg Tyr Leu Arg Lys Tyr Phe
      130          135          140
Val Glu Asn Arg Thr Ala Arg Phe Gly Phe Leu Ser Leu Phe Val Tyr
145          150          155          160
Asn Leu Val

```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

Leu Phe Glu Val Glu Glu Val Ser Asp His Gly Leu Thr Leu Tyr Thr
 1           5           10           15
Glu Arg Thr Asp Gly Thr Gly Gly Phe Pro Gly Asn Leu Lys Ile Trp
      20           25           30
Ile Ser Tyr His Leu Glu Glu Thr Gly Ala Ser Met Asn Ser Ile Tyr
      35           40           45

```

Lys Val Thr Thr Asp Gln Asp Thr Leu Val Asn Pro Thr Asn His Ser
 50 55 60
 Tyr Phe Asn Leu Ser Gly Asp Phe Thr Gln Thr Ile Asp Arg His Val
 65 70 75 80
 Phe Gln Leu Asn Thr Glu Gly Ile Tyr Ser Ile Ala Pro Asp Gly Val
 85 90 95
 Pro Ala Lys Thr Pro Glu Ala Asn Arg Asp Val Val Lys His Ile Tyr
 100 105 110
 Asn Gly Ala Leu Leu Lys Asp Ile Phe Ala Glu Glu Asp Glu Gln Ile
 115 120 125
 Gln Leu Ala Ser Gly Leu Asp His Pro Phe Ala Leu Pro Ala Gly His
 130 135 140
 Asp Asn Ala Gly Phe Leu Tyr Asp Gln Asn Ser Gly Arg Phe Leu Leu
 145 150 155 160
 Phe Lys Thr Glu Ala Pro Cys Phe Val Val Tyr Thr Ala Asn Phe Val
 165 170 175
 Asp Glu Ser Val Ile Ile Gly Gly Gln Pro Met Leu Gln His Asn Gly
 180 185 190
 Ile Ala Leu Glu Ala Gln Ala Leu Pro Asp Ala Ile His Ser Asp Leu
 195 200 205
 Lys Gly Gln Val Ile Leu Lys Ala Gly Gln Thr Phe Thr Ser Lys Thr
 210 215 220
 Arg Tyr Glu Leu Val Val Lys
 225 230

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met Ile Asn Thr Leu Val Gly Met Arg Phe Asp Leu Lys Thr Arg Lys
 1 5 10 15
 Pro Ile Leu Ala Asn Gly Thr Gly Gly Met Ser Gly Pro Ala Val Phe
 20 25 30
 Pro Val Ala Leu Lys Leu Ile Arg Gln Val Ala Gln Thr Thr Asp Leu
 35 40 45

Pro Ile Ile Gly Met Gly Gly Val Asp Ser Ala Glu Ala Ala Leu Glu
 50 55 60
 Met Tyr Leu Ala Gly Ala Ser Ala Ile Gly Val Gly Thr Ala Asn Phe
 65 70 75 80
 Thr Asn Pro Tyr Ala Cys Pro Asp Ile Ile Glu Asn Leu Pro Lys Val
 85 90 95
 Met Asp Lys Tyr Gly Ile Ser Ser Leu Glu Glu Leu Arg Gln Glu Val
 100 105 110
 Lys Glu Ser Leu Arg
 115

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met Tyr Asn Lys Val Ile Met Ile Gly Arg Leu Thr Ser Thr Pro Glu
 1 5 10 15
 Leu His Lys Thr Asn Asn Asp Lys Ser Val Ala Arg Ala Thr Ile Ala
 20 25 30
 Val Asn Arg Arg Tyr Lys Asp Gln Asn Gly Glu Arg Glu Ala Asp Phe
 35 40 45
 Val Gln Tyr Gly Pro Tyr Gly Ala Arg Thr Ser Gln Lys Thr Leu Ala
 50 55 60
 Ser Leu Arg Gln Pro Lys Gly Ser Leu His Phe Arg
 65 70 75

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Met Val Lys Ser Ser Ile Gln Gly Pro Arg Leu Ser Lys Ile Trp Gly
 1 5 10 15
 Ser Thr Arg Gln Glu Ser Tyr Arg Leu Cys Leu Gly Ala Arg Leu Val
 20 25 30
 Tyr Ser Ala Thr Lys Ala Ala Val Lys Thr Phe Ser Asp Gly Leu Arg
 35 40 45
 Ile Asp Thr Ile Ala Thr Asp Ile Lys Val Thr Thr Ile Gln Pro Gly
 50 55 60
 Ile Val Glu Thr Asp Phe Ser Thr Val Arg Phe His Gly Asp Lys Glu
 65 70 75 80
 Arg Ala Ala Ser Val Tyr Gln Gly Ile Glu Ala Leu Gln Ala Gln Asp
 85 90 95
 Ile Ala Asp Thr Val Val Tyr Val Thr Ser Gln Pro Arg Arg Val Gln
 100 105 110
 Ile Thr Asp Met Thr Ile Met Ala Asn Gln Gln Ala Thr Gly Phe Met
 115 120 125
 Ile His Lys Lys
 130

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Met Lys Ser Glu Leu Arg Lys Gln Val Leu His Glu Met Lys Ala Leu
 1 5 10 15
 Ser Gln Glu Gln Lys Gln Ala Ile Asp Gln Ala Leu Thr Glu Arg Ile
 20 25 30
 Leu Gln His Pro Phe Tyr Gln Glu Ala Lys Val Ile Ala Thr Tyr Leu
 35 40 45
 Ser Phe Ser His Glu Phe Gln Thr Arg Glu Leu Ile Glu Gln Ala Leu
 50 55 60

(2) INFORMATION FOR SEO ID NO:457:

(A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457;

Met	Asp	Ser	Leu	Thr	Trp	Leu	Asn	Asp	Leu	Ile	Tyr	Pro	Met	Met	Val
1				5					10					15	
Val	Asn	Gln	Thr	Ile	Pro	Thr	Ile	Ala	Ile	Ala	Pro	Ile	Leu	Val	Leu
			20					25					30		
Trp	Leu	Gly	Tyr	Gly	Ile	Leu	Pro	Lys	Ile	Val	Leu	Ile	Ile	Leu	Thr
		35					40					45			
Thr	Thr	Phe	Pro	Ile	Ile	Val	Ser	Ile	Leu	Asp	Gly	Phe	Arg	His	Cys
	50					55					60				
Asp	Lys	Asp	Met	Leu	Thr	Leu	Phe	Ser	Leu	Met	Arg	Ala	Lys	Pro	Trp
65					70					75					80
Gln	Ile	Leu	Trp	His	Phe	Lys	Ile	Pro	Val	Ser	Leu	Pro	Tyr	Phe	Tyr
				85					90					95	
Ala	Gly	Leu	Arg	Val	Ser	Val	Ser	Tyr	Ala	Phe	Ile	Thr	Thr	Val	Val
			100						105					110	
									411						

Ser Glu Trp Leu Gly Gly Phe Glu Gly Leu Gly Val Tyr Met Ile Gln
 115 120 125
 Ser Lys Lys Leu Phe Gln Tyr Asp Thr Met Phe Ala Ile Ile Ile Leu
 130 135 140
 Val Ser Ile Ile Ser Leu Leu Gly Met Lys Leu Val Asp Ile Ser Glu
 145 150 155 160
 Lys Tyr Val Ile Lys Trp Lys Arg Ser
 165

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Asn Val Gly Tyr Glu Lys Ala Phe Leu Met Gln Thr Ser Leu Asn
 1 5 10 15
 Leu Pro Thr Ser Glu Ile Ile Ser Thr Tyr Val Tyr Lys Val Gly Leu
 20 25 30
 Val Ser Gly Asp Tyr Ser Tyr Ser Thr Ala Val Gly Leu Phe Asn Ala
 35 40 45
 Val Ile Asn Val Val Leu Leu Val Ala Val Asn Gln Ile Val Lys Arg
 50 55 60
 Met Asn Asn Gly Glu Gly Ile
 65 70

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```

Met Lys Arg Met Leu Ser Gly Leu Asn Val Val Phe Ser Trp Met Phe
 1             5             10             15
Thr Ile Lys Lys Asn Asp Gly Lys Thr Thr Ile Gly Thr Ala Lys Asp
      20             25             30
His Pro Thr Trp Val Asn Arg Thr Pro Lys Gly Thr Phe Ser Pro Glu
      35             40             45
Gly Tyr Pro Leu Tyr His Tyr Gln Thr Tyr Ile Leu Glu Asp Phe Ile
      50             55             60
Glu Asp Gly Ser His Arg Asp Gln Leu Asp Glu Ala Thr Thr Gly Thr
65             70             75             80
Asn

```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```

Met Ala Leu Val Tyr Asp Ala Lys Val Ala Glu Ala Lys Arg Leu Ser
 1             5             10             15
Glu Ala Leu Leu Met Leu Asp Thr Ser Arg Ile Val Ala Arg Gly Tyr
      20             25             30
Ala Ile Val Lys Lys Glu Glu Ser Val Val Asp Ser Val Glu Ser Leu
      35             40             45
Lys Lys Lys Asp Gln Val Thr Leu Leu Met Arg Asp Gly Gln Val Glu
      50             55             60
Leu Glu Val Lys Asp Val Lys Thr Lys Glu Ile
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

```

Met Ser Gln Ala Gln Tyr Ala Gly Thr Gly Arg Arg Lys Asn Ala Val
 1           5           10           15
Ala Arg Val Arg Leu Val Pro Gly Thr Gly Lys Ile Thr Val Asn Lys
      20           25           30
Lys Asp Val Glu Glu Tyr Ile Pro His Ala Asp Leu Arg Leu Val Ile
      35           40           45
Asn Gln Pro Phe Ala Val Thr Ser Thr Val Gly Ser Tyr Asp Val Phe
      50           55           60
Val Asn Val Val Gly Gly Gly Tyr Ala Gly Gln Ser Gly Ala Ile Arg
      65           70           75           80
His Gly Ile Ala Arg Ala Leu Leu Gln Val Asn Pro Asp Phe Arg Asp
      85           90           95
Ser Leu Lys Arg Ala Gly Leu Leu Thr Arg Asp Ser Arg
      100          105

```

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

```

Met Ala Gly Ala Ser Leu Met Phe Phe Gly Phe Leu Gly Phe Glu Ser
 1           5           10           15
Ile Ser Asn Gly Gly Ser Val Asp Glu Val Lys Thr Pro Gln Lys Asn
      20           25           30
Ile Pro Arg Gly Ile Val Leu Ser Leu Ser Ile Val Thr Ile Leu Tyr
      35           40           45
Ala Leu Val Thr Leu Val Leu Thr Gly Val Val His Tyr Ser His Leu
      50           55           60
Asn Val Asp Asp Ala Val Ala Phe Ala Leu Arg Ser Val Gly Ile Ser
      65           70           75           80

```

Trp Ala Ala Asn Tyr Val Ser Leu Val Ala Ile Leu Thr Leu Ile Thr
 85 90 95
 Val Cys Ile Ser Met Thr Tyr Ala Leu Ser Arg Met Ile Tyr Ser Leu
 100 105 110
 Ala Ser Asp Gly Leu Val Pro Ala Ala Phe Lys Glu Leu Thr Lys Thr
 115 120 125
 Ser Lys Ile Pro Lys Asn Ala Thr Ile Leu Thr Gly Leu Ala Ser Ala
 130 135 140
 Val Ala Ala Gly Met Phe Pro Leu Ala Ser Ile Ala Ala Phe Leu Asn
 145 150 155 160
 Ile Cys Thr Leu Ala
 165

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met Asn Lys Lys Glu Arg Leu Glu Lys Ile Arg Arg Leu Val Thr Asp
 1 5 10 15
 Tyr Gln Ile Gly Thr Gln Glu Glu Ile Val Glu His Leu Lys Glu Ala
 20 25 30
 Gly Ile Thr Ala Thr Gln Ala Thr Val Ser Arg Asp Ile Lys Glu Leu
 35 40 45
 Gly Ile Val Lys Ile Pro Leu Arg Asp Asn Thr Tyr Val Tyr Glu Leu
 50 55 60
 Pro Lys Ser Ile Val Lys Ser Leu Gln Leu Ala Glu Asp Asn Ile Glu
 65 70 75 80
 Ser Ala Glu Leu Met Asp Lys Met Ile Asn Leu Gln Val Ile Pro Gly
 85 90 95
 Asn Thr Ala Phe Val Lys Ala Gln Leu Ile Glu Thr Phe Ala Asp Lys
 100 105 110
 Ile Phe Ser Cys Leu Thr Asp Asp Ser Gly Pro Val Xaa Gly
 115 120 125

(2) INFORMATION FOR SEQ ID NO:464:

415

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```

Met Asn Thr Asn Leu Ala Ser Phe Ile Val Gly Leu Ile Ile Asp Glu
 1             5             10             15
Asn Asp Arg Phe Tyr Phe Val Gln Lys Asp Gly Gln Thr Tyr Ala Leu
      20             25             30
Ala Lys Glu Glu Gly Gln His Thr Val Gly Asp Thr Val Lys Gly Phe
      35             40             45
Ala Tyr Thr Asp Met Lys Gln Lys Leu Arg Leu Thr Thr Leu Glu Val
      50             55             60
Thr Ala Thr Gln Asp Gln Phe Gly Trp Gly Arg Val Thr Glu Val Arg
65             70             75             80
Lys Asp Leu Gly Val Phe Val Asp Thr Gly Leu Pro Asp Lys Glu Ile
      85             90             95
Val Val Val Thr Arg Tyr Ser Pro Cys Ala Gln Gly Thr Leu Ala
      100            105            110

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

```

Met Tyr Leu Lys Glu Ile Glu Ile Gln Gly Phe Lys Ser Phe Ala Asp
 1             5             10             15
Lys Thr Lys Val Val Phe Asp Gln Gly Val Thr Ala Val Val Gly Pro
      20             25             30

```

```

Asn Gly Ser Gly Lys Ser Asn Ile Thr Glu Ser Leu Arg Trp Ala Leu
   35                               40                   45
Gly Glu Ser Ser Val Lys Ser Leu Arg Gly Gly Lys Met Pro Asp Val
   50                               55                   60
Ile Phe Ala Gly Thr Glu Ser Arg Lys Pro Leu Asn Tyr Ala Ser Val
   65                               70                   75                   80
Val Val Thr Leu Asp Asn His Asp Gly Phe Ile Lys Asp Ala Gly Gln
                        85                               90                   95
Glu Ile Arg Val Glu Arg His Ile Tyr Arg Ser Gly Asp Ser Glu Tyr
                        100                              105                  110
Lys Ile Asp Gly Lys Lys Val Arg Leu Arg Asp Ile His Asp Leu Phe
                        115                              120                  125
Leu Asp Thr Gly Leu Gly Arg Asp Ser Phe Ser Ile Ile Ser Gln Gly
                        130                              135                  140
Lys Val Glu Glu Ile Phe Asn Ser Lys Pro Glu Glu Arg Arg Ala Ile
   145                              150                  155                  160
Phe Glu Glu Ala Ala Gly Val Leu Lys Tyr Lys Thr Arg Arg Lys Glu
                        165                              170                  175
Thr Glu Ser Lys Leu Gln Gln Thr Gln Asp Asn Leu Asp Arg Leu Glu
                        180                              185                  190
Asp Ile Ile Tyr Glu Leu Asp Asn Gln Ile Lys Pro Leu Glu Lys Gln
                        195                              200                  205
Ala Glu Asn Ala Arg Lys Phe Leu Asp Leu Glu Gly Gln Arg Lys Ala
                        210                              215                  220
Ile Tyr Leu Asp Val Leu Val Ala Gln Ile Lys Glu Asn Lys Ala Glu
   225                              230                  235                  240
Leu Glu Ser Thr Glu Glu Glu Ser Trp Leu Arg Phe Lys Asn Ser
                        245                              250                  255

```

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```

Met Asp Asp Tyr Asn Ala Thr Gln Ala Ser Thr Ile Ala Val Met Pro
 1              5              10              15

```

Val Arg Tyr Glu Glu Val Leu Leu Met Val
 20 25

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met Arg Ser Leu Asn Phe Met Arg Ala Leu Leu Thr Asp Lys Gln Met
 1 5 10 15
 Asn Tyr Ile Glu Leu Tyr Tyr Ala Asp Asp Tyr Ser Leu Ala Glu Ile
 20 25 30
 Ala Glu Glu Phe Gly Val Ser Arg Gln Ala Val Tyr Asp Asn Ile Lys
 35 40 45
 Arg Thr Glu Lys Ile Leu Glu Asp Tyr Glu Met Lys Leu His Met Tyr
 50 55 60
 Ser Asp Tyr Ile Val Arg Ser Gln Ile Phe Asp Gln Ile Leu Asp Arg
 65 70 75 80
 Tyr Pro Lys Asp Asp Phe Leu Gln Glu Gln Ile Glu Ile Leu Thr Ser
 85 90 95
 Ile Asp Asn Arg Glu
 100

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

```

Met Gly Trp Glu Ile Gly Ile Thr Pro Ser Thr Val Leu Val Ser His
 1             5             10             15
Leu Leu Val Gln Glu Ser Thr Ser Pro Asp Leu Leu Val Asn Glu Phe
      20             25             30
Leu Leu Phe Ala Ile Gly Thr Gly Phe Ala Leu Leu Val Asn Leu Tyr
      35             40             45
Met Pro Ser Arg Glu Glu Glu Ile Gln His Tyr His Thr Leu Val Glu
      50             55             60
Glu Lys Leu Lys Asp Ile Leu Gln Arg Phe Lys Tyr Tyr Leu Ser Arg
      65             70             75             80
Gly Asp Gly Arg Asn Arg Ala Gln Leu Val Ala Glu Leu Asp Thr Leu
      85             90             95
Leu Lys Glu Ala Leu Arg Leu Val Tyr Leu Asp His Ser Asp His Leu
      100            105            110
Phe His Gln Thr Asp Tyr His Ile His Tyr Phe Glu Met Arg Gln Arg
      115            120            125
Gln Ser Arg Ile Pro Glu Lys His Gly Pro Thr Asp
      130            135            140

```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```

Met Glu Leu Leu Ala Asn Ala Asn Lys Ile Met Glu Gly Lys Val Val
 1             5             10             15
Leu Asn Trp Asp Ile Gln Tyr Leu Gly Trp Gly Asp Tyr Gly Lys Glu
      20             25             30
Asn Val Ser Tyr Gln His His Leu Val Lys Thr Met Ile Ser Pro Leu
      35             40             45
Gln Ile Thr Ile Leu
      50

```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

419

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```

Met Glu Arg Asn Asn Arg Lys Val Leu Val Gly Arg Val Val Ser Asp
 1             5             10             15
Lys Met Asp Lys Thr Ile Thr Val Val Val Glu Thr Lys Arg Asn His
          20             25             30
Pro Val Tyr Gly Lys Arg Ile Asn Tyr Ser Lys Lys Tyr Lys Ala His
          35             40             45
Asp Glu Asn Asn Val Ala Lys Glu Gly Asp Ile Val Arg Ile Met Glu
          50             55             60
Thr Arg Pro Leu Ser Ala Thr Lys Arg Phe Arg Leu Val Glu Val Val
65             70             75             80
Glu Glu Ala Val Ile Ile
                      85

```

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

Met His Arg Lys Pro Arg Gly Val Asp Phe Gly Glu Gly Ser Ile Val
 1             5             10             15
Gln Lys Val Lys Ala Met Ile Pro Ile Leu Ile Leu Leu Phe Ala Thr
          20             25             30
Ser Leu Lys Arg Ala Asp Ser Leu Ala Ile Ala Met Glu Ala Arg Gly
          35             40             45
Tyr Gln Gly Gly Lys Gly Arg Ser Gln Tyr Arg Gln Leu Lys Trp Thr
50             55             60

```

(2) INFORMATION FOR SEO ID NO:472:

(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

(2) INFORMATION FOR SEQ ID NO:473:

(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

Leu Arg Val Ala Tyr Phe Lys Val His His Pro Ile Tyr Tyr Tyr Cys
 1           5           10           15
Ala Tyr Phe Ser Ile Arg Ala Lys Ala Phe Asp Ile Lys Thr Met Gly
          20           25           30
Ala Gly Leu Glu Val Ile Lys Arg Arg Met Glu Glu Ile Ser Glu Lys
          35           40           45
Arg Lys Asn Asn Glu Ala Ser Asn Val Glu Ile Asp Leu Tyr Thr Thr
          50           55           60
Leu Glu Ile Val Asn Glu Met Trp Glu Arg Gly Phe Lys Phe Gly Lys
65           70           75           80
Leu Asp Leu Tyr Cys Ser Gln Thr Thr Glu Phe Leu Ile Asp Gly Asp
          85           90           95
Thr Leu Ile Pro Pro Phe Val Ala Met Asp Gly Leu Gly Glu Asn Val
          100          105          110
Ala Lys Gln Leu Val Arg Ala Arg Glu Glu Gly Glu Phe Leu Ser Lys
          115          120          125
Thr Glu Leu Arg Lys Arg Gly Gly Leu Ser Ser Thr Leu Val Glu Lys
          130          135          140
Met Asp Glu Met Gly Ile Leu Gly Asn Met Pro Glu Asp Asn Gln Leu
145          150          155          160
Ser Leu Phe Asp Glu Leu Phe
          165

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

Met Ser Glu Asn Gln Gln Ala Leu Asn His Val Val Ser Met Glu Asp
 1           5           10           15

```

Leu Thr Val Asp Gln Val Met Lys Leu Ile Lys Arg Gly Ile Glu Phe
 20 25 30
 Lys Asn Gly Ala Gln Ile Pro Tyr Glu Asp His Pro Ile Val Ser Asn
 35 40 45
 Leu Phe Phe Glu Asp Ser Thr Arg Thr His Lys Ser Phe Glu Val Ala
 50 55 60
 Glu Ile Lys Leu Gly Leu Glu Arg Leu Asp Phe Asp Val Lys Thr Ser
 65 70 75 80
 Ser Val Asn Lys Gly
 85

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Met Ser Met Phe Leu Asp Thr Ala Lys Ile Lys Val Lys Ala Gly Asn
 1 5 10 15
 Gly Gly Asp Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Asn
 20 25 30
 Gly Gly Pro Trp Gly Gly Asp Gly Gly Arg Gly Gly Asn Val Val Phe
 35 40 45
 Val Val Asp Glu Gly Leu Arg Thr Leu Met Asp Phe Arg Tyr Asn Arg
 50 55 60
 His Phe Lys Ala Asp Ser Gly Glu Lys Gly Met Thr Lys Gly Met His
 65 70 75 80
 Gly Arg Gly Ala Glu Asp Leu Arg Val Arg Val Pro Gln Gly Thr Thr
 85 90 95
 Val Arg Asp Ala Glu Thr Gly Lys Val Leu Thr Asp Leu Ile Glu His
 100 105 110
 Gly Gln Glu Phe Ile Val Ala His Gly Gly Arg Gly Gly Arg Gly Asn
 115 120 125
 Ile Arg Phe Ala Thr Pro Lys Asn Pro Ala Pro Glu Ile Ser Glu Asn
 130 135 140
 Gly Glu Pro Gly Ser Gly Thr
 145 150

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```

Met Gly Ser Phe Leu Met Pro Lys Ser Glu Val Tyr Met Lys Gln Glu
 1             5             10             15
Ser Thr Val Asp Leu Leu Leu Asp Val Asp Gln Arg Pro Ser Asp Gly
          20             25             30
Lys Gly Ile Leu Leu Ser Phe Gln His Val Phe Ala Met Phe Gly Ala
      35             40             45
Thr Ile Leu Val Pro Leu Ile Leu Gly Met Pro Val Ser Val Ala Leu
      50             55             60
Leu Cys Phe Gln Leu Phe Gly Thr Leu Ile Leu His Asp Cys Tyr Trp
65             70             75             80
Phe

```

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```

Met Ala Asn Tyr Asp Ile Phe Thr Ser Pro Pro Thr Asn Ser Gly Ile
 1             5             10             15
Ala Pro Val Thr Val Ile Val Lys Lys Ser Tyr Gly Phe Tyr Thr Glu
      20             25             30

```

Ala Lys Thr Phe His Thr Thr Arg Phe Gly Thr Ile Val Leu His Ser
 35 40 45
 Arg Lys Gln Asn Ile Pro Asp Ile Ile Ala Leu His Thr Ala Pro Pro
 50 55 60
 Leu Pro Gly Leu Met Glu Ile Trp Lys Gln Asp Leu Asn Ile Ile His
 65 70 75 80
 Asn Gln Leu Ala Ser Lys Tyr Pro Lys Ala Ile Ile Ala Gly Asp Phe
 85 90 95
 Asn Ala Thr Met Arg His Gly Ala Leu Ala Lys Ile Ser Ser His Arg
 100 105 110
 Asp Ala Leu Asn Val Leu Pro Pro Phe Glu Arg Gly Thr Trp Asn Ser
 115 120 125
 Gln Ser Pro Lys Leu Phe Asn Ala Thr Ile Asp His Ile Leu Leu Pro
 130 135 140
 Lys Asn His Tyr Tyr Val Lys Asp Leu Asp Ile Val Ser Phe Gln Asn
 145 150 155 160
 Ser Asp His Arg Cys Ile Phe Thr Glu Ile Thr Phe
 165 170

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Met Asn Leu Gly Ala Asp Gly Val Ile Ser Val Ala Ser His Thr Asn
 1 5 10 15
 Gly Asp Glu Met His Glu Met Phe Thr Ala Ile Ala Glu Ser Asp Met
 20 25 30
 Lys Lys Ala Ala Ala Ile Gln Arg Lys Phe Ile Pro Lys Val Asn Ala
 35 40 45
 Leu Phe Ser Tyr Pro Ser Pro Ala Pro Val Lys Ala Ile Leu Asn Tyr
 50 55 60
 Met Gly Phe Glu Ala Gly Pro Thr Arg Leu Pro Leu Val Pro Ala Pro
 65 70 75 80
 Glu Glu Asp Val Lys Arg Ile Ile Lys Val Val Val Asp Gly Asp Tyr
 85 90 95

Glu Ala Thr Lys Ala Thr Val Thr Gly Val Leu Arg Pro Asp Tyr
 100 105 110

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Met Glu Ser Leu Ile Gln Thr Tyr Leu Pro Asn Val Tyr Lys Met Gly
 1 5 10 15
 Trp Ser Gly Gln Ala Gly Trp Gly Thr Ala Ile Tyr Leu Thr Leu Tyr
 20 25 30
 Met Thr Val Leu Ser Phe Ile Ile Gly Gly Phe Leu Gly Leu Val Ala
 35 40 45
 Gly Leu Phe Leu Val Leu Thr Ala Pro Gly Gly Val Leu Glu Asn Lys
 50 55 60
 Val Val Phe Trp Ile Leu Asp Lys Ile Thr Ser Ile Phe Arg Ala Val
 65 70 75 80
 Pro Phe Ile Ile Leu Leu Ala Ile Leu Ser Pro Leu Ser His Leu Ile
 85 90 95
 Glu Lys Thr Ser Ile Gly Pro Asn Ala Ser Pro Cys Pro Thr Phe Phe
 100 105 110
 Cys Ser Leu Cys Leu Leu Cys Pro Ser Gly Ala Gly Cys Leu Gly
 115 120 125

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

```

Met Asp Ser Gln Asp Asn Lys Arg Lys Trp Lys Asn Arg Asp Leu Ile
 1             5             10             15
Ser Ser Leu Glu Phe Ala Ile Thr Gly Ile Phe Thr Ala Ile Lys Glu
             20             25             30
Glu Arg Asn Met Arg Lys His Ala Val Thr Ala Leu Val Val Ile Leu
             35             40             45
Ala Gly Phe Gly Phe Gln Val Ser Arg Ile Glu Trp Leu Phe Leu Leu
             50             55             60
Leu Ser Ile Phe Leu Val Val Ala Phe Glu Ile Ile Asn Ser Ala Ile
65             70             75             80
Glu Asn Val Val Asp Leu Ala Ser His Tyr His Phe Ser His Ala Gly
             85             90             95

```

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

```

Leu Ser Glu Ile Asp Glu Val Ile Leu Val Gly Gly Ser Thr Arg Ile
 1             5             10             15
Pro Ala Val Val Glu Ala Val Lys Ala Glu Thr Gly Lys Glu Pro Asn
             20             25             30
Lys Ser Val Asn Pro Asp Glu Val Val Ala Met Gly Ala Ala Ile Gln
             35             40             45
Gly Gly Val Ile Thr Gly Asp Val Lys Asp Val Val Leu Leu Asp Val
             50             55             60
Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val Phe Thr Lys
65             70             75             80
Leu Ile Asp Arg Asn Thr Thr Ile Pro Thr Ser Lys Ser Gln Val Phe
             85             90             95
Ser Thr Ala Ala Asp Asn Gln Pro Ala Val Asp Ile His Val Leu Gln
             100            105            110
Gly Glu Arg Pro Met Ala Ala Asp Asn Lys Thr Leu Gly Arg Phe Gln
             115            120            125

```


Leu Thr Asp Ile Pro Ala Ala Pro Arg Gly Ile Pro Gln Ile Glu Val
 130 135 140
 Thr Phe Asp Ile Asp Lys Asn Gly Ile Val Ser Val Lys Ala Lys Asp
 145 150 155 160
 Leu Gly Thr Gln Lys Glu Gln Thr Ile Val Ile Gln Ser Asn Ser Gly
 165 170 175
 Leu Thr Asp Glu Glu Ile Asp Arg Met Met Lys Asp Ala Glu Ala Asn
 180 185 190
 Ala Glu Ala Asp Lys Lys Arg Lys Glu Glu Val Asp Leu Arg Asn Glu
 195 200 205
 Val Asp Gln Ala Ile Phe Ala Thr Glu Lys Thr Ile Lys Glu Thr Glu
 210 215 220
 Gly Lys Gly Phe Asp Ala Glu Arg Asp Ala Ala Gln Ala Ala Leu Asp
 225 230 235 240
 Asp Leu Lys Lys Ala Gln Glu Asp Asn Asn Leu Asp Asp Met Lys Ala
 245 250 255
 Lys Leu Glu Ala Leu Asn Glu Lys Ala Gln Gly Leu Ala Val Lys Leu
 260 265 270
 Tyr Glu Gln Ala Ala Ala Gln Gln Ala Gln Glu Gly Ala Glu Gly
 275 280 285
 Ala Gln Ala Thr Gly Asn Ala Gly Asp Asp Val Val Asp Gly Glu Phe
 290 295 300
 Thr Glu Lys
 305

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

Met Ile Leu Ala Phe Leu Leu Ser Leu Cys Ser Glu Ala Asp Ala Phe
 1 5 10 15
 Ile Gly Ala Ser Leu Leu Ser Ser Phe Gly Leu Ala Pro Val Leu Ala
 20 25 30
 Phe Leu Val Ile Gly Pro Met Leu Asp Ile Lys Asn Ile Leu Met Met
 35 40 45
 428

Lys Asn Tyr Leu Lys Ala Arg Phe Ile Ser His Phe Ile Thr Ile Val
 50 55 60
 Thr Leu Val Val Leu Val Tyr Ser Leu Leu Ile Gly Val Ile Leu
 65 70 75

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

Leu Tyr Asn Ile Ile Phe Leu Ser Ser Met Trp Glu Pro Tyr Gly Gln
 1 5 10 15
 Leu Ser Asp Leu Pro Val Ala Val Val Asn Asn Asp Lys Glu Ala Ser
 20 25 30
 Tyr Asn Gly Asn Thr Met Ala Ile Gly Lys Asp Met Val Ser Asn Leu
 35 40 45
 Lys Glu Asn Lys Thr Leu Asp Phe His Phe Val Asp Glu Glu Glu Gly
 50 55 60
 Lys Lys Gly Leu Glu Asp Gly Asp Tyr Tyr Met Val Val Thr Leu Pro
 65 70 75 80
 Ser Asp Leu Ser Glu Lys Thr Thr Thr Leu Ser Asn Ile Gln Ser Thr
 85 90 95
 Ala Ala Tyr Gln Ser Leu Thr Ser Glu Gln Gln Thr Glu Ile Ser Asp
 100 105 110
 Ser Val Ser Gln Asn Ser Thr Asp Ser Ile Gln Ser Ala Gln Ser Ile
 115 120 125
 Val Ala Leu Val Gln Asp Leu Gln Gly Ser Leu Glu Asn Leu Gln Asn
 130 135 140
 Gln Ser Ser Asn Leu Ser Thr Leu Lys Asn Gln Ser Asn Gln Val Ser
 145 150 155 160
 Pro Ile Thr Ser Thr Ser Leu Ile Gly Leu Ser Ser Gly Leu Thr Glu
 165 170 175
 Ile Gln Gly Asp Val Thr Ser Lys Leu Val Pro Ala Ser Gln Ser Ile
 180 185 190
 Ala Ser Gly Val Asn Ala Tyr Thr Thr Gly Val Asp Lys Val Ser Gln
 195 200 205

Gly Ala Ser Gln Leu Ser Glu Lys Asn Ala Thr Leu Thr Gly Ser Leu
 210 215 220
 Asp Gln Leu Val Ser Gly Ser Asn Thr Leu Thr Gln Lys Ser Ser Arg
 225 230 235 240
 Leu Thr Ala Gly Val Gly
 245

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

Met Ala Asp Leu Asp His Pro His Ile Val Arg Ile Thr Asp Ile Gly
 1 5 10 15
 Glu Glu Asp Gly Gln Gln Tyr Leu Ala Met Glu Tyr Val Ala Gly Leu
 20 25 30
 Asp Leu Lys Arg Tyr Ile Lys Glu His Tyr Pro Leu Ser Asn Glu Glu
 35 40 45
 Ala Val Arg Ile Met Gly Gln Ile Leu Leu Ala Met Arg Leu Ala His
 50 55 60
 Thr Arg Gly Ile Val His Arg Asp Leu Lys Pro Gln Asn Ile Leu Leu
 65 70 75 80
 Thr Pro Asp Gly Thr Ala Lys Val Thr Asp Phe Gly Ile Ala Val Ala
 85 90 95
 Phe Ala Glu Thr Ser Leu Thr Gln Thr Asn Ser Asp Val Trp Ala Gln
 100 105 110
 Phe Ile Thr Cys His Gln Ser Arg Arg Val Val Leu Arg Arg Leu Cys
 115 120 125
 Arg Val Ile Ser Met Pro Trp Gly Leu Phe Ser Met Arg Cys
 130 135 140

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid

430

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

```

Met Leu Ala Thr Ala Ile Leu Gly Val Val Ile Glu Phe Leu Ala Tyr
 1           5           10           15
Arg Pro Leu Arg His Ser Thr Arg Ile Ala Val Leu Ile Thr Ala Ile
      20           25           30
Gly Val Ser Phe Leu Leu Glu Tyr Gly Met Val Tyr Leu Val Gly Ala
      35           40           45
Asn Thr Arg Ala Phe Pro Gln Ala Ile Gln Thr Val Arg Tyr Asp Leu
 50           55           60
Gly Pro Ile Ser Leu Thr Asn Val Gln Leu Met Ile Leu Ala Ile Ser
65           70           75           80
Leu Ile Leu Met Ile Leu Leu Gln Val Ile Val Gln Lys Thr Lys Met
      85           90           95
Gly Lys Ala Met Arg Ala Val Ser Val Asp Ser Asp Ala Ala Gln Leu
      100           105           110
Met Gly Ile Asn Val Asn Arg Thr Ile Ser Phe Thr Phe Ala Leu Gly
      115           120           125
Ser Ala Leu Ala Gly Ala Ala Gly Val Leu Ile Ala Leu Tyr Tyr Asn
      130           135           140
Ser Leu Glu Pro Leu Met Gly Val Thr Pro Gly Leu Lys Ser Phe Val
145           150           155           160
Ala Ala Val Leu Gly Gly Ile Gly Ile Ile Pro Gly Ala Ala Leu Gly
      165           170           175
Gly Phe Val Ile Gly Leu Leu Glu Thr Phe Ala Thr Ala Phe Gly Met
      180           185           190
Ser Asp Phe Arg Asp Ala Ile Val Tyr Gly Ile Leu Leu Leu Ile Leu
      195           200           205
Ile Val Arg Pro Ala Gly Ile Leu Gly Lys Asn Val Lys Glu Lys Val
      210           215           220

```

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```

Met Ser Leu Ala Met Lys Glu Met Gly Gly Asp Val Ser Ala Ala Gln
 1             5             10             15
Thr Gly Val Ile Leu Thr Gly Leu Val Tyr Val Leu Val Ala Thr Ser
      20             25             30
Ile Arg Phe Val Gly Thr Lys Trp Ile Asp Lys Leu Leu Pro Pro Ile
      35             40             45
Ile Ile Gly Pro Met Ile Ile Val Ile Gly Leu Gly Leu Ala Gly Ser
      50             55             60
Ala Val Thr Asn Ala Gly Leu Val Ala Asp Gly Asn Trp Lys Asn Ala
      65             70             75             80
Leu Val Ala Val Val Thr Phe Leu Ile Ala Ala Phe Ile Asn Thr Lys
      85             90             95
Gly Lys Gly Phe Leu Arg Ile Ile Pro Phe Leu Phe Ala Ile Ile Gly
      100            105            110
Gly Tyr Leu Phe Ala Leu Thr Leu Gly Leu Val Asp Phe Thr Pro Val
      115            120            125
Leu Lys Ala Asn Trp Phe Glu Ile Pro Gly Phe Tyr Leu Pro Phe Ser
      130            135            140
Thr Gly Gly Ala Phe Lys Glu Tyr Asn Leu Tyr Phe Gly Pro Glu Pro
      145            150            155            160
Ser Leu Ser Xaa Gln Ser Xaa Xaa
      165

```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

Met Val Lys Val Leu Ala Ala Cys Gly Asn Gly Met Gly Ser Ser Met
 1             5             10             15

```

Val Ile Lys Met Lys Val Glu Asn Ala Leu Arg Lys Leu Asn Gln Thr
 20 25 30
 Asp Phe Thr Val Asn Ser Trp Pro Val Ser Val Lys Leu Lys Val
 35 40 45

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Met Ala Ser Val Gly Glu Ala Lys Gly Leu Ala Val Gly Tyr Asp Ile
 1 5 10 15
 Val Ile Ala Ser Leu His Leu Ile Gln Glu Leu Glu Gly Arg Thr Asn
 20 25 30
 Gly Lys Leu Ile Gly Leu Asp Asn Leu Met Asp Asp Lys Glu Ile Thr
 35 40 45
 Glu Lys Leu Ser Gln Ala Leu Gln
 50 55

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

Leu Ile Ser Leu Gly Leu Glu His Ser Leu Pro Leu Ser Ser His Leu
 1 5 10 15
 Asn Ile Ser Ile Gly Pro Leu Ile Gln Thr Trp Arg Ile Gly Phe Ser
 20 25 30

Asp Ala Lys Val Ala Gln Pro Gln Lys Ile Glu Ser Val Leu Pro Leu
 35 40 45
 Ile Asn Pro His Gly Ile Glu Leu Asp Ser Ser Thr Ser Thr Val Phe
 50 55 60
 Leu Lys Gln Lys Gly Met Lys Ile Asp Leu Gly Cys Leu Ala Lys Gly
 65 70 75 80
 Tyr Ser Ala Asp Lys Val Ala Gln Phe Leu Arg Lys Glu Gly Val Thr
 85 90 95
 Ser Ala Leu Ile Asn Leu Gly Gly Asn Ile Leu Thr Ile Gly Lys Asn
 100 105 110
 Gln Ala Arg Gly Asp Asn Pro Trp Gln Ile Gly Asp Ser Arg Thr Gln
 115 120 125
 Pro Ile Leu Gly Glu Ile Ile
 130 135

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met Ile Asn Lys Tyr Phe Asp Gly Gln Ile Pro Ala Tyr Val Glu Gly
 1 5 10 15
 Val Thr Glu Phe Asp His Val Leu Ala Glu Val Ala Glu Lys Ser Ile
 20 25 30
 Ala Asp Phe His Thr His Met Glu Ala Val Asp Tyr Pro Arg Ala Leu
 35 40 45
 Glu Ala Val Trp Thr Leu Ile Ser Arg Thr Asn Lys Tyr Ile Asp Glu
 50 55 60
 Thr Ala Pro Trp Val Leu Asp Lys Asp Glu Ala Leu Arg Asp Gln Leu
 65 70 75 80
 Ala Ser Val Met Ser His Leu Ala Ala Ser Ile Arg Val Val Ala His
 85 90 95
 Leu Ile Glu Pro Phe Met Met Glu Thr Ser Arg Ala Val Leu Thr Gln
 100 105 110
 Leu Gly Leu Glu Glu Val Ser Ser Leu Glu Asn Leu Lys Phe Gly
 115 120 125

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```

Met Leu Val Val Ile Arg Phe Leu Lys Lys Leu Ser Leu Trp Leu Ser
 1             5             10             15
Lys His Arg Lys Pro Val Pro Ser Met Ile Gln Arg Arg Leu Ser Val
          20             25             30
Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu Leu Glu Met Ala Gly
          35             40             45
Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg Lys Val Xaa Gln Gln
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```

Met Val Gly Asn Pro Arg Leu Ala Asp Leu Gly Phe Glu Glu Glu Ala
 1             5             10             15
Val Gly His His Ala Leu Val Thr Gly Phe Gln Gly Gln Arg Gln Trp
          20             25             30
Thr Asp His Phe Pro Asn Gly Asp Phe Met Glu Thr Phe Leu Asn Thr
          35             40             45
Gln Phe Asp Trp Asn Gly Ile Arg Lys Pro Phe Val Phe Ala Cys Ile
 50             55             60

```


Cys Asp Arg Glu

65

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

```

Met Gly Thr Leu Trp Lys Leu Ser Ser Ile Leu Ser Leu Thr Gly Met
 1             5             10             15
Val Phe Glu Asn His Leu Tyr Leu Leu Val Phe Ala Thr Glu Asn Asp
          20             25             30
Ser Leu Asn Gly Val Ser Met Leu Phe Asn Tyr Leu Leu Thr Asn Thr
      35             40             45
Pro Gln Ile Phe Ala Asp Val Arg Thr Tyr Trp Ser Pro Glu Ala Val
      50             55             60
Lys Arg Val Thr Gly His Thr Leu Glu Gly Cys Ala Ala Ala Gly Phe
65             70             75             80
Leu His Leu Ile Asn Ser Gly Ser Cys Thr Leu Asp Gly Thr Gly Gln
          85             90             95
Ala Thr Arg Asn Gly Lys Pro Val Met Lys Pro Phe Trp Glu Leu Glu
          100             105             110
Glu Ser

```

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

```

Met Lys Leu His Glu Leu Lys Pro Ala Glu Gly Ser Arg Lys Val Arg
 1           5           10           15
Asn Arg Val Gly Arg Gly Thr Ser Ser Gly Asn Gly Lys Thr Ser Gly
 20           25           30
Arg Gly Gln Lys Gly Gln Lys Ala Arg Ser Gly Gly Gly Val Arg Leu
 35           40           45
Gly Phe Glu Gly Gly Gln Thr Pro Leu Phe Arg Arg Leu Pro Lys Arg
 50           55           60
Gly Phe Thr Asn Ile Asn Ala Lys Glu Tyr Ala Ile Val Asn Leu Asp
 65           70           75           80
Gln Leu Asn Val Phe Glu Asp Gly Ala Glu Val Thr Pro Val Val Leu
 85           90           95
Ile Glu Ala Gly Ile Val Lys Ala Glu Lys Ser Gly Ile Lys Ile Leu
 100          105          110
Gly Asn Gly Glu Leu Thr Lys Lys Leu Thr Val Lys Ala Ala Lys Phe
 115          120          125
Ser Lys Ser Ala Glu Glu Ala Ile Thr Ala Lys Gly Gly Ser Val Glu
 130          135          140
Val Ile
145

```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

```

Met Gly Ala Ala Lys Leu Val Val Phe Ala Asn Ala Val Glu Asp Asn
 1           5           10           15
Pro Phe Met Ala Gly Ala Phe His Gly Val Gly Glu Ala Asp Val Ile
 20           25           30
Ile Asn Val Gly Val Ser Gly Pro Gly Val Val Lys Arg Ala Leu Glu
 35           40           45
Lys Val Arg Gly Gln Ser Phe Asp Val Ser Lys Pro Lys Thr Ser
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```

Met Thr Glu Lys Arg Leu Ala Trp Asp Glu Tyr Phe Ala Ala Gln Ala
 1             5             10             15
Leu Leu Ile Ala Asn Arg Ser Thr Cys Lys Arg Ala Lys Val Gly Ala
      20             25             30
Ile Leu Val Lys Asp Asn Lys Val Ile Ser Thr Gly Tyr Asn Gly Ser
      35             40             45
Val Ser Gly Thr Glu His Cys Ile Asp His Glu Cys Leu Val Ile Glu
      50             55             60
Gly His Cys Val Arg Thr Leu His Ala Glu Val Asn Ala Ile Leu Gln
      65             70             75             80
Gly Ala Glu Arg Gly Val Pro Lys Gly Phe Thr Ala Tyr Val Thr His
      85             90             95
Phe Pro Cys Leu Asn Cys Thr Lys Gln Leu Leu Gln Val Gly Cys Lys
      100            105            110
Arg Val Val Tyr Ile Asn Gln Tyr Arg Met Asp Asp Tyr Ala Gln Tyr
      115            120            125
Leu Tyr Gln Glu Lys Gly Thr Glu Leu Thr His Leu Pro Leu Glu Thr
      130            135            140
Val Gln Thr Ala Leu Lys Glu Ala Asp Leu Met
      145            150            155

```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```

Leu Trp Asp Gln Xaa Gln Leu Asp Ile Ser Lys Thr Asn Tyr Leu Arg
 1             5             10             15
Val Ile Asn Ala Phe Thr Gln Ile Glu Ala Ala Lys Ala Tyr Leu Phe
          20             25             30
Ala Asn Ser Glu Phe Ser Gly Ala Asp Trp Asp Thr Lys Ile Ser Arg
          35             40             45
Asp Ile Phe Trp Glu Glu Ser Met His Gly Ile Tyr Pro Glu Asn Val
 50             55             60
Gly Val Asn Ala Arg Leu Leu Asn Asp Glu Ala Asp Phe Phe Asp Tyr
 65             70             75             80
Leu Asn His Ser Ala Ile Phe Thr Ala Glu Arg Asp Gly Gln Thr Tyr
          85             90             95
Tyr Phe Tyr Pro Ile Gln Ala Gly Asp Tyr Leu Ala Thr Pro Glu Ile
          100            105            110
Gln Ala Phe Ala Leu Asn Gly Asp Glu Val Ile Ile Tyr Pro Gln Glu
          115            120            125
Lys Asp Phe Glu Thr His Arg Ser Tyr Gln Tyr Gln Asp Leu Thr Thr
          130            135            140
Arg Gly Thr Val Glu Phe Arg Ser Val Cys Thr Gln Pro Leu Asp Arg
          145            150            155            160
Thr Phe Ala Ser Ala Ala Phe His Leu Gly Leu Leu Val Asn Leu Asp
          165            170            175
Lys Leu Glu Ala Tyr Leu Glu Thr Ala Pro Phe Leu
          180            185

```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```

Met Asp Ser Lys Ala Lys Lys Asp Phe Glu Asn Met Val Ala Ile Val
 1             5             10             15
Ala Gln Lys Ala Arg Ser Leu Ser Met Gly Val Cys Ile Val Met Gln
          20             25             30

```

439

Gln Pro Arg Ser Asp Ser Leu Ser Thr Asn Ile Arg Glu Gln Leu Val
 35 40 45
 Asn Ala Ile Phe Leu Gly Ala Pro Thr Arg Glu Ser Ser His Met Met
 50 55 60
 Phe Gly Thr Thr Asp Val Pro Gln Val Lys Lys Asp Lys Gly Val Gly
 65 70 75 80
 Leu Tyr Ser Thr Asp Arg Glu Pro Pro Lys Glu Phe His Ser Pro Met
 85 90 95
 Phe Asp Arg Asp Val Phe Glu Val Ile Leu Pro Val Trp Glu Trp Ala
 100 105 110
 Ala Lys Asp Tyr Met Lys Asp Glu Asp Glu Asp Val
 115 120

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

Met Arg His Ser Ile Tyr Asp Gly Lys Leu Gly Phe Asp Leu Lys Glu
 1 5 10 15
 Glu Gly Lys Gln Val Asp Leu Thr Leu Trp Ser Pro Ser Ala Asp Lys
 20 25 30
 Val Ser Val Val Val Tyr Asp Lys Asn Asp Pro Asp Lys Val Val Gly
 35 40 45
 Thr Val Ala Leu Glu Lys Gly Glu Arg Gly Thr Trp Lys Gln Thr Leu
 50 55 60
 Asp Ser Thr Asn Lys Leu Gly Ile Thr Asp Phe Thr Gly Tyr Tyr Tyr
 65 70 75 80
 Gln Tyr Gln Ile Glu Arg Gln Gly Lys Thr Val Leu Ala Leu Asp Pro
 85 90 95
 Tyr Ala Lys Ser Leu Ala Ala Trp Asn Ser Asp Asp Ala Lys Ile Asp
 100 105 110
 Asp Ala His Lys Val Ala Lys Ala Ala Phe Val Asp Pro Ala Gln Leu
 115 120 125
 Gly Pro Gln Asp Pro Phe Leu Arg Gly Leu Met Gly Gln Ile Arg Phe
 130 135 140

Thr Ile Ser Arg Leu Val Lys Thr Pro Leu Ser Thr Lys Leu Met Cys
 145 150 155 160
 Val Thr Ser Leu Gln Ile Leu Pro Leu Gln Lys Thr
 165 170

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

Met Cys Met Phe Glu Val Glu Glu Trp Leu His Ser Arg Ile Gly Leu
 1 5 10 15
 Asn Phe Arg Ser Gly Leu Ala Arg Ile Gln Gln Ala Val Asp Leu Leu
 20 25 30
 Gly Asn Pro Glu Gln Ser Tyr Pro Ile Ile His Val Thr Gly Thr Asn
 35 40 45
 Gly Lys Gly Ser Thr Ile Ala Phe Met Arg Glu Leu Phe Met Gly His
 50 55 60
 Gly Lys Lys Val Ala Thr Phe Thr Ser Pro His Ile Val Ser Ile Asn
 65 70 75 80
 Asp Arg Ile Cys Ile Asn Gly Gln Pro Ile Ala Asp Ala Asp Phe Ile
 85 90 95
 Arg Leu Ala Asp Gln Val Lys Glu Met Glu Lys Thr Leu Leu Gln Thr
 100 105 110
 Pro Asp Gln Leu Ser Phe Phe Glu Leu Leu Thr Leu Val Ala Phe Leu
 115 120 125
 Tyr Phe Arg Glu Gln Glu Val Asp Leu Val Leu Leu Glu Val Gly Ile
 130 135 140
 Gly Gly Leu Leu Asp Thr Thr Asn Val Val Thr Gly Glu Leu Ala Val
 145 150 155 160
 Ile Thr Ser Ile Gly Leu Asp His Gln Lys Thr Leu Gly Asp Ser Ser
 165 170 175

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

Met Ile Ser Tyr Asp Thr Arg Met Leu Leu Leu Ile Ala Ile Phe Ser
 1             5             10             15
Val Phe Leu Leu Tyr Leu Ser Glu Ile Arg Phe Lys Asp Val Ser Phe
          20             25             30
Val Ala Val Phe Ala Thr Val Phe Ala Val Leu Asn Val Leu Met Val
      35             40             45
Tyr Leu Phe Ser Pro Glu Tyr Gly Val Gly Leu Tyr Gly Glu Arg Ser
 50             55             60
Val Ile Trp Gln Gly Ile Gly Val Tyr Thr Leu Thr Ser Gln Glu Leu
65             70             75             80
Phe Tyr Leu Leu Asn Leu Val Ile Lys Tyr Leu Cys Thr Ile Pro Leu
          85             90             95
Ala Ile Ile Phe Leu Met Thr Thr His Pro Ser Gln Phe Ala Ser Ser
      100             105             110
Leu Asn Gln Ile Gly Val Pro Tyr Lys Ile Ala Tyr Ser Val Ser Leu
      115             120             125
Thr Leu Arg Tyr Ile Pro Asp Leu Gln Glu Glu Phe Phe Thr Ile Lys
      130             135             140
Met Ser Gln Glu Ala Arg Gly Met Glu Leu Ser Lys Lys Ala Ser Leu
      145             150             155             160
Met Gln Arg Ile Lys Gly Asn Leu Leu Ile Ile Thr Pro Leu Ile Phe
          165             170             175
Ser Ser Leu Glu Thr His
          180

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

Met Pro Ile Ser Glu Arg Thr Val Tyr Gln Ile Gln Ser Asp Gln Glu
 1             5             10             15
Ser Leu Tyr Ala Lys Phe Asn Pro Ala Leu Thr Phe Val Pro Val Asp
             20             25             30
Phe Glu Asp Leu Ser Ser Gln Met Thr Tyr Asn Lys Cys Val Thr Ala
             35             40             45
Phe Ala Gln Glu Pro Leu Asp Ala Ala Ile Gln Lys Ile Ser Pro Glu
             50             55             60
Leu Phe Asp Gln Tyr Glu Ile Phe Lys Ser Arg Glu Met Leu Leu Glu
65             70             75             80
Trp Ser Pro Lys Asn Val His Lys Ala Thr Gly Leu Ala Lys Leu Ile
             85             90             95
Ser His Leu Gly Ile Asn Gln Ser Gln Val Met Ala Cys Gly Asp Glu
             100            105            110
Ala Asn Asp Leu Ser Met Ile Glu Trp Ala Gly Leu Gly Val Ala Met
             115            120            125
Gln Asn Ala Val Pro Glu Val Lys Ala Ala Ala Asn Val Val Thr Pro
             130            135            140
Met Thr Asn Asp Glu Glu Ala Val Ala Arg Ala Ile Glu Gln Tyr Val
145            150            155            160
Leu Lys Glu Asn

```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```

Met Lys Ile Lys Val Val Thr Val Gly Lys Leu Lys Glu Lys Tyr Leu
 1             5             10             15
Lys Asp Gly Ile Ala Glu Tyr Ser Lys Arg Ile Ser Arg Phe Ala Lys
             20             25             30

```


Phe Glu Met Ile Glu Leu Ser Asp Glu Lys Thr Pro Asp Lys Ala Ser
 35 40 45
 Glu Ser Glu Asn Gln Lys Ile Leu Glu Ile Glu Gly Gln Arg Ile Leu
 50 55 60
 Ser Lys Ile Ala Asp Arg Asp Phe Val Ile Val Leu Ala Ile Glu Gly
 65 70 75 80
 Lys Thr Phe Phe Ser Glu Glu Phe Ser Lys Gln Leu Glu Glu Thr Ser
 85 90 95
 Ile Arg Arg Asp Phe Tyr Ser Tyr Phe Tyr Tyr Trp Gly Lys Phe Arg
 100 105 110
 Ile Val Ile Ile Cys Lys Lys
 115

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Leu Glu Gln Ala Pro Gly Leu Ser Leu Ala Asp Thr Leu Ser Leu His
 1 5 10 15
 Tyr Ala Met Arg Asn Glu Leu Thr Leu Ser Pro Val Asp Phe Leu Leu
 20 25 30
 Arg Arg Thr Asn His Met Leu Phe Met Arg Asp Ser Leu Asp Ser Ile
 35 40 45
 Val Glu Pro Val Leu Asp Glu Met Gly Arg Phe Tyr Asp Trp Thr Glu
 50 55 60
 Glu Glu Lys Ala Thr Tyr Arg Ala Asp Val Lys Ala Ala Leu Ala Gln
 65 70 75 80
 Asn Asp Leu Ala Glu Leu Lys Asn
 85

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```

Met Glu Asp Ile Leu Tyr Ala Pro Ala Glu Gln Asn Asn Gly Ser Ala
 1             5             10             15
Ile Glu Lys Ala Phe Gly Lys Asn Gly Lys Ile Ala Phe Gln Lys Ser
      20             25             30
Val Asp Lys Tyr Trp Lys Asn Leu Ile Phe Met Phe Lys Asn Thr Pro
      35             40             45
Ala Ala Glu Gly Asn Asp Ser Thr Thr Glu Ser Tyr Met Lys Gly Leu
      50             55             60
Trp Leu Ser Asn His Thr Tyr Gln Trp Gly Gly Leu Met Asp Thr Trp
      65             70             75             80
Lys Trp Tyr Glu Thr Gly Lys Trp Lys Leu Phe Ala Ser Gly Asn Ile
      85             90             95
Gly Lys Ser Gln Gly Asp Arg Gln Trp Leu Thr Glu Pro Glu Ser Met
      100            105            110
Leu Gly Glu Glu Ala Leu Gly Val Tyr Leu Asn Gly Gly Val Val Tyr
      115            120            125
Asn Phe Glu His Pro Ala Tyr Thr Tyr Gly Val Asn Asn Lys Glu Ser
      130            135            140
Leu Leu Phe Ser Glu Val Ile Lys Glu Phe Phe Arg Tyr Val Ile Ala
      145            150            155            160
His Pro Ala Pro Ser Lys Glu Lys Tyr Leu Arg Ile Gln Lys Tyr Ser
      165            170            175
Tyr Met Glu Thr Ile Gln Ile Lys Glu Met Val Ser Ser Leu
      180            185            190

```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Met Thr Ile Glu Leu Leu Thr Pro Phe Thr Lys Val Glu Leu Glu Pro
1 5 10 15
Glu Ile Lys Glu Lys Lys Arg Lys Gln Val Gly Ile Leu Gly Gly Asn
20 25 30
Phe Asn Pro Val His Asn Ala His Leu Ile Val Ala Asp Gln Val Arg
35 40 45
Gln Gln Leu Gly Leu Asp Gln Val Leu Leu Met Pro Glu Tyr Gln Pro
50 55 60
Pro His Val Asp Lys Lys Glu Thr Ile Pro Glu His His Arg Leu Lys
65 70 75 80
Met Leu Glu Phe Gly Asn
85

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

Leu Leu Xaa Gly Ser Leu Thr Xaa Thr His Val Ala Met Thr Trp Gln
1 5 10 15
Gln Leu Val Val Thr Lys Ser Ile Glu Lys Leu Asn Val Lys Thr Arg
20 25 30
Cys Val Gln Pro Asn His Trp Gln Glu Pro Leu Val Asp Pro Glu Thr
35 40 45
Gly Glu Ile Leu Val Glu Ala Gly Thr Ile Met Thr Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

Met Lys Lys Lys Leu Leu Ala Gly Ala Ile Thr Leu Leu Ser Val Ala
 1             5             10             15
Thr Leu Ala Ala Cys Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser
             20             25             30
Met Lys Gly Asp Val Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys
             35             40             45
Asn Asn Pro Ser Ala Gln Xaa Val Leu Leu Asn Met Thr Ile Gln Lys
             50             55             60
Val Phe Glu Lys Thr Ile Trp Leu Arg Ala
65             70

```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

```

Met Thr Gly Glu Ile Arg Asn Leu Gln Ala Gln Asp Tyr Asp Ala Ser
 1             5             10             15
Gln Ile Gln Val Leu Glu Gly Leu Glu Ala Xaa Xaa Met Arg Ser Gly
             20             25             30
Xaa Tyr Ile Gly Ser Thr Ser Lys Glu Gly Leu His His Leu Val Trp
             35             40             45
Glu Ile Val Asp Asn Ser Ile Asp Glu Ala Leu Ala Gly Phe Ala Ser
             50             55             60
His Ile Gln Val Phe Ile Glu Pro Asp Asp Ser Ile Thr Val Val Asp
65             70             75             80
Asp Gly Arg Gly Ile Pro Val Asp Ile Gln Glu Phe Thr Gly Arg Pro
             85             90             95
Ala Val Glu Thr Val Phe Thr Val Leu His Ala Gly Gly Lys Phe Gly
             100             105             110
Gly Gly Gly Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Ser Ser
             115             120             125

```

Val Val Asn Ala Leu Ser Thr Gln Leu Asp Val His Val His Lys Asn
 130 135 140
 Gly Lys Ile His Tyr Gln Glu Tyr Arg Arg Gly His Val Val Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

Met Val Leu Ser Lys Tyr Tyr Gly Val Ala Asp Gly Met Asn Val Glu
 1 5 10 15
 Gly Arg Gly Ser Ala Asn Phe Ile Lys Asp Asn Val Leu Ile Thr Ser
 20 25 30
 Gly Leu Thr Thr Asn Tyr Arg His Asp Tyr Gly Lys Glu Ala Asp Asp
 35 40 45
 Ile Tyr Val Leu Pro Ala Val Ser Pro Ser Gln Glu Leu Phe Gly Lys
 50 55 60
 Ile Lys Val Lys Glu Val Cys Tyr Leu Lys Glu Phe Arg Asn Leu Asn
 65 70 75 80
 Ser Lys Asp Ala Arg Glu Tyr Asp Leu Ala Leu Leu Ile Leu Glu Glu
 85 90 95
 Pro Ile Gly Ala Lys Leu Gly Thr Leu Gly Leu Pro Thr Ser Gln Lys
 100 105 110
 Asn Leu Thr Gly Ile Thr Val Thr Ile Thr Gly Tyr Pro Ser Tyr Asn
 115 120 125
 Phe Lys Ile His Gln Met Tyr Thr Asp Lys Lys Gln Val Leu Ser Asp
 130 135 140
 Asp Gly Met Phe Leu Asp Tyr Gln Val Asp Thr Leu Glu Gly Ser Ser
 145 150 155 160
 Gly Tyr Tyr Ser Leu
 165

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

448

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```

Met Val Glu Asn Pro Ile Leu Gly Thr Ala Glu Glu Gly Ala Leu Phe
 1             5             10             15
Ser Leu Thr Ala Glu Gly Lys Ile Val Val Asn Asn Pro His Lys Ala
          20             25             30
Asp Ile Glu Pro Ser Leu Leu Asp His Phe Phe Val Asp Thr His Gln
          35             40             45
Asp Pro Ser Tyr Gln Ala Cys
          50             55

```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

Leu Lys Lys Ile Ser Lys Gln Glu Leu Val Asn Thr Arg Phe Ser Arg
 1             5             10             15
Leu Phe Ala His Phe Gly Gln Glu Lys Asp Gly Ser Phe Leu Ala Gln
          20             25             30
Arg Tyr Gln Phe Tyr Leu Ala Gln Gln Gly Gln Thr Leu Ser Gly Ala
          35             40             45
His Asp Leu Leu Asp Ser Leu Ile Glu Arg Asp Tyr Asn Leu Tyr Ala
          50             55             60
Ala Thr Asn Gly Ile Thr Ala Ile Gln Thr Gly Arg Leu Ala Gln Ser
          65             70             75             80
Gly Leu Ala Pro Tyr Phe Asn Gln Val Phe Ile Ser Glu Gln Leu Gln
          85             90             95

```

Thr Gln Lys Pro Asp Ala Leu Phe Tyr Glu Lys Ile Gly Gln Gln Ile
 100 105 110
 Ala Gly Phe Ser Lys Glu Lys Thr Leu Met Ile Gly Asp Ser Leu Thr
 115 120 125
 Ala Asp Ile Gln Gly Gly Asn Asn Ala Gly Ile Asp Thr Ile Trp Tyr
 130 135 140
 Asn Pro His His Leu Glu Asn His Thr Gln Ala Gln Pro Thr Tyr Glu
 145 150 155 160
 Val Tyr Ser Tyr Gln Asp Leu Leu Asp Cys Leu Asp Lys Asn Ile Leu
 165 170 175
 Glu Lys Ile Thr Phe
 180

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

Met Lys Tyr Asp Asp Ala Met Ala Leu Tyr Gly Ser Asp Lys Pro Asp
 1 5 10 15
 Thr Arg Phe Asp Met Leu Leu Gln Asp Leu Thr Glu Val Val Lys Gly
 20 25 30
 Val Asp Phe Lys Val Phe Ser Glu Ala Leu Ala Val Lys Ala Ile Val
 35 40 45
 Val Asn Gly Leu Glu Pro Leu Thr Ala Asp Asn Tyr Ser Arg Lys Asp
 50 55 60
 Ile Asp Lys Met Thr Glu Val Ala Lys Gln Tyr Gly Ala Lys Gly Leu
 65 70 75 80
 Ala Trp Val Lys Val Val Asp Gly Glu Leu Asn Gly Pro Val Ala Lys
 85 90 95
 Phe Leu Thr Gly Ile Gln Glu Glu Leu Thr Thr Ala Leu Ala Leu Glu
 100 105 110
 Asp Lys Asp Leu Val Leu Phe Val Ala Asp Thr Leu Glu Val Ala Asn
 115 120 125
 Ala Thr Leu Gly Ala Leu Arg Gly Arg Ile Ala Lys Glu Leu Gly Leu
 130 135 140
 450

Ile Asp Asn Asp Lys Phe Asn Phe Leu Trp Val Val Asp Trp Pro Met
 145 150 155 160
 Phe

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

Met Val Lys Tyr Gly Val Val Gly Ala Gly Tyr Phe Gly Ala Glu Leu
 1 5 10 15
 Ala Arg Tyr Met Gln Lys Asn Asp Gly Ala Glu Ile Thr Leu Leu Tyr
 20 25 30
 Asp Pro Asp Asn Ala Glu Ala Ile Ala Glu Glu Leu Gly Ala Lys Val
 35 40 45
 Ala Ser Ser Leu Asp Glu Leu Val Ser Ser Asp Glu Val Asp Cys Val
 50 55 60
 Ile Val Ala Thr Pro Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met Lys Ile Asp Lys Tyr Ser Ala Ile Leu Gly Asn Thr Val Gly Phe
 1 5 10 15

His Asn Met Ser Thr Leu Thr Asp His Arg Pro Val Ala Ser Leu Pro
 20 25 30
 Phe Gly Gly Lys Tyr Arg Leu Ile Asp Phe Pro Leu Ser Ser Leu Ala
 35 40 45
 Asn Ala Gly Val Arg Ser Val Phe Gly Ile Phe Gln Gln Asp Asn Ile
 50 55 60
 Ser Ser Val Phe Asp His Ile Arg Ser Gly Arg Glu Trp Gly Leu Ser
 65 70 75 80
 Thr Leu Leu Ser His Tyr Tyr Leu Gly Ile Tyr Asn Thr Arg Val Glu
 85 90 95
 Ser

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

Met Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val
 1 5 10 15
 Lys Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro
 20 25 30
 Asn Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr
 35 40 45
 Gln Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu
 50 55 60
 Arg Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe
 65 70 75 80
 Leu Cys Arg Arg Ser Gln His Pro Phe Pro Ser Asn Lys Ser Arg
 85 90 95

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

```

Met Lys Ile Gly Ile Ile Ala Ala Met Pro Glu Glu Leu Ala Tyr Leu
 1             5             10             15
Val Gln His Leu Asp Asn Ala Gln Glu Gln Val Val Leu Gly Asn Thr
          20             25             30
Tyr His Thr Gly Thr Ile Ala Ser His Glu Val Val Leu Val Glu Ser
          35             40             45
Gly Ile Gly Lys Val Met Ser Ala Met Asn Cys Val Ala Asn Phe Gly
50             55             60

```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

```

Met Leu His Asn Ala Phe Ala Tyr Val Thr Arg Lys Phe Phe Lys Ser
 1             5             10             15
Ile Val Ile Phe Leu Ile Ile Leu Leu Met Ala Ser Leu Ser Leu Val
          20             25             30
Gly Leu Ser Ile Lys Gly Ala Thr Ala Lys Ala Ser Gln Glu Thr Phe
          35             40             45
Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile Asn Arg Arg Val Asn
50             55             60
Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys Gly Glu Asp Ile Lys
65             70             75             80
Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr Val Lys Arg Ile Asn
          85             90             95
Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile Glu Thr Pro Glu Thr
100             105             110

```

Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg Phe Gly Ser Ser Leu
 115 120 125
 Thr Ile Thr Gly Val Asn Asp Ser Ser Lys Glu Asp Lys Phe Val Ser
 130 135 140
 Gly Pro Ile
 145

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

Leu Arg Lys Asn Ile Gly Leu Val Leu Gln Asp Leu Ser Ile Arg Glu
 1 5 10 15
 Leu Leu Ser Pro Ile Ser Pro Cys Thr Lys Lys Ser Val Met Ser Arg
 20 25 30
 Phe Lys Ala Ala Ala Phe Val Asp Ala Asp Ser Phe Ile Gln Glu
 35 40 45
 Leu Pro Gln Arg Tyr Asp Ser Pro Val Ser Glu Arg Gly Ser Ser Phe
 50 55 60
 Ser Thr Gly Gln Arg Gln Leu Leu Ala Phe Ala Arg Thr Val Ala Ser
 65 70 75 80
 Gln Pro Lys Ile Leu Ile Leu Asp Glu Ala Thr Ala Asn Ile Asp Ser
 85 90 95
 Glu Thr Glu Ser Leu Val Gln Ala Ser Leu Ala Lys Met Arg Gln Gly
 100 105 110
 Arg Thr Thr Ile Ala Ile Ala His Arg Leu Ser Thr Ile Gln Asp Ala
 115 120 125
 Asn Cys Ile Tyr Val Leu Asp Lys Gly Arg Ile Ile Glu Ser Gly Thr
 130 135 140
 His Glu Glu Leu Leu Ala Leu Gly Gly Thr Tyr His Lys Met Tyr Ser
 145 150 155 160
 Leu Gln Ala Gly Ala Met Ala Asp Thr Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:520:

454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

```

Met Arg Asn Met Lys Ala Lys Tyr Ala Val Trp Val Ala Phe Phe Leu
 1           5           10           15
Asn Leu Thr Tyr Ala Ile Val Glu Phe Ile Ala Gly Gly Val Phe Gly
          20           25           30
Ser Ser Ala Val Leu Ala Asp Ser Val His Asp Leu Gly Asp Ala Ile
          35           40           45
Ala Ile Gly Ile Ser Ala Phe Leu Glu Thr Ile Ser Asn Arg Glu Glu
          50           55           60
Asp Asn Gln Tyr Thr Leu Gly Tyr Lys Arg Phe Ser Leu Leu Gly Ala
          65           70           75           80
Leu Val Thr Ala Val Ile Leu Val Thr Gly Ser Val Leu Val Ile Leu
          85           90           95
Glu Asn Val Thr Lys Ile Leu His Pro Gln Pro Val Asn Asp Glu Gly
          100          105          110
Ile Leu Trp Leu Gly Ile Ile Ala Ile Thr Ile Asn Leu Leu Ala Ser
          115          120          125
Leu Val Val Gly Lys Gly Lys Thr Lys Asn Glu Ser Ile Leu Ser Leu
          130          135          140
His Phe Leu Glu Asp Thr Leu Gly Trp Val Ala Val Ile Leu Met Ala
          145          150          155          160
Ile Val Pro Ser Ile
          165

```

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

```

Met Glu Thr Ala Leu Ile Ser Val Ile Val Pro Val Tyr Asn Val Ala
 1              5              10              15
Gln Tyr Leu Glu Lys Ser Ile Ala Ser Ile Gln Lys Gln Thr Tyr Gln
      20              25              30
Asn Leu Glu Ile Ile Leu Val Asp Asp Gly Ala Thr Asp Glu Ser Gly
      35              40              45
Arg Leu Cys Asp Ser Ile Ala Glu Gln Asp Asp Arg Val Ser Val Leu
      50              55              60
His Lys Lys Asn Glu Gly Leu Ser Gln Ala Arg Asn Asp Gly Met Lys
      65              70              75              80
Gln Ala His Gly Asp Tyr Leu Ile Phe Ile Asp Ser Lys
      85              90

```

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

Met Ile Lys Asp Ile Gln Gly Asp Lys Met Asn Asn Asn Leu Leu Val
 1              5              10              15
Leu Gln Ser Asp Phe Gly Leu Val Asp Gly Ala Val Ser Ala Met Ile
      20              25              30
Gly Val Ala Leu Glu Glu Ser Pro Thr Leu Lys Ile His His Leu Thr
      35              40              45
His Asp Ile Thr Pro Tyr Asn Ile Phe Glu Gly Ser Tyr Arg Leu Phe
      50              55              60
Gln Thr Val Asp Tyr Trp Pro Glu Gly Thr Thr Phe Val Ser Val Val
      65              70              75              80
Asp Pro Gly Val Gly Ser Lys Arg Lys Ser Val Val Ala Lys Thr Ala
      85              90              95
Gln Lys Ser Ile His Cys His Ala Arg
      100              105

```

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

```

Leu Val Glu Val Gln Lys Ile Lys Val Ile Arg Thr Lys Lys Gly Glu
 1             5             10             15
Asn Met Ala Phe Leu Gln Ala Asp Asp Ser Lys Lys Lys Leu Asp Val
          20             25             30
Thr Leu Phe Ser Asp Leu Tyr Arg Gln Val Gly Gln Glu Ile Lys Glu
      35             40             45
Gly Ala Phe Tyr Tyr Val Lys Gly Lys Ile Gln Ser Arg Asp Gly Arg
      50             55             60
Leu Gln Met Ile Ala Gln Glu Ile Arg Glu Ala Val Ala Glu Arg Phe
      65             70             75             80
Trp Ile Gln Val Lys Asn His Glu Ser Asp Gln Glu Ile Ser Arg Ile
          85             90             95
Leu Glu Gln Phe Lys Gly Pro Ile Pro Val Ile Ile Arg Tyr Glu Glu
          100             105             110
Glu Gln Lys Thr Ile Val Ser Pro His His Phe Val Ala Lys Ser Asn
          115             120             125
Glu Leu Glu Glu Lys Leu Asn Glu Ile Val Met Lys Thr Ile Tyr Arg
          130             135             140

```

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met Asn Ser Phe Lys Asn Phe Leu Lys Glu Trp Gly Leu Phe Leu Leu
 1 5 10 15
 Ile Leu Ser Leu Leu Ala Leu Ser Arg Ile Phe Phe Trp Ser Asn Val
 20 25 30
 Arg Val Glu Gly His Ser Met Asp Pro Thr Leu Ala Asp Gly Glu Ile
 35 40 45
 Leu Phe Val Val Lys His Leu Pro Ile Asp Arg Phe Asp Ile Val Val
 50 55 60
 Ala His Glu Glu Asp Gly Asn Lys Asp Ile Val Lys Arg Val Ile Gly
 65 70 75 80
 Met Pro Gly Asp Thr Ile Arg Tyr Glu Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Met Val Leu Gln Arg Asn Glu Ile Asn Glu Lys Asp Thr Trp Asp Leu
 1 5 10 15
 Ser Thr Ile Tyr Pro Thr Asp Gln Ala Trp Glu Glu Ala Leu Lys Asp
 20 25 30
 Leu Thr Glu Gln Leu Glu Thr Val Ala Gln Tyr Glu Gly His Leu Leu
 35 40 45
 Asp Ser Ala Asp Asn Leu Leu Glu Ile Thr Glu Phe Ser Leu Glu Met
 50 55 60
 Glu Arg Gln Met Glu Lys Leu Tyr Val Tyr Ala His Met Lys Asn Asp
 65 70 75 80
 Gln Asp Thr Arg Glu Ala Lys Tyr Gln Glu Tyr Tyr Ala Lys Ala Met
 85 90 95
 Thr Leu Leu Gln Pro Val Arg Pro Ser Leu Phe Ile Leu
 100 105

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

458

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

```

Met Met Ile Glu Lys Glu Asp Leu Thr Pro Phe Ile His Leu Gln His
 1             5             10             15
His Gln Gln Glu Leu Thr Leu Lys Asp Gly Ile Val Ile Thr Ala Lys
          20             25             30
Leu Ala Gln Leu Ala Gly Val Lys Val Gly Gln Thr Leu
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

```

Leu Ala Leu Phe Asp Glu Lys Asp Gln Phe Val Gln Thr Val Thr Ile
 1             5             10             15
Ala Ser His Arg Lys Gln Lys Asn Phe Asp Ile Ile Lys Phe Lys Asp
          20             25             30
Met Tyr His Ile Asn Thr Ile Glu Lys Tyr Lys Gly Tyr Ser Leu Lys
      35             40             45
Val Ala Glu Glu Asp Leu Asn Asp Leu Asp Asp Gly Glu Phe Tyr Tyr
      50             55             60
His Glu Ile Ile Gly Leu Glu Val Tyr Glu Gly Asp Ser Leu Val Gly
65             70             75             80
Thr Ile Lys Glu Asn Pro Ala Thr Arg Cys
          85             90

```

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

```

Met Pro Val Ser Arg Met Trp Cys Ser Thr Ser Ile Leu Arg Ile Leu
 1             5             10             15
Thr Val Trp Ser Thr Ser Met Ile Lys Arg Lys Thr Tyr Trp Lys Asp
      20             25             30
Leu Ile Gln Ser Phe Thr Gly Ser Lys Gly Arg Phe Leu Ser Ile Leu
      35             40             45
Ile Leu Met Met Leu Gly Ser Leu Ala Leu Val Gly Leu Lys Val Thr
      50             55             60
Ser Pro Asn Met Glu Thr Thr Ala Asn Ala Tyr Leu Thr Thr Ala Gln
65             70             75             80
Thr Leu Asp Leu Ala Val Met Ser Asn Tyr Gly Leu Asp Gln Ala Tyr
      85             90             95
Gln Glu Glu Leu Lys Gln Thr Glu Gly Ala Glu Val Glu Phe Gly Tyr
      100            105            110
Leu Thr Asp Val Thr Met Asp Asn Gly Gln Asp Ala Ile Arg Leu Tyr
      115            120            125
Ser Lys Pro Glu Arg Ile Ser Thr Phe Gln Leu Arg Lys Gly
130            135            140

```

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

```

Met Tyr Val Ala Thr Glu Arg Glu Ile Ala Lys His Ile Ser Arg Leu
 1             5             10             15
                                     460

```

Gly Trp Tyr Arg Asn Lys Asp Lys Phe Leu Lys Lys Cys Ala Gln Gln
 20 25 30
 Leu Ala Lys Arg Phe
 35

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met Lys His Gln Gln Lys Phe Val Pro Tyr Lys Thr Leu Gly Ala Asp
 1 5 10 15
 Ala Val Gly Met Ser Thr Val Pro Glu Val Ile Val Ala Ala His Ser
 20 25 30
 Gly Leu Lys Val Leu Gly Ile Ser Cys Ile Thr Asn Phe Ala Ala Gly
 35 40 45
 Phe Gln Glu Glu Leu Asn His Glu Glu Val Val Glu Val Thr Glu Arg
 50 55 60
 Val Lys Gly Asp Phe Lys Gly Leu Leu Lys Ala Ile Leu Ala Glu Leu
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Leu Leu Glu Ile Leu Asp Phe Asp Trp Ser Ile Phe Leu His Asp Val
 1 5 10 15

Glu Lys Thr Glu Lys Phe Val Phe Leu Leu Leu Val Phe Ser Met Ser
 20 25 30
 Ile Thr Cys Leu Leu Ala Leu Phe Trp Arg Gly Ile Glu Glu Leu Ser
 35 40 45
 Leu Arg Lys Met Gln Ala Asn Leu Lys Arg Leu Leu Ala Gly Gln Glu
 50 55 60
 Val Val Gln Val Ala Asp Pro Asp Leu Asp Ala Ser Phe Lys Ser Leu
 65 70 75 80
 Ser Gly Lys Leu Asn Leu Leu Thr Glu Ala Leu Gln Lys Ala Glu Asn
 85 90 95
 His Ser Leu Ala His Glu Glu Glu Ile Ile Glu Lys Glu Arg Lys Arg
 100 105 110
 Ile Ala Arg Asp Leu His Asp Thr Val Ser Gln Glu Leu Phe Ala Ala
 115 120 125
 His Met Ile Leu Ser Gly Phe Ser Gln Gln Ala Leu Lys Phe Gly
 130 135 140

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Met Asn Lys Leu Ile Ala Phe Ile Glu Lys Gly Lys Pro Phe Phe Glu
 1 5 10 15
 Lys Leu Ser Arg Asn Ile Tyr Leu Arg Ala Ile Arg Asp Gly Phe Ile
 20 25 30
 Ala Gly Met Pro Val Ile Leu Phe Ser Ser Ile Phe Ile Leu Ile Ala
 35 40 45
 Phe Val Pro Asn Ser Trp Gly Phe Lys Trp Ser Asp Ala Ser Cys Ser
 50 55 60
 Leu Ser Asp
 65

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

462

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

```

Met Ile Ser Lys Cys Cys Val Arg Trp Ala Ile Pro Met Gly Leu Lys
 1             5             10             15
Ile Ile Leu Ala Asn Met Asp Gly Arg Ser Glu Gly Glu Pro Pro Tyr
 20             25             30
Thr Leu Leu Asp Phe Phe Pro Asp Asp Phe Leu Ile Met Ile Asp Glu
 35             40             45
Ser His Met Thr Ile Gly Gln Ile Lys Gly Met Tyr Asn Gly Asp Arg
 50             55             60
Ser Arg Lys Glu Met Leu Val Asn Tyr Gly Phe Arg Leu Pro Ser Ala
 65             70             75             80
Leu Asp Asn Arg Pro Leu Arg Arg Glu Glu Phe
             85             90

```

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE--DESCRIPTION: SEQ ID NO:534:

```

Met Lys Gln Val Glu Ala Lys Glu Glu Glu Gln Glu Gln Ala Glu Arg
 1             5             10             15
Glu Ala Glu Ser Lys Lys Glu Pro Tyr Ile Tyr Tyr Ile Leu Ser Phe
 20             25             30
Ala Lys Leu Ala Asp Leu Val Ala Phe Ala Lys Thr Val Thr Phe Glu
 35             40             45
Met Glu Thr Ser Glu Leu Tyr Lys Met Asn Glu Arg Tyr Tyr Gly Leu
 50             55             60

```

Phe Asp Arg Leu
65

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Met	Lys	Ala	Pro	Gln	Ala	Ala	Gly	Ile	Ile	His	Ser	Asp	Phe	Glu	Lys
1				5				10					15		
Gly	Phe	Ile	Arg	Ala	Val	Thr	Met	Ser	Tyr	Glu	Asp	Leu	Val	Lys	Tyr
			20					25				30			
Gly	Ser	Glu	Lys	Ala	Val	Lys	Lys	Ala	Gly	Arg	Leu	Arg	Glu	Glu	Gly
		35					40				45				
Lys	Glu	Tyr	Ile	Val	Gln	Asp	Gly	Asp	Ile	Met	Glu	Phe	Arg	Phe	Asn
	50					55				60					
Val															
65															

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

Met	Ile	Lys	Thr	Thr	Ser	Leu	Val	Val	Leu	Ile	Gly	Val	Val	Glu	Val
1				5					10				15		
Thr	Lys	Val	Gly	Gln	Gln	Ile	Ile	Asp	Ser	Asn	Arg	Leu	Thr	Ile	Pro
			20					25				30			

Thr Gly Ser Phe Trp Val Tyr Gly Thr Ile Leu Val Leu Tyr Phe Ala
 35 40 45
 Val Cys Tyr Pro Ile Ser Lys Leu Ser Thr His Leu Glu Lys His Trp
 50 55 60
 Ser Asn
 65

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

Met Glu Val Val Met Asp Asn Ile Ile Asp Val Ser Ile Pro Val Ala
 1 5 10 15
 Glu Val Val Asp Lys His Pro Glu Val Leu Glu Ile Leu Val Glu Leu
 20 25 30
 Gly Phe Lys Pro Leu Ala Asn Pro Leu Met Arg Asn Thr Val Gly Arg
 35 40 45
 Lys Val Ser Leu Lys Gln Gly Ser Lys Leu Ala Gly Thr Pro Met Asp
 50 55 60
 Lys Ile Val Arg Thr Leu Glu Ala Asn Gly Tyr Glu Val Ile Gly Leu
 65 70 75 80
 Asp

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Met Ile Phe Leu Ile Arg Met Ile Tyr Asn Ala Val Asp Ile Tyr Ser
 1 5 10 15
 Leu Ile Leu Val Ala Phe Ala Val Met Ser Trp Phe Pro Gly Ala Tyr
 20 25 30
 Glu Ser Ser Leu Gly Arg Trp Ile Val Ala Leu Val Lys Pro Val Leu
 35 40 45
 Ala Pro Leu Gln Arg Leu Pro Leu Gln Ile Ala Gly Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Met Lys Tyr Ile Ser Tyr Arg Ser Glu Pro Asn Val Asn Pro Glu Ser
 1 5 10 15
 Thr Thr Glu Thr Phe Thr Ser Gly Ala Phe Phe Val Asp Ser Asp Arg
 20 25 30
 Phe Arg Gly Val Arg Ser Phe Leu Phe Pro Tyr Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Met Thr Lys Ile Ser Ile Tyr Glu Leu Val Lys Arg Ala Gly Val Ser
 1 5 10 15

```

Arg Ala Ala Phe Tyr Arg Asn Tyr Asp Ser Lys Glu Glu Ile Ser Glu
      20              25              30
Ser Val Phe Lys Arg Thr Val His Asn Ile Met Glu Gln Met His His
      35              40              45
Tyr Asp Leu Lys Thr Asp Leu Tyr Val Val Cys Phe Thr Phe Ser Gly
      50              55              60
Arg Pro Glu Arg Lys Leu Glu
      65              70

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

```

Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val Glu Tyr Asp
 1              5              10              15
Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala Ile Pro Lys
      20              25              30
Asp Lys Val Asp Ser Tyr His Thr Phe Glu Val Leu Gly Lys Val Glu
      35              40              45
Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Asp Gly Ile Val
      50              55              60
Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu Ala Pro Gln
      65              70              75              80
Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His Val Ser Ser
      85              90              95
Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu
      100             105             110
Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr
      115             120             125
Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile
      130             135             140
Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp
      145             150             155             160
Ser Asn His Lys Arg Pro Ser Phe Lys Cys Ser
      165             170

```


(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

```

Met Glu Leu Arg Arg Pro Arg Leu Ala Asp Lys Lys Ala Val Leu Asp
 1             5             10             15
Met Met Thr Glu Phe Glu Lys Ser Gln Ser Ala His Asp Gly Gly Phe
      20             25             30
Trp Asp Thr Glu Asn Phe Val Tyr Glu Glu Trp Leu Glu Ser Asn Gln
      35             40             45
Glu Gln Glu Met Gly Ile Asn Leu Pro Glu Gly Trp Val Pro Ala Ile
      50             55             60
Gln Leu Val Ala Phe Ser Glu Lys Gly Gln Ala Val Gly Phe Leu Asn
      65             70             75             80
Leu Arg Leu Arg Leu Ser Asn Phe Leu Leu Glu Glu Gly Gly His Ile
      85             90             95
Gly Tyr Ser Ile Arg Pro Ser Glu Arg Gly Lys Gly Tyr Ala Lys Glu
      100            105            110
Leu Ser Val Arg Ala Cys Lys Leu Leu Arg Lys Arg Thr Ser Arg Lys
      115            120            125
Leu Trp
      130

```

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

```

Leu Leu Leu Ile Phe Ala Val Ile Gly Val Leu Val Ala Leu Ile Ala
 1               5               10               15
Gln Phe Tyr Ser Ala Lys Ala Ala Val Gly Phe Ala Lys Glu Leu Thr
      20               25               30
Asn Asp Leu Tyr Arg His Ile Leu Ser Leu Pro Lys Asp Ser Arg Asp
      35               40               45
Arg Leu Thr Thr Ser Ser Leu Val Thr Arg Leu Thr Ser Asp Thr Tyr
      50               55               60
Gln Ile Gln Thr Gly Ile Asn Gln Phe Leu Leu Ser Leu Phe Thr Ser
      65               70               75               80
Ala His Ile Ser Phe Leu Val Pro Phe Leu Trp Leu Ile Glu Ser Gln
      85               90               95
Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

```

Met Ala Tyr Arg Ile Ser Ala Glu Leu Thr Phe Trp Phe Leu Ile Met
 1               5               10               15
Val Ala Ile Leu Thr Ile Val Ile Val Arg Val Ile Ser Ile Gly Gln
      20               25               30
Ser Ser Leu Gln
      35

```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

```

Met Thr Thr Phe Lys Asp Arg Phe Leu Trp Gly Gly Ala Val Ala Ala
 1             5             10             15
His Gln Leu Glu Gly Gly Trp Gln Glu Gly Gly Lys Gly Ile Ser Val
          20             25             30
Ala Asp Val Met Thr Ala Gly Arg His
      35             40

```

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

```

Met Leu Asp Met Leu Arg Asp Met Gln Asp Lys Ala Arg Lys Asn Lys
 1             5             10             15
Ile Asp Phe Ala Val Ala Gly Tyr Leu Asn Thr Ser Phe Ile Gln Lys
          20             25             30
Met Asn Gln Leu Gly Ile Lys Cys Ile Ile His Tyr Ser Ser Ile Pro
      35             40             45
Glu Ile Phe Asp Leu Glu Ile Asp His Pro Asp His Leu Lys His Ile
      50             55             60
Lys Glu Glu Lys
65

```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```

Met Lys Asn Val Glu Leu Lys Glu Glu Asn Met Thr Phe Glu Glu Ile
 1           5           10           15
Leu Pro Gly Leu Lys Ala Lys Arg Lys Tyr Val Arg Thr Gly Trp Gly
          20           25           30
Gly Ala Glu Asn Tyr Val Gln Leu Phe Asp Thr Ile Glu Gln Asn Gly
          35           40           45
Leu Ala Leu Glu Met Thr Pro Tyr Phe Leu Ile Asn Val Ser Gly Glu
          50           55           60
Gly Glu Gly Phe Ser His Val Gly Ala Arg Gln Phe Val Met Phe Trp
65           70           75           80
Gln Arg Ile Gly Leu Glu Leu His Asp
          85

```

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

```

Leu Asp Ser Gln Thr Val Ser Ala Lys Gly Tyr His Phe Pro Leu Ser
 1           5           10           15
Glu Gly Thr Asp Leu Ala Ile Xaa Thr Ser Glu Gly Thr Thr Ser Gln
          20           25           30
Tyr Leu Lys Pro Asp Thr Ser Ser Tyr Phe Ser Lys Ser Ala Tyr Glu
          35           40           45
Lys Glu Met Arg Thr Ala Ala Asp Lys Tyr Leu Ser Gln Asp Ser Ile
          50           55           60
Gln Ile Thr Asn Glu Asn Tyr Met Gly Gly His Gly Gly Tyr Leu Arg
65           70           75           80
Leu Ser Gln Met Asn Leu Arg Val Lys Thr Ile Gln Phe Asn Arg Leu
          85           90           95
Cys Leu

```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```

Met Lys Lys Leu Val Phe Val Cys Leu Gly Asn Ile Cys Arg Thr Pro
 1               5               10               15
Met Ala Glu Phe Val Met Lys Ser Met Thr Asp Asn Tyr Glu Ile Gln
                20               25               30
Ser Arg Ala Thr Ser Ser Trp Glu His Gly Asn Pro Ile His Lys Gly
                35               40               45
Thr Gln Gly Ile Phe Gln Glu Tyr Glu Ile Pro Tyr Asp Lys Asn Lys
                50               55               60
Thr Ser Leu Gln Ile Ser Lys Glu Asp Phe Glu Ala Phe Asp Tyr Ile
                65               70               75               80
Ile Gly Met Asp Ala Ser Asn Val Ser Asp Leu Arg Gln Met Cys Pro
                85               90               95
Val His Cys Gln Asp Lys Ile Tyr Ser Phe Ser Ser Glu Ser Val Pro
                100              105              110
Glu Pro Trp Tyr Thr Gly Arg Phe
                115              120

```

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```

Met Lys Thr Thr Phe Ser Tyr Pro Lys Trp Ala Glu Ile Pro Asn Ile
 1               5               10               15

```

```

Asp Leu Tyr Leu Asp Gln Val Leu Leu Tyr Val Asn Gln Val Cys Ala
      20                      25                      30
Pro Ile Ser Pro Asn Lys Asp Lys Gly Leu Thr Ala Ser Met Val Asn
      35                      40                      45
Asn Tyr Val Lys Asn Gly Tyr Leu Thr Lys Pro Asp Lys Lys Lys Tyr
      50                      55                      60
Gln Arg Gln Gln Ile Ala Pro Phe Asp Cys Tyr His Asn Pro Gln Val
      65                      70                      75                      80
Leu Tyr Phe Pro Ile Pro Arg Lys
                        85

```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

```

Met Pro Thr Ala Phe Tyr Leu Phe Phe Ser Ser Met Tyr Gln Asp Thr
  1                      5                      10                      15
Pro Gly Gly Pro Ala Asn Phe Met Arg Asp Tyr Leu Ile Ser Met Thr
      20                      25                      30
Ala Phe Ser Met Met Ser Thr Ala Ile Phe Ser Phe Pro Val Val Leu
      35                      40                      45
His Thr Asp Lys Met Ser Asn Trp Gln Lys Thr Leu Arg His Ser Pro
      50                      55                      60
Val Asn Met Val Glu Tyr Tyr Leu Ser Lys Ile Thr Val Cys Trp Val
      65                      70                      75                      80
Asp Tyr Leu Val Phe His Ser Trp Trp Phe Phe Leu Ser Leu Gly Phe
      85                      90                      95
Leu Leu Glu Gly Val Gly Leu Val Leu
      100                      105

```

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

```

Met Ala Ser Pro Tyr Tyr Leu Asp Glu Glu Ala Leu Lys Tyr Ile Asp
 1             5             10             15
Tyr Asp Leu Asp Val Lys Ile Phe Thr Asp Gly Glu Lys Arg Leu Leu
      20             25             30
Asp Val Glu Glu Tyr Glu Arg His Lys Arg Lys Met Asn Tyr Ser Asp
      35             40             45
Asp Leu Asp Tyr Ile Leu Lys Glu His Val Lys Ile Leu Val Asp Trp
      50             55             60
Ile Asn Asn Gly Arg Gly Pro Phe Ser Glu Ala Tyr Val Asn Ile Trp
65             70             75             80
Tyr Lys Arg Tyr Val Glu Leu Lys Asn Arg
      85             90

```

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:
 - 5 (a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of selected from the group consisting of SEQ ID NO:263 through 552,
 - (b) a polynucleotide which is complementary to the polynucleotide of (a);
 - (c) a polynucleotide having at least a 70% identity to a polynucleotide encoding the
10 same mature polypeptide expressed by the a gene comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1 through 262 contained in the DNA of the deposited clone; and
 - (d) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).
- 15 2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
4. The polynucleotide of Claim 2 comprising the nucleic acid sequence set forth in SEQ ID NO:1 THROUGH 262.
5. The polynucleotide of Claim 2 comprising a nucleotide sequence selected from
20 the group consisting of SEQ ID NO:1 through 262.
6. The polynucleotide of Claim 2 which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:263 through 552.
7. A vector comprising the polynucleotide of Claim 1.
8. A host cell comprising the vector of Claim 7.
- 25 9. A process for producing a polypeptide comprising: expressing from the host cell of Claim 8 a polypeptide encoded by said DNA.
10. A process for producing a noval polypeptide or fragment comprising culturing a host of claim 8 under conditions sufficient for the production of said polypeptide or fragment.
- 30 11. A polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:263 through 552.
12. A polypeptide comprising an amino acid selected from the group consisting of SEQ ID NO:263 through 552.

13. An antibody against the polypeptide of claim 11.
14. An antagonist which inhibits the activity or expression of the polypeptide of claim 11.
15. A method for the treatment of an individual in need of a Streptococcal polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 11.
16. A method for the treatment of an individual having need to inhibit a bacterial polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.
17. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 11 in an individual comprising:
 - (a) determining a nucleic acid sequence encoding said polypeptide, and/or
 - (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.
18. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 11 comprising:
 - contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of providing a detectable signal in response to the interaction of the polypeptide with the compound;
 - and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.
19. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with Streptococcal polypeptide of claim 11, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.
20. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of Streptococcal polypeptide of claim 11, or fragment or a variant thereof, for expressing said Streptococcal polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/ or T cell immune response to protect said animal from disease.
22. An isolated nucleic acid encoding one of the amino acid sequences of

Claim 21 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.

23. Recombinant vectors comprising the nucleic acid sequences of Claim 22 and host cells transformed or transfected therewith.

5 24. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 21 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.

25. Antimicrobial compounds identified by the method of Claim 24.

10 26. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of SEQ ID NO: 389,

(b) a polynucleotide which is complementary to the polynucleotide of (a);

15 (c) a polynucleotide having at least a 70% identity to a polynucleotide encoding the same mature polypeptide expressed by the a gene comprising a polynucleotide sequence of SEQ ID NO: 389 contained in the DNA of the deposited clone; and

(d) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).

20 27. A polypeptide encoded by the polynucleotide of claim 26.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/07950

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/320.1, 183.1, 91.1, 91.4; 536/23.1, 23.5, 24.1; 530/300, 333, 350; 424/184.1, 244.1, 237.1, 234.1; 514/44

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	PAPE et al. Cloning and characterization of the gene for the yeast cytoplasmic threonyl-tRNA synthetase. Nucleic Acids Research. 1985, Vol. 13, No. 17, pages 6171-6183, see entire document.	1-12, 15
A	TATUSOV et al. Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coli. Current Biology. 1996, Vol. 6, No. 3, pages 279-291, see entire document.	1-12, 15
A	SHARP et al. Roles of selection and recombination in the evolution of type I restriction-modification systems in enterobacteria. Proc. Natl. Acad. Sci. USA. 1992, Vol. 89, pages 9836-9840, see entire document.	1-12, 15

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 21 AUGUST 1997	Date of mailing of the international search report 15 OCT 1997
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer NITA M. MINNIFIELD Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/07950

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 22-25
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

It is noted that there is no claim 21 and that claims 22-25 depend from claim 21.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
1-12, 15; Species 1-4

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/07950

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C07K 5/00, 14/00; C07H 21/04; C12N 15/63, 9/00; A61K 48/00, 39/00, 39/085, 39/09, 39/02; C12P 19/34

A. CLASSIFICATION OF SUBJECT MATTER: US CL :

435/320.1, 183.1, 91.1, 91.4; 536/23.1, 23.5, 24.1; 530/300, 333, 350; 424/184.1, 244.1, 237.1, 234.1; 514/44

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

maspar, medline, embase, biosis, biotechds, lifesci, confsci, caplus, japio, wpids, aps, dissabs

search terms: streptococcal polypeptide, inventor names, polynucleotide, DNA helicase, prolyl tRNA synthetase, proline tRNA ligase, alanyl tRNA synthetase, isopropylmalate dehydratase

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1.

Group I, claims 1-12 and 15, drawn to Streptococcal polypeptides, polynucleotide, vector, host cells.

Group II, claim 13, drawn to an antibody.

Group III, claim 14, drawn to an antagonist.

Group IV, claim 16, drawn to a method of using an antagonist.

Group V, claims 17 and 18, drawn to a process of diagnosis.

Group VI, claim 19, drawn to a method of inducing an immunological response in a mammal using a polypeptide.

Group VII, claim 20, drawn to a knighthood of inducing an immunological response in a mammal using a nucleic acid vector.

Group VIII, claims 26 and 27, drawn to a polynucleotide with specific sequences.

The inventions listed as Groups I-VIII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The special technical feature of Group I is considered to be Streptococcal polypeptides, polynucleotide sequences that encode the Streptococcal polypeptides, vectors and host cells.

The special technical feature of Group II is considered to be an antibody directed against the polypeptide.

The special technical feature of Group III is considered to be an antagonist.

The special technical feature of Group IV is considered to be a method of using an antagonist.

The special technical feature of Group V is considered to be a process of diagnosis of a disease.

The special technical feature of Group VI is considered to be a method of inducing an immunological response in a mammal using a polypeptide.

The special technical feature of Group VII is considered to be a to a method of inducing an immunological response in a mammal using a polypeptide.

The special technical feature of Group VIII is considered to be a to a polynucleotide with specific sequences.

Accordingly, Groups I-VIII are not so linked by the same or corresponding special technical feature as to form a single inventive concept.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

Species 1: SEQ ID No. 1-10

Species 2: SEQ ID No. 247, 279, 282, 283

Species 3: SEQ ID No. 310, 313, 339, 356

Species 4: SEQ ID No. 358, 368, 388, 418

Species 5-136: each species consists of 4 SEQ ID Nos. taken from the remaining 530 SEQ ID NOs.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/07950

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the reasons given above and the species are different structurally and/or functionally with regard to their site of action.